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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 3.97883 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1' GKICTAGVKCPAALPCCPGLRCLTGGVNNKVC 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: Geneseq1980s: \*  
2: Geneseq1990s: \*  
3: Geneseq2000s: \*  
4: Geneseq2001s: \*  
5: Geneseq2002s: \*  
6: Geneseq2003as: \*  
7: Geneseq2003bs: \*  
8: Geneseq2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	194	100.0	33	4	AAB66900	Insectici
2	194	100.0	33	6	AAB66283	Paeicilomy
3	194	100.0	34	6	AAB66261	Insectici
4	194	100.0	34	6	AAB66295	Insectici
5	194	100.0	34	6	AAB66260	Insectici
6	194	100.0	34	6	AAB66294	Insectici
7	194	100.0	34	6	AAB66259	Insectici
8	194	100.0	34	6	AAB66290	Insectici
9	194	100.0	34	6	AAB66292	Insectici
10	194	100.0	34	6	AAB66287	Insectici
11	194	100.0	34	6	AAB66289	Insectici
12	194	100.0	34	6	AAB66263	Insectici
13	194	100.0	34	6	AAB66284	Insectici
14	194	100.0	34	6	AAB66288	Insectici
15	194	100.0	34	6	AAB66296	Insectici
16	194	100.0	34	6	AAB66286	Insectici
17	194	100.0	34	6	AAB66291	Insectici
18	194	100.0	34	6	AAB66264	Insectici
19	194	100.0	34	6	AAB66285	Insectici
20	194	100.0	34	6	AAB66262	Insectici
21	194	100.0	34	6	AAB66297	Insectici
22	194	100.0	34	6	AAB66298	Insectici
23	194	100.0	34	6	AAB66293	Insectici
24	194	100.0	35	4	AAB66901	Insectici
25	194	100.0	35	6	AAB66281	Insectici

ALIGNMENTS

RESULT 1

AAB66900

ID AAB66900 standard; peptide; 33 AA.

XX

AC AAB66900;

XX

DT 12-APR-2001 (first entry)

XX

DE Insecticidal protein #2.

XX

KW Insecticide; transgenic plant; insect-resistance.

XX

OS Paecilomyces sp.

XX

PN WO200100841-A1.

XX

PD 04-JAN-2001.

XX

PF 23-JUN-2000; 2000WO-GB002457.

XX

PR 29-JUN-1999; 99GB-00015215.

PR

PR 23-DEC-1999; 99GB-00030536.

XX

(ZENE ) ZENECA LTD.

PA

Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

PI

Vincent JL, Lee MD;

XX

WPI; 2001-123015/13.

XX

Novel insecticidal protein obtained from species of Paecilomyces for

PT

controlling insects, and for insect-resistant transgenic plant

PT

production.

XX

Claim 3; Page 30; 72pp; English.

XX

The present invention relates to novel insecticidal proteins obtained

CC

from Paecilomyces sp. (see AAB6699 to AAB6691 and AAB66913). The

CC

insecticidal proteins can be used to produce transgenic plants, which are

CC

insect-resistant. Also, the insecticidal proteins are useful for

CC

controlling insects by providing them at a locus where insects feed

XX

Sequence 33 AA;

SQ

Query Match 100.0%; Score 194; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 9.6e-15;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
 PD |||||  
 Db 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33

RESULT 2  
 AAE36283  
 ID AAE36283 standard; peptide; 33 AA.  
 XX  
 AC AAE36283;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Paecilomyces farinosus insecticidal protein.  
 XX  
 KW Insecticidal protein; pesticide.  
 XX  
 OS Paecilomyces farinosus.

PN WO200298911-A2  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 PI Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Example 2; Page 62; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Paecilomyces farinosus insecticidal protein

Query Match 100.0%; Score 194; DB 6; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
 PD |||||  
 Db 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33

RESULT 3  
 AAE36261  
 ID AAE36261 standard; peptide; 34 AA.  
 XX  
 AC AAE36261;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Insecticidal protein #3.  
 XX  
 KW Insecticidal protein; pesticide.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200298911-A2.

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
 PD |||||  
 Db 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33

XX 12-DEC-2002.  
 PD |||||  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 PI Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX  
 PS Claim 6; Page 23; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

Query Match 100.0%; Score 194; DB 6; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
 PD |||||  
 Db 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 4  
 AAE36295  
 ID AAE36295 standard; peptide; 34 AA.  
 XX  
 AC AAE36295;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Insecticidal protein #25.  
 XX  
 KW Insecticidal protein; pesticide.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200298911-A2.  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 PI Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Example 1; Page 66; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the

CC invention are useful for producing plants or plant parts that are  
CC resistant to insects. The protein or synergistic combination is useful as  
CC an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify  
CC other proteins with insecticidal activity. The present sequence is  
CC insecticidal protein  
XX  
SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33  
|||  
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34  
|||

RESULT 5  
AAE36260  
ID AAE36260 standard; peptide; 34 AA.

AC AAE36260;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #2.

KW Insecticidal protein; pesticide.

OS Unidentified.

PN WO200298911-A2.

PD 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

PA (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;

DR WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Claim 5; Page 23; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33  
|||  
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34  
|||

RESULT 6  
AAE36294

ID AAE36294 standard; peptide; 34 AA.

AC AAE36294;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #24.

KW Insecticidal protein; pesticide.

OS Unidentified.

PN WO200298911-A2.

PD 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

PA (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;

DR WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Example 1; Page 66; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 33  
|||  
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCR 34  
|||

RESULT 7

AAE36259

ID AAE36259 standard; peptide; 34 AA.

AC AAE36259;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #1.

KW Insecticidal protein; pesticide.

OS Unidentified.

PN Key Location/Qualifiers

FT Misc-difference 1 /note= "Xaa = any amino acid"

PN WO200298911-A2.

PD 12-DEC-2002.

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PF 30-MAY-2002; 2002WO-GB002666.
XX
XX PR 07-JUN-2001; 2001GB-00013900.
XX
XX PA (SYGN ) SYNGENTA LTD.
XX
XX PI Vincent JL, Viner R;
XX
XX DR WPI; 2003-175137/17.
XX
XX PT New insecticidal protein comprising an X-glycine motif at the amino-
XX PT terminus, useful as an active ingredient of a pesticide.
XX
XX PS Claim 1; Page 23; 67pp; English.
XX
XX CC The invention relates to insecticidal protein comprising an X-glycine
XX CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
XX CC invention are useful for producing plants or plant parts that are
XX CC resistant to insects. The protein or synergistic combination is useful as
XX CC an active ingredient of a pesticide or for controlling insects.
XX CC Antibodies raised to the insecticidal proteins can be used to identify
XX CC other proteins with insecticidal activity. The present sequence is
XX CC insecticidal protein
XX
XX SQ Sequence 34 AA;
XX
XX Query Match 100.0%; Score 194; DB 6; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 9.9e-15;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
XX |||||
XX DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34
XX |||||
XX
XX RESULT 9
XX AAE36292
XX ID AAE36292 standard; peptide; 34 AA.
XX
XX AC AAE36292;
XX
XX DT 26-JUN-2003 (first entry)
XX
XX DE Insecticidal protein #22.
XX
XX KW Insecticidal protein; pesticide.
XX
XX OS Unidentified.
XX
XX PN WO200298911-A2.
XX
XX PD 12-DEC-2002.
XX
XX PF 30-MAY-2002; 2002WO-GB002666.
XX
XX PR 07-JUN-2001; 2001GB-00013900.
XX
XX PA (SYGN ) SYNGENTA LTD.
XX
XX PI Vincent JL, Viner R;
XX
XX DR WPI; 2003-175137/17.
XX
XX PT New insecticidal protein comprising an X-glycine motif at the amino-
XX PT terminus, useful as an active ingredient of a pesticide.
XX
XX PS Example 1; Page 65; 67pp; English.
XX
XX CC The invention relates to insecticidal protein comprising an X-glycine
XX CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
XX CC invention are useful for producing plants or plant parts that are
XX CC resistant to insects. The protein or synergistic combination is useful as
XX CC an active ingredient of a pesticide or for controlling insects.
XX CC Antibodies raised to the insecticidal proteins can be used to identify
XX CC other proteins with insecticidal activity. The present sequence is
XX CC insecticidal protein
XX
XX SQ Sequence 34 AA;
XX
XX Query Match 100.0%; Score 194; DB 6; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 9.9e-15;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
XX |||||
XX DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34
XX |||||
XX
XX RESULT 8
XX AAE36290
XX ID AAE36290 standard; peptide; 34 AA.
XX
XX AC AAE36290;
XX
XX DT 26-JUN-2003 (first entry)
XX
XX DE Insecticidal protein #20.
XX
XX KW Insecticidal protein; pesticide.
XX
XX OS Unidentified.
XX
XX PN WO200298911-A2.
XX
XX PD 12-DEC-2002.
XX
XX PF 30-MAY-2002; 2002WO-GB002666.
XX
XX PR 07-JUN-2001; 2001GB-00013900.
XX
XX PA (SYGN ) SYNGENTA LTD.
XX
XX PI Vincent JL, Viner R;
XX
XX DR WPI; 2003-175137/17.
XX
XX PT New insecticidal protein comprising an X-glycine motif at the amino-
XX PT terminus, useful as an active ingredient of a pesticide.
XX
XX PS Example 1; Page 64; 67pp; English.
XX
XX CC The invention relates to insecticidal protein comprising an X-glycine
XX CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
XX CC invention are useful for producing plants or plant parts that are
XX CC resistant to insects. The protein or synergistic combination is useful as
XX CC an active ingredient of a pesticide or for controlling insects.
XX
XX QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33
XX |||||
XX DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34
XX |||||
XX
XX RESULT 10
XX AAE36287
XX ID AAE36287 standard; peptide; 34 AA.
XX
XX AC AAE36287;

```

XX DT 26-JUN-2003 (first entry)  
XX DE Insecticidal protein #17.  
XX KW Insecticidal protein; pesticide.  
XX OS Unidentified.  
XX XX WO200298911-A2.  
XX PD 12-DEC-2002.  
XX PF 30-MAY-2002; 2002WO-GB002666.  
XX PR 07-JUN-2001; 2001GB-00013900.  
XX PA (SYGN ) SYNGENTA LTD.  
XX PI Vincent JL, Viner R;  
XX DR WPI; 2003-175137/17.  
XX XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX PS Example 1; Page 63; 67pp; English.  
XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein  
XX SQ Sequence 34 AA;  
Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 34  
RESULT 11  
AAE36289  
ID AAE36289 standard; peptide; 34 AA.  
AC AAE36289;  
XX 26-JUN-2003 (first entry)  
XX DE Insecticidal protein #19.  
XX KW Insecticidal protein; pesticide.  
XX OS Unidentified.  
XX XX WO200298911-A2.  
XX PD 12-DEC-2002.  
XX PF 30-MAY-2002; 2002WO-GB002666.  
XX PR 07-JUN-2001; 2001GB-00013900.  
XX PA (SYGN ) SYNGENTA LTD.  
XX PI Vincent JL, Viner R;  
XX DR WPI; 2003-175137/17.  
XX XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX PS Example 1; Page 63; 67pp; English.  
XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein  
XX SQ Sequence 34 AA;  
Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 34  
RESULT 11  
AAE36289  
ID AAE36289 standard; peptide; 34 AA.  
AC AAE36289;  
XX 26-JUN-2003 (first entry)  
XX DE Insecticidal protein #19.  
XX KW Insecticidal protein; pesticide.  
XX OS Unidentified.  
XX XX WO200298911-A2.  
XX PD 12-DEC-2002.  
XX PF 30-MAY-2002; 2002WO-GB002666.  
XX PR 07-JUN-2001; 2001GB-00013900.  
XX PA (SYGN ) SYNGENTA LTD.  
XX PI Vincent JL, Viner R;

XX WPI; 2003-175137/17.  
XX DR New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX PT Example 1; Page 64; 67pp; English.  
XX PS The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein  
XX SQ Sequence 34 AA;  
Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCR 34  
RESULT 12  
AAE36263  
ID AAE36263 standard; peptide; 34 AA.  
AC AAE36263;  
XX 26-JUN-2003 (first entry)  
XX DE Insecticidal protein #5.  
XX KW Insecticidal protein; pesticide.  
XX OS Unidentified.  
XX XX WO200298911-A2.  
XX PD 12-DEC-2002.  
XX PF 30-MAY-2002; 2002WO-GB002666.  
XX PR 07-JUN-2001; 2001GB-00013900.  
XX PA (SYGN ) SYNGENTA LTD.  
XX PI Vincent JL, Viner R;  
XX DR WPI; 2003-175137/17.  
XX XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX PS Claim 40; Page 35; 67pp; English.  
XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein  
XX SQ Sequence 34 AA;  
Query Match 100.0%; Score 194; DB 6; Length 34;

Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 13  
AAE36284  
ID AAE36284 standard; peptide; 34 AA.

AC AAE36284;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #14.

KW Insecticidal protein; pesticide.

OS Unidentified.

PN WO20029894-A2-

PD 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

PA (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;

DR WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Example 1; Page 62; 67pp; English.

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 14  
AAE36288  
ID AAE36288 standard; peptide; 34 AA.

AC AAE36288;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #18.

KW Insecticidal protein; pesticide.

OS Unidentified.

PN WO200298911-A2.

PD 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

PA (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;

DR WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Example 1; Page 64; 67pp; English.

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is insecticidal protein

SQ Sequence 34 AA;

Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33  
DB 2 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 34

RESULT 15  
AAE36296  
ID AAE36296 standard; peptide; 34 AA.

AC AAE36296;

DT 26-JUN-2003 (first entry)

DE Insecticidal protein #26.

KW Insecticidal protein; pesticide.

OS Unidentified.

PN WO200298911-A2.

PD 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

PA (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;

DR WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Example 1; Page 66; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine  
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
CC invention are useful for producing plants or plant parts that are  
CC resistant to insects. The protein or synergistic combination is useful as  
CC an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify  
CC other proteins with insecticidal activity. The present sequence is  
CC insecticidal protein  
XX  
SQ Sequence 34 AA;  
Query Match 100.0%; Score 194; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 9.9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCVCR 33  
DB 2 GKICTPAGVKCPAALPCCPGRLRCIGGVNNKVCVCR 34  
Search completed: October 28, 2004, 18:19:40  
Job time : 4.97883 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 0.88081 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GKICTPAGVKCPAALPCCGRLCIGGVNKKVCR 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	64	33.0	1064	2 A40136	fibropellin Ia - s
2	60	30.9	422	2 S48564	probable membrane
3	60	30.9	570	2 A48836	fibropellin C prec
4	58.5	30.2	34	2 A31043	mu-conotoxin GS -
5	58	29.9	37	2 E44007	aptotoxin III - tr
6	57.5	29.6	417	2 T08724	hypothetical prote
7	57	29.4	1221	2 T23472	hypothetical prote
8	56.5	29.1	585	2 S43572	C05B5.5 protein (c
9	56.5	29.1	585	2 E88571	protein C05B5.5 [i
10	56.5	29.1	1390	2 T30346	insulin receptor -
11	56	28.9	197	2 T10081	sperm mitochondria
12	56	28.9	238	2 T04166	thauromatin-like pro
13	56	28.9	2352	2 T30201	Notch homolog prot
14	56	28.9	2531	2 S18188	notch protein homo
15	56	28.9	2531	2 A46019	notch-1 protein -
16	55	28.4	132	2 H75335	hypothetical prote
17	54.5	28.1	218	2 T03287	osmotin protein ho
18	54.5	28.1	601	2 T22025	hypothetical prote
19	54.5	28.1	601	2 D89711	protein F40E10.4 [i
20	54.5	28.1	768	2 A87722	protein ZC123.1 [i
21	54.5	28.1	1207	1 EGHU	epidermal growth f
22	54.5	28.1	4543	1 A53102	alpha-2-macroglobu
23	54	27.8	73	2 H43019	platelet aggregati
24	54	27.8	74	2 S25773	testis-specific pr
25	54	27.8	269	2 T26957	hypothetical prote
26	54	27.8	283	2 E88597	protein Y47D3B.6 [i
27	54	27.8	2318	2 S45306	notch3 protein - h
28	54	27.8	2321	2 S78549	notch3 protein - h
29	53	27.3	375	2 A41428	CEF-10 protein pre

30	53	27.3	456	1 KXBC	protein C (activat
31	53	27.3	686	2 JC7569	Delta-4 protein -
32	53	27.3	2139	2 A35672	crumbs protein - f
33	53	27.3	2524	2 A35844	Xotch protein - Af
34	52.5	27.1	596	2 T26950	hypothetical prote
35	52.5	27.1	4544	1 S02392	alpha-2-macroglobu
36	52.5	27.1	4545	1 S25111	alpha-2-macroglobu
37	52	26.8	64	2 A25775	metallothionein A
38	52	26.8	71	2 G43019	platelet aggregati
39	52	26.8	134	2 AD0652	conserved hypotet
40	52	26.8	1203	2 A49175	Notch B protein -
41	52	26.8	1449	2 S47423	E2 glycoprotein pr
42	52	26.8	2437	2 S42612	transmembrane prot
43	51.5	26.5	233	2 S31829	pathogenesis-relat
44	51.5	26.5	238	2 S28001	osmotin-like prote
45	51.5	26.5	246	2 S30144	osmotin-like prote

## ALIGNMENTS

### RESULT 1

A40136

fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)

N;Alternate names: epidermal growth factor homolog precursor

N;Contains: alternatively spliced fibropellin Ib (EGFI)

C;Species: Strongylocentrotus purpuratus (purple urchin)

C;Date: 13-May-1992 #sequence revision 17-Sep-1997 #text\_change 09-Jul-2004

C;Accession: A40136; B40136; C40136; A29316; A43131

R;Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.

J. Mol. Evol. 29, 314-327, 1989

A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpur

A;Reference number: A40136; MUID:90112459; PMID:2514273

A;Accession: A40136

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-114 <DEL>

A;Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g567061

A;Accession: B40136

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>

A;Accession: C40136

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 'K',747-821,898-978 <DE3>

R;Hursh, D.A.; Andrews, M.E.; Raff, R.A.

Science 237, 1487-1490, 1987

A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.

A;Reference number: A29316; MUID:87319677; PMID:3498216

A;Accession: A29316

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 'S',280-481,786-1064 <HUR>

A;Cross-references: GB:M17421; NID:g161474; PIDN:AAA30050.1; PID:g552260

R;Hunt, L.T.; Barker, W.C.

FASEB J. 3, 1760-1764, 1989

A;Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.

A;Reference number: A43131; MUID:89196806; PMID:2784773

A;Contents: annotation

C;Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib).

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-1064/Product: fibropellin I #status predicted <FIB>

F;23-54/Domain: EGF homology <EG01>

F;57-175/Domain: C1r/C1s repeat homology <C1r>

F;180-211/Domain: EGF homology <EG02>

F;218-249/Domain: EGF homology <EG03>

F;256-287/Domain: EGF homology <EG04>

F;294-325/Domain: EGF homology <EG05>

F;332-363/Domain: EGF homology <EG06>

F;370-401/Domain: EGF homology <EG07>

F;408-439/Domain: EGF homology <EG08>

F;446-477/Domain: EGF homology <EG09>

```

A;Cross-references: UNIPROT:P49013; GB:L07045; NID:g310659; PID:g310660
A;Note: sequence extracted from NCBI backbone (NCBIN:132724, NCBI:P:132725)
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-570/Product: fibropellin C #status predicted <FIB>
F;19-54/Domain: EGF homology <EGL>
F;57-175/Domain: C1r/C1s repeat homology <C1R>
F;176-211/Domain: EGF homology <EG2>
F;214-249/Domain: EGF homology <EG3>
F;252-287/Domain: EGF homology <EG4>
F;290-325/Domain: EGF homology <EG5>
F;328-363/Domain: EGF homology <EG6>
F;366-401/Domain: EGF homology <EG7>
F;404-439/Domain: EGF homology <EG8>
F;442-570/Region: avidin-like
F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-276
fide bonds: #status predicted

Query Match          30.9%; Score 60; DB 2; Length 570;
Best Local Similarity 35.1%; Pred. No. 12;
Matches 13; Conservative 4; Mismatches 12; Indels 8; Gaps 2;

QY      4   CTPA--GVKCP-----AALPCGPGRLRCIGGVNNKVC 32
Db       240 CIPGFNGVNCENNINECASIPCUNGICVDGINQFAC 276
              ||| ||| |::|||::|||::|||
RESULT 4
A31043
mu-conotoxin GS - cone shell (Conus geographus)
C;Species: Conus geographus (geography cone)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: A31043
R;Yanagawa, Y.; Abe, T.; Satake, M.; Odani, S.; Suzuki, J.; Ishikawa, K.
Biochemistry 27, 6256-6262, 1988
A;Title: A novel sodium channel inhibitor from Conus geographus: purification, structure,
A;Reference number: A31043; MUID:89118210; PMID:2851318
A;Accession: A31043
A;Molecule type: protein
A;Residues: 1-34 <VAN>
A;Cross-references: UNIPROT:P15472
C;Superfamily: unassigned conotoxins
C;Keywords: carboxylglutamic acid; hydroxyproline; myotoxin; sodium channel inhibitor; ver
F;10,11/Modified site: 4-hydroxyproline (Pro) #status experimental
F;32/Modified site: gamma-carboxylglutamic acid (Glu) #status experimental
F;34/Modified site: amidated carboxyl end (Val) #status absent

Query Match          30.2%; Score 58.5; DB 2; Length 34;
Best Local Similarity 44.8%; Pred. No. 1.9;
Matches 13; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

QY      4   CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db       2   CSGRGSRCPP--QCQMGLRC-GRGNPKC 27
              ||| ||| |::|||::|||::|||
RESULT 5
E44007
aptotoxin III - trap-door spider (Aptostichus schlingeri)
N;Alternate names: insecticidal peptide Aps III
C;Species: Aptostichus schlingeri
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E44007
R;Skinner, W.S.; Dennis, P.A.; Li, J.P.; Quistad, G.B.
Toxicol 30, 1043-1050, 1992
A;Title: Identification of insecticidal peptides from venom of the trap-door spider, Aptoc
A;Reference number: A44007; MUID:93069259; PMID:1440641
A;Accession: E44007
A;Molecule type: protein
A;Residues: 1-37 <SKI>
A;Cross-references: UNIPROT:P49268; PID:NAB24051.1; PID:g259281
A;Note: sequence extracted from NCBI backbone (NCBI:P:119526)
C;Keywords: disulfide bond; toxin; venom

```



RESULT 11  
T10081  
sperm mitochondrial capsule selenoprotein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Jul-1999 #sequence\_revision 04-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: T10081; A37199  
R;Kleene, K.C.; Smith, J.; Bozorgzadeh, A.; Harris, M.; Hahn, L.; Karimpour, I.; Gerstel  
Dev. Biol. 137, 395-402, 1990  
A;Title: Sequence and developmental expression of the mRNA encoding the seleno-protein c  
A;Reference number: A37199; MUID:90152148; PMID:2303168  
A;Accession: T10081  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-6, 'X', 8-16, 'X', 18-33, 'X', 35-197 <KLE1>  
A;Cross-references: UNIPROT:P15265; EMBL:M29603; NID:gl99088; PIDN:AAA53045.1; PID:g5672  
A;Experimental source: strain CD-1  
A;Note: in Genbank entry MUSMCS, release 113.0, PIDN:AAA53045.1, the selenocysteine UGA  
A;Accession: A37199  
A;Molecule type: mRNA  
A;Residues: 55-197 <KLE2>  
A;Cross-references: GB:M29603; NID:gl99088  
A;Note: the authors translated the codon TGT for residue 112 as Pro  
C;Genetics:  
A;Gene: MCS  
A;Genome: nuclear  
C;Keywords: mitochondrion; selenocysteine; sperm  
F;7,17,34/Modified site: selenocysteine #status predicted  
Query Match 28.9%; Score 56; DB 2; Length 197;  
Best Local Similarity 45.0%; Pred. No. 15;  
Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 4 CTPAGVKCPAALPCCPGRLC 23  
DB 87 CCPKSPCCPPKSPCCPPKPC 106  
RESULT 12  
T04166  
thaumatin-like protein - rice  
C;Species: Oryza sativa (rice)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T04166  
R;Cole, K.C.; Velazhahan, R.; Anuratha, C.S.; Muthukrishnan, S.  
submitted to the EMBL Data Library, November 1996  
A;Description: Induction of thaumatin-like proteins (TLPs) in Rhizoctonia solani- infect  
A;Reference number: Z15250  
A;Accession: T04166  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-238 <COL>  
A;Cross-references: UNIPROT:O04364; EMBL:U77657; NID:g2062388; PIDN:AAB53368.1; PID:g206  
C;Superfamily: thaumatin I  
Query Match 28.9%; Score 56; DB 2; Length 238;  
Best Local Similarity 45.2%; Pred. No. 17;  
Matches 14; Conservative 2; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GKICTPAGVKCPAALPCCPG-LRCIGVNN 29  
DB 146 GAGCPKGGPCATAITPQCPSELRAPGCCNN 176  
RESULT 13  
T30201  
Notch homolog protein - sea squirt (Halocynthia roretzi)  
C;Species: Halocynthia roretzi  
C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 08-Sep-2002  
C;Accession: T30201  
R;Hori, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.  
Dev. Genes Evol. 207, 371-380, 1997  
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the ced

A;Reference number: Z20775  
A;Accession: T30201  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-2352 <HOR>  
A;Cross-references: EMBL:AB001327; NID:di204472; PID:di026501; PIDN:BAA25571.1  
C;Genetics:  
A;Gene: Notch  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
Query Match 28.9%; Score 56; DB 2; Length 2352;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;  
QY 4 CTP--AGVKCPAALPCCPGRLCIGVNNKVC 33  
DB 593 CTPGTYGHCDDTDINECDNPNMNGATCQNEVNNFVCQ 630  
RESULT 14  
S18188  
notch protein homolog - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 02-Aug-2002  
C;Accession: S18188  
R;Weinmaster, G.; Roberts, V.J.; Lemke, G.  
Development 113, 199-205, 1991  
A;Title: A homolog of Drosophila Notch expressed during mammalian development.  
A;Reference number: S18188; MUID:92111383; PMID:1764995  
A;Accession: S18188  
A;Molecule type: mRNA  
A;Residues: 1-2531 <WEI>  
A;Cross-references: EMBL:X57405; NID:g57634; PID:g57635  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F;1987-1018/Domain: EGF homology <EGF1>  
F;1025-1056/Domain: EGF homology <EGF>  
F;1233-1264/Domain: EGF homology <EGF2>  
F;1917-1949/Domain: ankyrin repeat homology <AN1>  
F;1950-1982/Domain: ankyrin repeat homology <AN2>  
F;1984-2016/Domain: ankyrin repeat homology <AN3>  
F;2017-2049/Domain: ankyrin repeat homology <AN4>  
F;2050-2082/Domain: ankyrin repeat homology <AN5>  
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Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;  
QY 4 CTP--AGVKCPAALPCCPGRLR-----CIGVNNKVC 33  
DB 245 CLPFGAGQCEENVDDCPGNCKNGGACVGVNTYNC 282  
RESULT 15  
A46019  
notch-1 protein - mouse  
N;Alternate names: notch protein  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2004  
C;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109  
R;Idel Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gridl  
Genomics 15, 259-264, 1993  
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of I  
A;Reference number: A46019; MUID:93194170; PMID:8449489  
A;Accession: A46019  
A;Status: not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-2531 <DEL>  
A;Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1; I  
A;Note: sequence extracted from NCBI backbone (NCBIP:127318)  
R;Franco dal Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; N  
submitted to the EMBL Data Library, April 1992  
A;Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggeste  
A;Reference number: S25144

A:Accession: S25144  
A:Molecule type: mRNA  
A:Residues: 1551-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <FRA>  
A:Cross-references: EMBL:Z11886  
R:Liardelli, M.; Lendahl, U.  
Exp. Cell Res. 204, 364-372, 1993  
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of  
A:Reference number: A49175; MUID:93178563; PMID:8440332  
A:Accession: C49175  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1161-1547 <LAR>  
A:Cross-references: EMBL:X68278; NID:G287987; PIDN:CAA48339.1; PID:G287988  
A:Experimental source: embryo  
A:Note: sequence extracted from NCBI backbone (NCBIP:126159)  
R:Kopan, R.; Weintraub, H.  
J. Cell Biol. 121, 631-641, 1993  
A:Title: Mouse notch: expression in hair follicles correlates with cell fate determination  
A:Reference number: A46438; MUID:93252998; PMID:8486742  
A:Accession: B46438  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054  
A:Experimental source: embryo  
A:Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)  
C:Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.  
C:Comment: This protein is one of the neurogenic proteins controlling the decision between  
C:Genetics:  
A:Gene: notch-1  
A:Map position: 2  
A:Note: proximal region of chromosome 2  
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology  
F:106-138/Domain: EGF homology <EGF1>  
F:144-175/Domain: EGF homology <EGF1>  
F:222-254/Domain: EGF homology <EGF2>  
F:261-292/Domain: EGF homology <EGF2>  
F:339-370/Domain: EGF homology <EGF3>  
F:416-449/Domain: EGF homology <EGF3>  
F:456-487/Domain: EGF homology <EGF4>  
F:494-525/Domain: EGF homology <EGF5>  
F:532-563/Domain: EGF homology <EGF6>  
F:607-638/Domain: EGF homology <EGF7>  
F:682-713/Domain: EGF homology <EGF8>  
F:757-788/Domain: EGF homology <EGF9>  
F:795-826/Domain: EGF homology <EGF10>  
F:873-904/Domain: EGF homology <EGF11>  
F:911-942/Domain: EGF homology <EGF12>  
F:949-980/Domain: EGF homology <EGF13>  
F:987-1018/Domain: EGF homology <EGF14>  
F:1025-1056/Domain: EGF homology <EGF15>  
F:1063-1094/Domain: EGF homology <EGF16>  
F:1149-1180/Domain: EGF homology <EGF17>  
F:1187-1218/Domain: EGF homology <EGF18>  
F:1233-1264/Domain: EGF homology <EGF19>  
F:1352-1383/Domain: EGF homology <EGF20>  
F:1391-1425/Domain: EGF homology <EGF21>  
F:1491-1521/Domain: ankyrin repeat homology <AN1>  
F:1521-1551/Domain: ankyrin repeat homology <AN2>  
F:1551-1581/Domain: ankyrin repeat homology <AN3>  
F:1581-1611/Domain: ankyrin repeat homology <AN4>  
F:1611-1641/Domain: ankyrin repeat homology <AN5>

Query Match 28.9%; Score 56; DB 2; Length 2531;  
Best Local Similarity 36.8%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 14; Indels 8; Gaps 2;  
QY 4 CTP--AGVKCPAALPCPGRLR-----CIGGVNKKVCR 33  
DB 245 CLFGAGQNCENVDGCGNCKNGGACVDGWTYNCR 282

Search completed: October 28, 2004, 18:31:45  
Job time : 2.88081 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 3.0145 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GKICTPAGVKCPALPCCPGLRCIGGVNNKVC 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 segs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	82	42.3	36	9	US-09-894-882-3
2	79	40.7	36	9	US-09-894-882-4
3	73	37.6	35	14	US-10-072-602B-571
4	73	37.6	82	14	US-10-072-602B-140
5	72.5	37.4	37	9	US-09-894-882-5
6	69.5	35.8	30	14	US-10-072-602B-570
7	69.5	35.8	77	14	US-10-072-602B-137
8	69	35.6	31	9	US-09-894-882-461
9	69	35.6	39	9	US-09-894-882-497
10	69	35.6	67	9	US-09-894-882-247
11	68	35.1	3501	14	US-10-123-155-37
12	68	35.1	3501	14	US-10-146-731-37
13	68	35.1	3501	14	US-10-140-472-37

14	68	35.1	3501	14	US-10-141-761-37	Sequence 37, Appl
15	68	35.1	3501	14	US-10-142-885-37	Sequence 37, Appl
16	68	35.1	3501	14	US-10-158-790-37	Sequence 37, Appl
17	68	35.1	3501	14	US-10-137-871-37	Sequence 37, Appl
18	68	35.1	3501	14	US-10-140-923-37	Sequence 37, Appl
19	68	35.1	3501	14	US-10-141-756-37	Sequence 37, Appl
20	68	35.1	3501	14	US-10-141-759-37	Sequence 37, Appl
21	68	35.1	3501	14	US-10-140-805-37	Sequence 37, Appl
22	68	35.1	3501	14	US-10-140-864-37	Sequence 37, Appl
23	68	35.1	3501	15	US-10-142-426-37	Sequence 37, Appl
24	67	34.5	32	9	US-09-894-882-470	Sequence 470, App
25	67	34.5	32	14	US-10-072-602B-581	Sequence 581, App
26	67	34.5	40	9	US-09-894-882-498	Sequence 498, App
27	67	34.5	68	9	US-09-894-882-274	Sequence 274, App
28	67	34.5	79	14	US-10-072-602B-255	Sequence 255, App
29	65	33.5	77	14	US-10-072-602B-191	Sequence 191, App
30	65	33.5	2292	14	US-10-184-644-493	Sequence 493, App
31	65	33.5	2292	14	US-10-184-634-493	Sequence 493, App
32	64.5	33.2	86	15	US-10-424-539-240605	Sequence 240605,
33	64	33.0	30	14	US-10-072-602B-576	Sequence 576, App
34	64	33.0	566	10	US-09-900-449A-6	Sequence 6, Appli
35	64	33.0	572	10	US-09-900-449A-7	Sequence 7, Appli
36	64	33.0	601	10	US-09-900-449A-5	Sequence 5, Appli
37	64	33.0	639	10	US-09-900-449A-4	Sequence 4, Appli
38	64	33.0	1064	14	US-10-173-461-5	Sequence 5, Appli
39	63	32.5	1971	14	US-10-123-155-139	Sequence 139, App
40	63	32.5	1971	14	US-10-146-731-139	Sequence 139, App
41	63	32.5	1971	14	US-10-140-472-139	Sequence 139, App
42	63	32.5	1971	14	US-10-141-761-139	Sequence 139, App
43	63	32.5	1971	14	US-10-142-885-139	Sequence 139, App
44	63	32.5	1971	14	US-10-158-790-139	Sequence 139, App
45	63	32.5	1971	14	US-10-137-871-139	Sequence 139, App

ALIGNMENTS

RESULT 1  
US-09-894-882-3  
; Sequence 3, Application US/09894882  
; Patent No. US20020102607A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren M.  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-3

Query Match 42.3%; Score 82; DB 9; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.022;  
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33  
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Db 2 ICTGADRPCAACCCPCCPCTSCQGPESGVVYCR 34  
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RESULT 2  
US-09-894-882-4  
; Sequence 4, Application US/09894882  
; Patent No. US20020102607A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.

TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-4

Query Match 40.7%; Score 79; DB 9; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.047;  
Matches 17; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33  
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Db 2 ICTGADRPCAACCCPCCPCTSCQGPPEPVGVSICR 34  
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RESULT 3  
US-10-072-602B-571  
; Sequence 571, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.

TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 571  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Conus lividus  
US-10-072-602B-571

Query Match 37.6%; Score 73; DB 14; Length 35;  
Best Local Similarity 43.3%; Pred. No. 0.22;  
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKVCR 33  
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Db 2 CGESGQGCYSVRPCCPGLICKGTGGGLCR 31  
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RESULT 4  
US-10-072-602B-140  
; Sequence 140, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.

TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 140  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Conus lividus  
US-10-072-602B-140

Query Match 37.6%; Score 73; DB 14; Length 82;  
Best Local Similarity 43.3%; Pred. No. 0.47;  
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKVCR 33  
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Db 49 CGESGQGCYSVRPCCPGLICKGTGGGLCR 78  
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RESULT 5  
US-09-894-882-5  
; Sequence 5, Application US/09894882  
; Patent No. US20020102607A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.

APPLICANT: McIntosh, J. Michael  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Watkins, Maren  
APPLICANT: Jones, Robert M.  
APPLICANT: Shen, Greg S.  
TITLE OF INVENTION: I-Superfamily Conotoxins  
FILE REFERENCE: 2314-238  
CURRENT APPLICATION NUMBER: US/09/894,882  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/243,410  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/246,581  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/247,714  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/264,256  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 506  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Hadronyche versuta  
US-09-894-882-5

Query Match 37.4%; Score 72.5; DB 9; Length 37;  
Best Local Similarity 46.9%; Pred. No. 0.27;  
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGLRCIGGVNN-KVCR 33  
DB 2 ICTGADRPCAACCCPCPGTSCKAESNGVSYCR 33

RESULT 6  
US-10-072-602B-570  
Sequence 570, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 538  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 570  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Conus lividus  
US-10-072-602B-570

Query Match 35.8%; Score 69.5; DB 14; Length 30;  
Best Local Similarity 44.8%; Pred. No. 0.48;  
Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;  
QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32

DB 2 CGHSGAGC-YTRPCCPGLHCSGGAGGLC 29  
RESULT 7  
US-10-072-602B-137  
Sequence 137, Application US/10072602B  
Publication No. US20030109670A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Watkins, Maren  
APPLICANT: Garrett, James E.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Grilley, Michelle  
APPLICANT: Schoenfeld, Robert M.  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Cone Snail Peptides  
FILE REFERENCE: 2314-249  
CURRENT APPLICATION NUMBER: US/10/072,602B  
CURRENT FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/267,408  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 638  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 137  
LENGTH: 77  
TYPE: PRT  
ORGANISM: Conus lividus  
US-10-072-602B-137

Query Match 35.8%; Score 69.5; DB 14; Length 77;  
Best Local Similarity 44.8%; Pred. No. 1.1;  
Matches 13; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNNKVC 32  
DB 49 CGHSGAGC-YTRPCCPGLHCSGGAGGLC 76

RESULT 8  
US-09-894-882-461  
Sequence 461, Application US/09894882  
Patent No. US20020102607A1  
GENERAL INFORMATION:  
APPLICANT: University of Utah Research Foundation  
APPLICANT: Cognetix, Inc.  
APPLICANT: Walker, Craig S.  
APPLICANT: Shetty, Reshma  
APPLICANT: Jimenez, Elsie C.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Watkins, Maren  
APPLICANT: Jones, Robert M.  
APPLICANT: Shen, Greg S.  
TITLE OF INVENTION: I-Superfamily Conotoxins  
FILE REFERENCE: 2314-238  
CURRENT APPLICATION NUMBER: US/09/894,882  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/243,410  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/246,581  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/247,714  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/264,256  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 506

us-10-019-823b-2.rapb

Fri Oct 29 15:06:22 2004

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

Query Match          35.6%; Score 69; DB 9; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.57;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; CURRENT APPLICATION NUMBER: US 09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 2000-11-08
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          35.6%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.7;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; CURRENT APPLICATION NUMBER: US 09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 2000-11-08
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          35.6%; Score 69; DB 9; Length 67;
Best Local Similarity 44.8%; Pred. No. 1.1;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db      29 CFPFGIYCTPYLPCCWGICC--GTCRNVC 55

RESULT 11
US-10-123-155-37
; Sequence 37, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-123-155-37

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

Query Match          35.6%; Score 69; DB 9; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.57;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; CURRENT APPLICATION NUMBER: US 09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 2000-11-08
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          35.6%; Score 69; DB 9; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.7;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db      1 CFPFGIYCTPYLPCCWGICC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; CURRENT APPLICATION NUMBER: US 09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 2000-11-08
; PRIOR FILING DATE: 2000-11-14
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match          35.6%; Score 69; DB 9; Length 67;
Best Local Similarity 44.8%; Pred. No. 1.1;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
Db      29 CFPFGIYCTPYLPCCWGICC--GTCRNVC 55

RESULT 11
US-10-123-155-37
; Sequence 37, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-123-155-37

```

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
DB 888 GACCAAAGTACCAAGCCTGTGCTGG 913

## RESULT 12

US-10-146-731-37

; Sequence 37, Application US/10146731

; Publication No. US20030129692A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C323

; CURRENT APPLICATION NUMBER: US/10/146,731

; CURRENT FILING DATE: 2002-05-15

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 37

; LENGTH: 3501

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 2762, 2778

; OTHER INFORMATION: unknown base

US-10-146-731-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
DB 888 GACCAAAGTACCAAGCCTGTGCTGG 913

## RESULT 13

US-10-140-472-37

; Sequence 37, Application US/10140472

; Publication No. US20030138888A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C168  
; CURRENT APPLICATION NUMBER: US/10/140,472  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37  
; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2762, 2778  
; OTHER INFORMATION: unknown base  
US-10-140-472-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGRLRCIGG 26  
DB 888 GACCAAAGTACCAAGCCTGTGCTGG 913

## RESULT 14

US-10-141-761-37

; Sequence 37, Application US/10141761

; Publication No. US20030148432A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C198

; CURRENT APPLICATION NUMBER: US/10/141,761

; CURRENT FILING DATE: 2002-05-08

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 37

; LENGTH: 3501

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 2762, 2778

; OTHER INFORMATION: unknown base

US-10-141-761-37

Query Match 35.1%; Score 68; DB 14; Length 3501;

Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGG 26  
Db 888 GACCAAGTACCCCAAGCCTGTGCTGG 913

RESULT 15

US-10-142-885-37  
; Sequence 37, Application US/10142885  
; Publication No. US20030157604A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C248  
; CURRENT APPLICATION NUMBER: US/10/142,885  
; CURRENT FILING DATE: 2002-05-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 37  
; LENGTH: 3501  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2762, 2778  
; OTHER INFORMATION: unknown base  
US-10-142-885-37

Query Match 35.1%; Score 68; DB 14; Length 3501;  
Best Local Similarity 46.2%; Pred. No. 50;  
Matches 12; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GKICTPAGVKCPAALPCCPGLRCIGG 26  
Db 888 GACCAAGTACCCCAAGCCTGTGCTGG 913

Search completed: October 28, 2004, 18:40:50  
Job time : 4.0145 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 4.51795 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-2  
Perfect score: 194  
Sequence: 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVCYR 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	42.3	36	1 TXJA_HADVE	P82227 hadronyche
2	79	40.7	36	1 TXJB_HADVE	P82226 hadronyche
3	73	37.6	72	2 QTVN1	Q9tvm1 conus livid
4	73	37.6	72	2 Q9UAA2	Q9uaa2 conus livid
5	73	37.6	72	2 Q9UAA4	Q9uaa4 conus livid
6	73	37.6	72	2 Q9UAA7	Q9uaa7 conus livid
7	73	37.6	72	2 Q9UAB0	Q9uab0 conus livid
8	73	37.6	72	2 Q9UAB1	Q9uab1 conus livid
9	72.5	37.4	37	1 TXJC_HADVE	P82228 hadronyche
10	72	37.1	72	2 Q9UAA3	Q9uaa3 conus livid
11	72	37.1	72	2 Q9UAA5	Q9uaa5 conus livid
12	72	37.1	2524	2 Q9GPA5	Q9gpa5 branchiosio
13	70.5	36.3	33	1 TXCS_PHONI	P84015 phonetria
14	69.5	35.8	3775	2 Q7PMF9	Q7pmf9 anopheles g
15	69	35.6	67	1 CKX CONVR	Q7vzs9 conus virgo
16	68	35.1	71	2 Q9UAA9	Q9uaa9 conus livid
17	66	34.0	71	2 Q9UAB3	Q9uab3 conus livid
18	65	33.5	71	2 Q9UW08	Q9tw08 conus livid
19	65	33.5	71	2 Q9UAA0	Q9uaa0 conus livid
20	65	33.5	71	2 Q9UAA1	Q9uaa1 conus livid
21	65	33.5	71	2 Q9UAA6	Q9uaa6 conus livid
22	65	33.5	71	2 Q9UAA8	Q9uaa8 conus livid
23	65	33.5	71	2 Q9UAB2	Q9uab2 conus livid
24	64.5	33.2	76	2 Q9BP93	Q9bp93 conus ventr
25	64	33.0	1064	1 FBPI STRPU	P10079 strongyloce
26	63	32.5	233	2 Q946Y8	Q946y8 hordeum vul
27	62.5	32.2	80	2 Q9BP85	Q9bp85 conus arena
28	62	32.0	77	2 Q7SWH6	Q7swh6 macrothel
29	62	32.0	77	2 BAD13402	Bad13402 macrothel
30	61.5	31.7	77	2 Q7SWH3	Q7swh3 macrothel
31	61.5	31.7	77	2 BAD13405	Bad13405 macrothel

ALIGNMENTS

RESULT 1

ID	TXJA_HADVE	STANDARD;	PRT;	36 AA.
AC	P82227;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Janus-atracotoxin-Hv1a (J-ActX-Hv1a).			
OS	Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).			
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;			
OC	Mygalomorphae; Hexathelidae; Hadronyche.			
OX	NCBI_TaxID=6904;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RX	MEDLINE=20343014; PubMed=10881200;			
RA	Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,			
RA	Nicholson G.M., Christie M.J., King G.F.;			
RT	"Discovery and characterization of a family of insecticidal			
RT	neurotoxins with a rare vicinal disulfide bridge.";			
RL	Nat. Struct. Biol. 7:505-513 (2000).			
CC	-!- FUNCTION: Insecticidal neurotoxin.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Expressed by the venom gland.			
DR	HSSP; P82228; 1DL0.			
KW	Direct protein sequencing; Neurotoxin; Toxin.			
FT	DISULFID 3 17 By similarity.			
FT	DISULFID 10 22 By similarity.			
FT	DISULFID 13 14 By similarity.			
FT	DISULFID 16 33 By similarity.			
SQ	SEQUENCE 36 AA; 3685 MW; D1598B2560BFE997 CRC64;			

Query Match 42.3%; Score 82; DB 1; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.0089;  
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

Qy 3 ICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33

Db 2 ICTGADRPCAACCCPCPGTSCQGPESGVVYCR 34

RESULT 2

ID	TXJB_HADVE	STANDARD;	PRT;	36 AA.
AC	P82226;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Janus-atracotoxin-Hv1b (J-ActX-Hv1b).			
OS	Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).			
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;			
OC	Mygalomorphae; Hexathelidae; Hadronyche.			

4

```

Q9UAA4
ID Q9UAA4 PRELIMINARY; PRT; 72 AA.
AC Q9UAA4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089955; AAD48210.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR NON_TER 1
FT SEQUENCE 72 AA; 7998 MW; B4DE7DDC87553B8D CRC64;
SQ

Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
: ||| | | | | | | | | | | | | |
Db 42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69

RESULT 6
Q9UAA7
ID Q9UAA7 PRELIMINARY; PRT; 72 AA.
AC Q9UAA7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089912; AAD48167.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR NON_TER 1
FT SEQUENCE 72 AA; 7970 MW; B7A0DDDC87533D8D CRC64;
SQ

Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
: ||| | | | | | | | | | | | | |
Db 42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69

Q9UAA7
ID Q9UAA7 PRELIMINARY; PRT; 72 AA.
AC Q9UAA7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089912; AAD48167.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR NON_TER 1
FT SEQUENCE 72 AA; 7970 MW; B7A0DDDC87533D8D CRC64;
SQ

Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
: ||| | | | | | | | | | | | | |
Db 42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69

```

```

RESULT 7
Q9UAB0
ID Q9UAB0 PRELIMINARY; PRT; 72 AA.
AC Q9UAB0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089905; AAD48161.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR NON_TER 1
FT SEQUENCE 72 AA; 8028 MW; B5720DDC87503E8D CRC64;
SQ

Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 2 KICTPAGVKCPAALPCCPGLRC--IGGV 27
: ||| | | | | | | | | | | | | |
Db 42 RTCSPAGEVCTSKSPCCTGFLCSHIGM 69

RESULT 8
Q9UAB1
ID Q9UAB1 PRELIMINARY; PRT; 72 AA.
AC Q9UAB1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Four-loop conotoxin LVVIA (Fragment).
OS Conus lividus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89426;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99289555; PubMed=10359796;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Molecular genetics of ecological diversification: duplication and
RL rapid evolution of toxin genes of the venomous gastropod Conus.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:6820-6823(1999).
DR EMBL; AF089904; AAD48160.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR NON_TER 1
FT SEQUENCE 72 AA; 7935 MW; 64C72DDC8755282F CRC64;
SQ

Query Match 37.6%; Score 73; DB 2; Length 72;
Best Local Similarity 46.4%; Pred. No. 0.2;
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

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QY 2 KICTAGVKCPAALPCCPGRLC--IGGV 27  
 TXJC HADVE STANDARD; PRT; 37 AA.  
 AC P82228;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Janus-atracotoxin-Hv1c (J-Actx-Hv1c).  
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).  
 OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Mygalomorphae; Hexathelidae; Hadronyche.  
 OC NCBI\_TaxID=6904;  
 RN [1]  
 RP SEQUENCE, FUNCTION, X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.  
 RC TISSUE=Venom;  
 RX MEDLINE=20343014; PubMed=10881200;  
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,  
 RA Nicholson G.M., Christie M.J., King G.F.;  
 RT "Discovery and characterization of a family of insecticidal  
 RT neurotoxins with a rare vicinal disulfide bridge."  
 RL Nat. Struct. Biol. 7:505-513(2000).  
 CC -!- FUNCTION: Insecticidal neurotoxin.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 DR PDB; 1DLO; NMR; A=1-37.  
 KN 3D-structure; Direct protein sequencing; Neurotoxin; Toxin.  
 FT DISULFID 3 17  
 FT DISULFID 10 22  
 FT DISULFID 13 14  
 FT DISULFID 16 32  
 FT TURN 6 7  
 FT STRAND 9 9  
 FT TURN 18 19  
 FT STRAND 20 24  
 FT TURN 26 27  
 FT STRAND 30 34  
 SQ SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;  
 Query Match 37.4%; Score 72.5; DB 1; Length 37;  
 Best Local Similarity 46.9%; Pred. No. 0.13;  
 Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
 QY 3 ICTAGVKCPAALPCCPGRLCIGGVNN-KVCR 33  
 TXJC HADVE STANDARD; PRT; 37 AA.  
 AC P82228;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Janus-atracotoxin-Hv1c (J-Actx-Hv1c).  
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).  
 OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Mygalomorphae; Hexathelidae; Hadronyche.  
 OC NCBI\_TaxID=6904;  
 RN [1]  
 RP SEQUENCE, FUNCTION, X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.  
 RC TISSUE=Venom;  
 RX MEDLINE=20343014; PubMed=10881200;  
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,  
 RA Nicholson G.M., Christie M.J., King G.F.;  
 RT "Discovery and characterization of a family of insecticidal  
 RT neurotoxins with a rare vicinal disulfide bridge."  
 RL Nat. Struct. Biol. 7:505-513(2000).  
 CC -!- FUNCTION: Insecticidal neurotoxin.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 DR PDB; 1DLO; NMR; A=1-37.  
 KN 3D-structure; Direct protein sequencing; Neurotoxin; Toxin.  
 FT DISULFID 3 17  
 FT DISULFID 10 22  
 FT DISULFID 13 14  
 FT DISULFID 16 32  
 FT TURN 6 7  
 FT STRAND 9 9  
 FT TURN 18 19  
 FT STRAND 20 24  
 FT TURN 26 27  
 FT STRAND 30 34  
 SQ SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;  
 Query Match 37.4%; Score 72.5; DB 1; Length 37;  
 Best Local Similarity 46.9%; Pred. No. 0.13;  
 Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
 QY 3 ICTAGVKCPAALPCCPGRLCIGGVNN-KVCR 33  
 TXJC HADVE STANDARD; PRT; 37 AA.  
 AC P82228;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Janus-atracotoxin-Hv1c (J-Actx-Hv1c).  
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).  
 OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Mygalomorphae; Hexathelidae; Hadronyche.  
 OC NCBI\_TaxID=6904;  
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 RP SEQUENCE, FUNCTION, X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.  
 RC TISSUE=Venom;  
 RX MEDLINE=20343014; PubMed=10881200;  
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,  
 RA Nicholson G.M., Christie M.J., King G.F.;  
 RT "Discovery and characterization of a family of insecticidal  
 RT neurotoxins with a rare vicinal disulfide bridge."  
 RL Nat. Struct. Biol. 7:505-513(2000).  
 CC -!- FUNCTION: Insecticidal neurotoxin.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 DR PDB; 1DLO; NMR; A=1-37.  
 KN 3D-structure; Direct protein sequencing; Neurotoxin; Toxin.  
 FT DISULFID 3 17  
 FT DISULFID 10 22  
 FT DISULFID 13 14  
 FT DISULFID 16 32  
 FT TURN 6 7  
 FT STRAND 9 9  
 FT TURN 18 19  
 FT STRAND 20 24  
 FT TURN 26 27  
 FT STRAND 30 34  
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 Query Match 37.4%; Score 72.5; DB 1; Length 37;  
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DR EMBL; AF089956; AAD48211.1; -  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR004214; Conotoxin.  
 DR Pfam; PF02950; Conotoxin; 1.  
 FT NON TER 1  
 SQ SEQUENCE 72 AA; 8014 MW; C2757DDC87553EDD CRC64;  
 Query Match 37.1%; Score 72; DB 2; Length 72;  
 Best Local Similarity 50.0%; Pred. No. 0.27;  
 Matches 13; Conservative 3; Mismatches 8; Indels 2; Gaps 1;  
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 TXJC HADVE STANDARD; PRT; 72 AA.  
 AC P82228;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Janus-atracotoxin-Hv1c (J-Actx-Hv1c).  
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).  
 OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Mygalomorphae; Hexathelidae; Hadronyche.  
 OC NCBI\_TaxID=6904;  
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 RC TISSUE=Venom;  
 RX MEDLINE=20343014; PubMed=10881200;  
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,  
 RA Nicholson G.M., Christie M.J., King G.F.;  
 RT "Discovery and characterization of a family of insecticidal  
 RT neurotoxins with a rare vicinal disulfide bridge."  
 RL Nat. Struct. Biol. 7:505-513(2000).  
 CC -!- FUNCTION: Insecticidal neurotoxin.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 DR PDB; 1DLO; NMR; A=1-37.  
 KN 3D-structure; Direct protein sequencing; Neurotoxin; Toxin.  
 FT DISULFID 3 17  
 FT DISULFID 10 22  
 FT DISULFID 13 14  
 FT DISULFID 16 32  
 FT TURN 6 7  
 FT STRAND 9 9  
 FT TURN 18 19  
 FT STRAND 20 24  
 FT TURN 26 27  
 FT STRAND 30 34  
 SQ SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;  
 Query Match 37.4%; Score 72.5; DB 1; Length 37;  
 Best Local Similarity 46.9%; Pred. No. 0.13;  
 Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
 QY 3 ICTAGVKCPAALPCCPGRLCIGGVNN-KVCR 33  
 TXJC HADVE STANDARD; PRT; 37 AA.  
 AC P82228;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Janus-atracotoxin-Hv1c (J-Actx-Hv1c).  
 OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax versutus).  
 OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Mygalomorphae; Hexathelidae; Hadronyche.  
 OC NCBI\_TaxID=6904;  
 RN [1]  
 RP SEQUENCE, FUNCTION, X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.  
 RC TISSUE=Venom;  
 RX MEDLINE=20343014; PubMed=10881200;  
 RA Wang X.-H., Connor M., Smith R., Maciejewski M.W., Howden M.E.H.,  
 RA Nicholson G.M., Christie M.J., King G.F.;  
 RT "Discovery and characterization of a family of insecticidal  
 RT neurotoxins with a rare vicinal disulfide bridge."  
 RL Nat. Struct. Biol. 7:505-513(2000).  
 CC -!- FUNCTION: Insecticidal neurotoxin.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 DR PDB; 1DLO; NMR; A=1-37.  
 KN 3D-structure; Direct protein sequencing; Neurotoxin; Toxin.  
 FT DISULFID 3 17  
 FT DISULFID 10 22  
 FT DISULFID 13 14  
 FT DISULFID 16 32  
 FT TURN 6 7  
 FT STRAND 9 9  
 FT TURN 18 19  
 FT STRAND 20 24  
 FT TURN 26 27  
 FT STRAND 30 34  
 SQ SEQUENCE 37 AA; 3768 MW; E4DDF046CC750FFC CRC64;  
 Query Match 37.4%; Score 72.5; DB 1; Length 37;  
 Best Local Similarity 46.9%; Pred. No. 0.13;  
 Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

RA Abi-Rached L., Pontarotti P., Lardelli M.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole larvae;  
 RA Lardelli M.T.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y12539; CAC19873.1; -;  
 DR HSP; P00740; IEDM.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0030154; P:cell differentiation; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; ASX\_hydroxyl\_S.  
 DR InterPro; IPR008985; ConA like lec\_gl.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR010660; NOD.  
 DR InterPro; IPR008000; Notch\_region.  
 DR Pfam; PF00023; Ank; 6.  
 DR Pfam; PF00008; EGF; 34.  
 DR Pfam; PF07645; EGF\_CA; 2.  
 DR Pfam; PF06816; NOD; 1.  
 DR Pfam; PF00066; Notch; 3.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR00010; EGFLOOD.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 6.  
 DR SMART; SM00179; EGF\_CA; 21.  
 DR SMART; SM00004; NL; 3.  
 DR PROSITE; PSS0088; ANK\_REPEAT; 4.  
 DR PROSITE; PSS0297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PSS0010; ASX\_HYDROXYL; 23.  
 DR PROSITE; PSS0190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PSS0022; EGF\_1; 34.  
 DR PROSITE; PSS1186; EGF\_2; 28.  
 DR PROSITE; PSS0026; EGF\_3; 36.  
 DR PROSITE; PSS0187; EGF\_CA; 22.  
 KW ANK repeat; EGF-like domain; Receptor.  
 SQ SEQUENCE 2524 AA; 270970 MW; C2CA57B306D23EC9 CRC64;

Query Match 37.1%; Score 72; DB 2; Length 2524;  
 Best Local Similarity 45.9%; Pred. No. 6.3;  
 Matches 17; Conservative 2; Mismatches 10; Indels 8; Gaps 2;

QY 4 CTPA--GVKCP-----AALPCCPGRLCIGGVNNKVC 32  
 DB 768 CLPGVGVNCDINTDECASNPQNGRCCLDGVNNYVC 804

RESULT 13  
 TXCS PHONI  
 ID TXCS PHONI \* STANDARD; PRT; 33 AA.  
 AC P84015;  
 DT 01-OCT-2004 (Rel. 45, Created)  
 DT 01-OCT-2004 (Rel. 45, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Venom protein PN10C5.  
 OS Phoneutria nigriventer (Brazilian armed spider).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.  
 OC NCBI\_TaxID=6918;  
 [1]  
 RN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS  
 RP SPECTROMETRY.  
 RC TISSUE=Venom;  
 RA Richards M., Pimenta A.M.C., Bemquerer M.P., Santoro M.M.,  
 RA Figueiredo S.G., Cordeiro M.N.;  
 RT "New peptide PN10C5 from venom of Brazilian armed spider Phoneutria

RT nigriventer has sequence similarities with snake disintegrins,  
 RT vasotocin-neurophysins and other spider toxins.";  
 RL Submitted (JUN-2004) to Swiss-Prot.  
 CC -!- FUNCTION: Non-toxic to mice.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -!- MASS SPECTROMETRY: MW=3672.7; METHOD=Electrospray; RANGE=1-33;  
 CC NOTE=Ref.1.  
 KW Direct protein sequencing.  
 SQ SEQUENCE 33 AA; 3679 MW; 77F1127D4785D6E1 CRC64;

Query Match 36.3%; Score 70.5; DB 1; Length 33;  
 Best Local Similarity 40.0%; Pred. No. 0.2;  
 Matches 12; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGRLCIGGVNNKVC 33  
 DB 3 CAQKGIC-KDHIHCTNLKCVREGSNERVC 31

RESULT 14  
 Q7PMF9  
 ID Q7PMF9 PRELIMINARY; PRT; 3775 AA.  
 AC Q7PMF9;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE ENSANGP0000011881 (Fragment).  
 GN Name=ENSANGG00000009392;  
 OS Anopheles gambiae str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
 OC NCBI\_TaxID=180454;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=PEST;  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAA01008980; EAA13897.2; -;  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR000152; ASX\_hydroxyl\_S.  
 DR InterPro; IPR000345; CytC\_heme\_BS.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00008; EGF; 3.  
 DR Pfam; PF07645; EGF\_CA; 16.  
 DR PROSITE; PSS0010; ASX\_HYDROXYL; 17.  
 DR PROSITE; PSS0190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PSS0615; C\_TYPE\_LECTIN\_1; UNKNOWN\_1.  
 DR PROSITE; PSS0022; EGF\_1; UNKNOWN\_1.  
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 DR PROSITE; PSS0026; EGF\_3; 25.  
 DR PROSITE; PSS1187; EGF\_CA; 16.  
 KW EGF-like domain.  
 FT NON\_TER 1 1  
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 SQ SEQUENCE 3775 AA; 396198 MW; 51C4106F6E9908F4 CRC64;

Query Match 35.8%; Score 69.5; DB 2; Length 3775;  
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 Matches 13; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 3 ICT-PAGVKCPAALPCCPGRLCIGGVNNKVC 32  
 DB 1353 VCTNPRQCQCGANMCCPPGVCVRGVNNLC 1383

RESULT 15

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CXK_CONVR
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DT  29-MAR-2004 (Rel. 43, Created)
DT  29-MAR-2004 (Rel. 43, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Kappa-conotoxin ViTx precursor.
GN  Name=ViTx;
OS  Conus virgo (Virgin cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=89427;
RN  [1]
SEQUENCE FROM N.A., SEQUENCE OF 27-53, SYNTHESIS OF 27-60, AND MASS
SPECTROMETRY.
RP  TISSUE=Venom, and Venom duct;
RC  TISSUE=Venom, and Venom duct;
RX  PubMed=12893060;
RA  Kaufenstein S., Huys I., Lanthanh H., Stocklin R., Sotto F., Menez A.,
RA  Tytgat J., Mebs D.;
RT  "A novel conotoxin inhibiting vertebrate voltage-sensitive potassium
RT  channels."
RL  Toxicol 42:43-52(2003).
RN  [2]
SEQUENCE FROM N.A.
RP  TISSUE=Venom duct;
RC  TISSUE=Venom duct;
RA  Kaufenstein S.;
RL  Thesis (2001), University of Darmstadt, Germany.
CC  -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC  potassium channels. This toxin inhibits the vertebrate potassium
CC  channels Kv1.1 and Kv1.3, but not Kv1.2. It has no effect on HERG-
CC  type channels, sodium hH1 channels and Kir-type channels (IRK1).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  -!- PTM: Contains four disulfide bonds.
CC  -!- MASS SPECTROMETRY: MW=3933.3; METHOD=Electrospray; RANGE=27-60;
CC  NOTE-Ref.1.
CC  -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC  family.
-----
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or send an email to license@isb-sib.ch).
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CC  EMBL; AJ560778; CAD90965.1; -.
KW  Direct protein sequencing; Signal; Toxin.
FT  SIGNAL 1 26
FT  CHAIN 27 60 Kappa-conotoxin ViTx.
FT  PROPEP 61 67
FT  CONFLICT 38 38 P -> S (in Ref. 1).
FT  CONFLICT 49 49 G -> S (in Ref. 1).
SQ  SEQUENCE 67 AA; 7599 MW; 46671D012446F62D CRC64;

Query Match 35.6%; Score 69; DB 1; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.57;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGRLRCIGGVNNKVC 32
DB 29 CFPFGIYCTPYLPCCWGICC--GTCRNV 55

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Search completed: October 28, 2004, 18:29:44  
Job time : 6.6608 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 1.02508 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-2

Perfect score: 194

Sequence: 1 GKICTPAGVKCPAALPCCPGLRCIGGVNNKVC 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	42.3	36	4	US-09-894-882-3
2	79	40.7	36	4	US-09-894-882-4
3	75	38.7	36	1	US-08-682-485A-7
4	75	38.7	36	2	US-08-933-314-7
5	75	38.7	37	1	US-08-682-485A-6
6	75	38.7	37	2	US-08-933-314-6
7	72.5	37.4	37	4	US-09-894-882-5
8	69	35.6	31	4	US-09-894-882-461
9	69	35.6	39	4	US-09-894-882-497
10	69	35.6	67	4	US-09-894-882-247
11	67	34.5	32	4	US-09-894-882-470
12	67	34.5	40	4	US-09-894-882-498
13	67	34.5	68	4	US-09-894-882-274
14	59	30.4	155	4	US-09-252-991A-28474
15	59	30.4	2471	1	US-08-185-432-16
16	59	30.4	2471	1	US-08-083-590A-19
17	59	30.4	2471	3	US-08-532-384-19
18	59	30.4	2471	4	US-08-899-232-1
19	59	30.4	2471	4	US-09-121-457-1
20	58.5	30.2	34	1	US-08-117-080-5
21	58.5	30.2	34	1	US-08-471-329-5
22	58.5	30.2	34	2	US-08-915-142-5
23	58.5	30.2	908	4	US-08-714-741-44
24	58	29.9	39	4	US-09-894-882-248
25	57.5	29.6	180	4	US-09-510-238A-286
26	57.5	29.6	281	4	US-09-252-991A-23962
27	57.5	29.6	420	4	US-09-907-794A-109

28	57.5	29.6	420	4	US-09-905-125A-109	Sequence 109, App
29	57.5	29.6	420	4	US-09-902-775A-109	Sequence 109, App
30	57.5	29.6	420	4	US-09-906-700-109	Sequence 109, App
31	57.5	29.6	420	4	US-10-140-002-290	Sequence 290, App
32	57.5	29.6	420	4	US-09-903-603A-109	Sequence 109, App
33	57	29.4	259	3	US-09-161-241-11	Sequence 11, Appl
34	57	29.4	493	4	US-09-252-991A-16925	Sequence 16925, A
35	56.5	29.1	30	4	US-09-894-882-474	Sequence 474, App
36	56.5	29.1	44	4	US-09-894-882-296	Sequence 296, App
37	56.5	29.1	44	4	US-09-894-882-502	Sequence 502, App
38	56.5	29.1	70	4	US-09-894-882-295	Sequence 295, App
39	56	28.9	642	3	US-08-872-855-10	Sequence 10, Appl
40	56	28.9	2732	4	US-09-086-436-30	Sequence 30, Appl
41	55.5	28.6	2211	3	US-09-738-884-1	Sequence 1, Appli
42	55.5	28.6	2211	4	US-10-096-961A-1	Sequence 1, Appli
43	54.5	28.1	30	4	US-09-894-882-471	Sequence 471, App
44	54.5	28.1	30	4	US-09-894-882-475	Sequence 475, App
45	54.5	28.1	44	4	US-09-894-882-278	Sequence 278, App

## ALIGNMENTS

RESULT 1  
US-09-894-882-3  
; Sequence 3, Application US/09894882  
; Patent No. 6767895  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Walker, Craig S.  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jimenez, Elsie C.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Watkins, Maren  
; APPLICANT: Jones, Robert M.  
; APPLICANT: Shen, Greg S.  
; TITLE OF INVENTION: I-Superfamily Conotoxins  
; FILE REFERENCE: 2314-238  
; CURRENT APPLICATION NUMBER: US/09/894,882  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 60/243,410  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/246,581  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: US 60/247,714  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 60/264,256  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Hadronyche versuta  
US-09-894-882-3

Query Match 42.3%; Score 82; DB 4; Length 36;  
Best Local Similarity 51.5%; Pred. No. 0.004;  
Matches 17; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGLRCIGGVNNKV--CR 33  
||| | | | | | | | | | | | | | | | | | | |  
Db 2 ICTGADRPCAACCCPCCPCTSCQGPESNGVVYCR 34

RESULT 2  
US-09-894-882-4  
; Sequence 4, Application US/09894882  
; Patent No. 6767895

APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Atrax formidabilis

US-08-682-485A-7

Query Match 38.7%; Score 75; DB 1; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.026;  
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

4 CTPAGVKCPAALPCCPGLCIGGVNKKV--CR 33  
||| |||||  
4 CTGADRPACACCPCPGTCKGPENGVS YCR 35

DB

RESULT 4  
US-08-933-314-7  
Sequence 7, Application US/08933314  
Patent No. 5959182  
GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET I  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
FUNNEL WEB (Atrax or Hadronyche Spiders)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,314  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.

```

; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
;
US-08-933-314-7

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```

Query Match      38.7%; Score 75; DB 2; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.026;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

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QY      4 CTGAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
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Db      4 CTGADRPCAACCCPCPGTCKGPEPNCVSYCR 35

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RESULT 5
US-08-682-485A-6
; Sequence 6, Application US/08682485A
; Patent No. 5763568
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PL0722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.
; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids

```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label= a
; OTHER INFORMATION: /note= "this site may be amidated without loss
; OTHER INFORMATION: of biological activity"
;
US-08-682-485A-6

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Query Match      38.7%; Score 75; DB 1; Length 37;
Best Local Similarity 50.0%; Pred. No. 0.027;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

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QY      4 CTGAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      4 CTGADRPCAACCCPCPGTCKGPEPNCVSYCR 35

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RESULT 6
US-08-933-314-6
; Sequence 6, Application US/08933314
; Patent No. 5959182
; GENERAL INFORMATION:
; APPLICANT: ATKINSON, RONALD K
; APPLICANT: HOWDEN, MERLIN E.H.
; APPLICANT: TYLER, MARGARET I
; APPLICANT: VONARX, EDWARD J
; TITLE OF INVENTION: Insecticidal Toxins Derived From
; TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zeneca, Inc.
; STREET: 1200 South 47th Street
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,314
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,485
; FILING DATE: 17-JULY-1996
; APPLICATION NUMBER: US/08/256,933
; FILING DATE: 27-JULY-1994
; APPLICATION NUMBER: WO 93/15108
; FILING DATE: 29-JAN-1993
; APPLICATION NUMBER: AU PL0722
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Shaw, Melissa A.
; REGISTRATION NUMBER: 38,301
; REFERENCE/DOCKET NUMBER: PPD 5099/D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-231-1542
; TELEFAX: 510-231-1112
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Atrax formidabilis
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 37
; OTHER INFORMATION: /label= a
; OTHER INFORMATION: /note= "this site may be amidated without loss
; OTHER INFORMATION: of biological activity"
US-08-933-314-6

Query Match 38.7%; Score 75; DB 2; Length 37;
Best Local Similarity 50.0%; Pred. No. 0.027;
Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKV--CR 33
||| ||| ||| ||| ||| ||| ||| |||
Db 4 CTGADRPCAACCCPCPGTSCKGPEPNGVSYCR 35

RESULT 7
US-09-894-882-5
; Sequence 5, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Hadronyche versuta
US-09-894-882-5

Query Match 37.4%; Score 72.5; DB 4; Length 37;
Best Local Similarity 46.9%; Pred. No. 0.053;
Matches 15; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 3 ICTPAGVKCPAALPCCPGLRCIGGVN--KVCR 33
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Db 2 ICTGADRPCAACCCPCPGTSCKAESNGVSYCR 33

RESULT 8
US-09-894-882-461
; Sequence 461, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
```

```
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 461
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-461

Query Match 35.6%; Score 69; DB 4; Length 31;
Best Local Similarity 44.8%; Pred. No. 0.12;
Matches 13; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 4 CTPAGVKCPAALPCCPGLRCIGGVNKKVC 32
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Db 1 CFPPGIYCTPLPCWGICC--GTCRNVC 27

RESULT 9
US-09-894-882-497
; Sequence 497, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 497
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; LENGTH: 39
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-497

Query Match      35.6%; Score 69; DB 4; Length 39;
Best Local Similarity 44.8%; Pred. No. 0.14;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLCGCVNNKVC 32
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Db      1 CFPFGIYCTPYLPCCGCGICC--GTCRNVC 27

RESULT 10
US-09-894-882-247
; Sequence 247, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      35.6%; Score 69; DB 4; Length 67;
Best Local Similarity 44.8%; Pred. No. 0.23;
Matches 13; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY      4 CTPAGVKCPAALPCCPGLCGCVNNKVC 32
      |||:|||||:|:|:|:|:|:|:|:|:|
Db      29 CFPFGIYCTPYLPCCGCGICC--GTCRNVC 55

RESULT 11
US-09-894-882-470
; Sequence 470, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren

; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Conus emaciatus
US-09-894-882-247

Query Match      34.5%; Score 67; DB 4; Length 32;
Best Local Similarity 50.0%; Pred. No. 0.2;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      4 CTPAGVKCPAALPCCPGLCG 25
      |||:|||||:|:|:|:|:|:|:|:|:|
Db      1 CFPGLTFCRSRYLPCCSGMCCSG 22

RESULT 12
US-09-894-882-498
; Sequence 498, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 498
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Conus virgo
US-09-894-882-498

Query Match      34.5%; Score 67; DB 4; Length 40;
Best Local Similarity 50.0%; Pred. No. 0.25;
Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
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QY 4 CTPAGVKCPAALPCCPGRLRCIG 25  
 Db 1 CFPGLTFCRSYLPCCSGMCCSG 22

RESULT 13

US-09-894-882-274  
 ; Sequence 274, Application US/09894882  
 ; Patent No. 6767895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Walker, Craig S.  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jimenez, Elsie C.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Jones, Robert M.  
 ; APPLICANT: Shen, Greg S.  
 ; TITLE OF INVENTION: I-Superfamily Conotoxins  
 ; FILE REFERENCE: 2314-238  
 ; CURRENT APPLICATION NUMBER: US/09/894,882  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 60/243,410  
 ; PRIOR FILING DATE: 2000-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/246,581  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/247,714  
 ; PRIOR FILING DATE: 2000-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/264,256  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 274  
 ; LENGTH: 68  
 ; TYPE: PRT  
 ; ORGANISM: Conus virgo  
 US-09-894-882-274

Query Match 34.5%; Score 67; DB 4; Length 68;  
 Best Local Similarity 50.0%; Pred. No. 0.41;  
 Matches 11; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CTPAGVKCPAALPCCPGRLRCIG 25  
 Db 29 CFPGLTFCRSYLPCCSGMCCSG 50

RESULT 14

US-09-252-991A-28474  
 ; Sequence 28474, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 28474  
 ; LENGTH: 155  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-28474

Query Match 30.4%; Score 59; DB 4; Length 155;  
 Best Local Similarity 52.6%; Pred. No. 7.4;  
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 TPAGVKCPAALPCCPGRLRC 23  
 Db 7 TPASPRRPSTAWCCPGRRRC 25

RESULT 15

US-08-185-432-16  
 ; Sequence 16, Application US/08185432  
 ; Patent No. 5750652  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Artavanis-Tsakonas, Spyridon  
 ; APPLICANT: Busseau, Isabelle  
 ; APPLICANT: Diederich, Robert J.  
 ; APPLICANT: Xu, Tian  
 ; APPLICANT: Matsuno, Kenji  
 ; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND  
 ; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/185,432  
 ; FILING DATE: 21-JAN-1994  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mirock, S. Leslie  
 ; REGISTRATION NUMBER: 18,872  
 ; REFERENCE/DOCKET NUMBER: 7326-006  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864/9741  
 ; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2471 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; US-08-185-432-16

Query Match 30.4%; Score 59; DB 1; Length 2471;  
 Best Local Similarity 36.8%; Pred. No. 94;  
 Matches 14; Conservative 4; Mismatches 12; Indels 8; Gaps 2;

QY 3 ICTPP-AGVKCP-----AALPCCPGRLRCIGVNNKVC 32  
 Db 669 VCSPGFTGQRGNIDIDECASNPCRKGATCINGVNGFRC 706

Search completed: October 28, 2004, 18:34:07  
 Job time : 3.02508 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.5697 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MKLKNQDKHQSPSSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3747	99.9	718	4	AAB66907 Insectici
2	3747	99.9	718	6	AAB66907 Insectici
3	3736.5	99.7	719	2	AAR08041 81 kD end
4	3732.5	99.6	719	4	AAR08041 81 kD end
5	3724.5	99.3	719	4	AAB66909 Insectici
6	3724.5	99.3	719	6	AAB66909 Insectici
7	3722.5	99.3	719	4	AAB66908 Insectici
8	3722.5	99.3	719	6	AAB66908 Insectici
9	3718.5	99.2	719	4	AAB66910 Insectici
10	3718.5	99.2	719	6	AAB66910 Insectici
11	3711.5	99.0	719	4	AAB66911 Insectici
12	3711.5	99.0	719	6	AAB66911 Insectici
13	3513.5	93.7	719	7	ADM74717 B. thurin
14	3482.5	92.9	719	6	AAB66912 Insectici
15	3482.5	92.9	719	6	AAB66912 Insectici
16	3439	91.7	710	4	AAR02041 B. thurin
17	3359.5	89.6	719	3	ABD07073 Bacillus
18	3358.5	89.6	719	2	AAW49089 Bacillus
19	3280.5	87.5	1217	4	AAU02092 Bacillus
20	2704.5	72.1	1208	4	AAU02093 Bacillus
21	2416.5	64.5	1230	8	ADK98484 B thuring
22	2416.5	64.5	1230	8	ADK98489 B thuring
23	2416.5	64.5	1230	8	ADK98481 B thuring
24	2416.5	64.5	1230	8	ADK98491 B thuring
25	2416.5	64.5	1230	8	ADK98487 B thuring

26	2415	64.4	1229	2	AAR54074
27	2415	64.4	1229	2	AAW35259
28	2415	64.4	1229	2	AAW17699
29	2415	64.4	1229	2	AAW87633
30	2415	64.4	1229	2	AAW87633
31	2415	64.4	1229	8	ADK98479
32	2319	61.9	488	2	AAW44322
33	2319	61.9	488	4	AAW19947
34	2249	60.0	1228	2	AAR50955
35	2244	59.9	1209	4	AAU02094
36	2235	59.6	1227	2	AAW31990
37	2165	57.7	1227	2	AAW44321
38	2165	57.7	1227	4	AAW19950
39	2156	57.5	1227	4	AAU02046
40	2141	57.1	1186	2	AAW16796
41	2121	56.6	1221	4	AAU00421
42	2107	56.2	1221	4	AAU00420
43	2085.5	55.6	1228	4	AAW84628
44	2085.5	55.6	1228	4	AAU02039
45	1902	50.7	643	2	AAW16797

ALIGNMENTS

RESULT 1  
AAB66907  
ID AAB66907 standard; protein; 718 AA.  
XX  
AC AAB66907;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryllal.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
(ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
PS Claim 14; Page 53-55; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB6699 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 718 AA;

Query Match 99.9% Score 3747; DB 4; Length 718;  
Best Local Similarity 100.0%; Pred. No. 9e-296;  
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

My people



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RESULT 3
ID AAR08041 standard; protein; 719 AA.
XX
AC AAR08041;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-FEB-1991 (first entry)
XX
DE 81 kD endotoxin deduced from DNA carried on pJH12.
XX
KW Crystal; insecticide; toxin; delta endotoxin.
XX
OS Bacillus thuringiensis; JHCC 4353 and 4835.
XX
PN WO9013651-A..
XX
PD 15-NOV-1990..
PF 09-MAY-1989; 89GB-00010624.
XX
PR 09-MAY-1989; 89GB-00010624.
XX
PA (ICIL) IMPERIAL CHEM IND PLC.
XX
PI Blenk RG, Ely S, Tailor RH, Tippet JM;
XX
DR WPI; 1990-361486/48.
DR N-PSDB; AAQ06636.
XX
PT Bacillus thuringiensis strains - used for producing an endotoxin for
PT protecting plants against insects, partic. Lepidoptera and Coleoptera.
XX
PS Claim 5; Fig. 5-10; 66pp; English.
XX
CC The sequence carried on pJH12 which was isolated from B. thurin- giensis
CC strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can
CC be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,
CC or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11
CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be
CC used in formulations for combatting Lepidoptera and Coleoptera pests.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 719 AA;
Query Match 99.7%; Score 3736.5; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 6.4e-295;
Matches 718; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPFVSASTI 60
Db 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKLGDALAYVHDSLESWGNRNTRARSVKSQYIALELMEVQKLPSFAVSG 180
Db 121 RNKALTDLKLGDALAYVHDSLESWGNRNTRARSVKSQYIALELMEVQKLPSFAVSG 180
QY 181 EEVPLLPYQAANLHLLLRDASIFGKWLSSSEISITFYNNQVERAGDYSYHCWKWYS 240
Db 181 EEVPLLPYQAANLHLLLRDASIFGKWLSSSEISITFYNNQVERAGDYSYHCWKWYS 240
QY 241 TGLNNLRGTNAGSWVRNQFRDMLVLDLVALFPSYDTQMYPIKTTAQLTREVTYDAI 300
Db 241 TGLNNLRGTNAGSWVRNQFRDMLVLDLVALFPSYDTQMYPIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360

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Db 301 GTVHPHPSFTSTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360
QY 361 GGHKLEFRTIGGTNLINISTOGSTNTSINPVTLPFTSRDVRYSLAGNLTLTQPVN-VPR 419
Db 361 GGHKLEFRTIGGTNLINISTOGSTNTSINPVTLPFTSRDVRYSLAGNLTLTQPVN-VPR 420
QY 420 VDFHWKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHLSHIGLIS 479
Db 421 VDFHWKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHLSHIGLIS 480
QY 480 ASHVZALVYSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN 539
Db 481 ASHVZALVYSWTHRSADRTNTEIPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDIILRTN 540
QY 540 TGTFGDIRVNINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNRGELDLYK 599
Db 541 TGTFGDIRVNINPPPAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATWNRGELDLYK 600
QY 600 TFXTVGFTTFPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 659
Db 601 TFXTVGFTTFPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM 719

RESULT 4
AAU02095
ID AAU02095 standard; protein; 719 AA.
XX
AC AAU02095;
XX
DT 07-SEP-2001 (first entry)
XX
DE Bacillus thuringiensis partial mutant CryIIa.
XX
KW Crystal protein; CryIIa; CrylBa; moth; butterfly; Colorado potato beetle;
KW mutant; mutein.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= Signal_peptide
FT Protein 20..719 /label= Mature_CryIIa
FT EP1099760-A1.
PN 16-MAY-2001.
XX
PD 09-NOV-1999; 99EP-00203723.
XX
PR 09-NOV-1999; 99EP-00203723.
XX
PA (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
XX
PI De Maagd RA, Bosch HJ;
XX
DR WPI; 2001-337141/36.
DR N-PSDB; AAS04855.
XX
PT New hybrid Bacillus thuringiensis hybrid toxins comprising structural
PT domains derived from at least 2 different crystal proteins, such as
PT CryIIa and CrylBa, and having insecticidal activity, useful for combating
PT insects.
XX
PS Example; Page 30-32; 43pp; English.
XX
CC The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA
CC encoding which was mutated to allow cloning of domain III or domains I

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CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
 CC of the invention, having structural domains I, II and III in this order  
 CC starting from the N-terminal derived from at least 2 different crystal  
 CC proteins, are useful for protecting plants against pest insects, e.g.  
 CC moths, butterflies and Colorado potato beetle or for combating insects  
 XX  
 SQ Sequence 719 AA;

Query Match 99.6%; Score 3732.5; DB 4; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 1.4e-294;  
 Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MRLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 Db 1 MRLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240

QY 241 TGLANLGRGTNAESWVRYNQFRRDWTMLVLDLVALFSPYDTQMPYPIKTTAQLTREYVTDI 300  
 Db 241 TGLANLGRGTNAESWVRYNQFRRDWTMLVLDLVALFSPYDTQMPYPIKTTAQLTREYVTDI 300

QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPFLDLFLEQVTTIYSLLSWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPFLDLFLEQVTTIYSLLSWSNTQYMNW 360

QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVR 419  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVR 419

QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 Db 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479

QY 480 ASHVKALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539  
 Db 480 ASHVKALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539

QY 540 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATNRGDELDYK 599  
 Db 540 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATNRGDELDYK 599

QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATNRGDELDYK 600  
 Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATNRGDELDYK 600

QY 600 TFXTVGFTTTPFLDQVSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 Db 600 TFXTVGFTTTPFLDQVSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659

QY 660 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 Db 660 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 5  
 AAB66909  
 ID AAB66909 standard; protein; 719 AA.  
 XX AC  
 XX AAB66909;  
 XX  
 DT 12-APR-2001 (first entry)  
 DE Insecticidal protein cryIIa3.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.  
 XX

OS Paecilomyces sp.  
 XX WO200100841-A1.  
 XX 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 XX 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 XX Griffen J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 XX Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 XX production.  
 XX Claim 14; Page 57-59; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 XX from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 XX insecticidal proteins can be used to produce transgenic plants, which are  
 XX insect-resistant. Also, the insecticidal proteins are useful for  
 XX controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;

Query Match 99.3%; Score 3724.5; DB 4; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 6.1e-294;  
 Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MRLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 Db 1 MRLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240

QY 241 TGLANLGRGTNAESWVRYNQFRRDWTMLVLDLVALFSPYDTQMPYPIKTTAQLTREYVTDI 300  
 Db 241 TGLANLGRGTNAESWVRYNQFRRDWTMLVLDLVALFSPYDTQMPYPIKTTAQLTREYVTDI 300

QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPFLDLFLEQVTTIYSLLSWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPFLDLFLEQVTTIYSLLSWSNTQYMNW 360

QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVR 419  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVR 419

QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 Db 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479

QY 480 ASHVKALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539  
 Db 480 ASHVKALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539

QY 540 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATNRGDELDYK 599  
 Db 540 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATNRGDELDYK 599

Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAFMNGBEDLDYK 600  
QY 600 TFXTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659  
Db 601 TFRVGVFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELFELFVVKYAKOLHIERNM 718  
Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELFELFVVKYAKOLHIERNM 719

RESULT 6  
AAE36273  
ID AAE36273 standard; protein; 719 AA.  
XX  
AC AAE36273;  
DT 26-JUN-2003 (first entry)  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
OS Bacillus thuringiensis.  
PN WO200298911-A2.  
PD 12-DEC-2002.  
PF 30-MAY-2002; 2002WO-GB002666.  
XX  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX Vincent JL, Viner R;  
XX WPI; 2003-175137/17.  
DR  
XX  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
PT  
XX  
PS Claim 12; Page 47-50; 67pp; English.  
XX  
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
CC  
XX  
SQ Sequence 719 AA;

Query Match 99.3%; Score 3724.5; DB 6; Length 719;  
Best Local Similarity 99.3%; Pred. No. 6.1e-294;  
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSNAKVDKSTDSLKNETDIELQININHEDECKMSEYENVEFVSASTI 60  
Db 1 MCLKNQDKHQSFSNAKVDKSTDSLKNETDIELQININHEDECKMSEYENVEFVSASTI 60  
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKLGDALAYVHDSLESWGNRNNTARSVVKSOYIALELMFVQKLPSPFAVSG 180  
Db 121 RNKALTDLKLGDALAYVHDSLESWGNRNNTARSVVKSOYIALELMFVQKLPSPFAVSG 180

QY 181 EEVPLLPYQAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKWYS 240  
Db 181 EEVPLLPYQAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKWYS 240  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTAQLTREVYTDAL 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTAQLTREVYTDAL 300  
QY 301 GTVHPHPSFTSTTWYNNNAPSFSIAEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWYNNNAPSFSIAEAAVVRNPHLLDLEQVTIYSLLSRWSTQYNNMW 360  
QY 361 GGHKLEFRTIGTGLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVN-VPR 419  
Db 361 GGHKLEFRTIGTGLNISTOGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFTQPVN-VPR 420  
QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLIS 479  
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTOLQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
QY 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
Db 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAFMNGBEDLDYK 599  
Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAFMNGBEDLDYK 600  
QY 600 TFXTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659  
Db 601 TFRVGVFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELFELFVVKYAKOLHIERNM 718  
Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELFELFVVKYAKOLHIERNM 719

RESULT 7  
AAB66908  
ID AAB66908 standard; protein; 719 AA.  
XX  
AC AAB66908;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa2.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX WO200100841-A1.  
PN  
XX 04-JAN-2001.  
XX  
XX 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.  
PT  
XX  
PS Claim 14; Page 55-57; 72pp; English.  
XX

CC The present invention relates to novel insecticidal proteins obtained  
 CC from *Paecilomyces* sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;

Query Match 99.3%; Score 3722.5; DB 4; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 8.9e-294;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVSASTI 60  
 Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDKGLDALAVYHDSLESWGNRNTRARSVVKSQVIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDKGLDALAVYHDSLESWGNRNTRARSVVKSQVIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
 QY 301 GTVHPHPSFTSTTYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLLNISTQSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVN-VPR 419  
 Db 361 GGHKLEFRITGGTLLNISTQSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVN-VPR 420  
 QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
 Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATNRRGEDLDYK 599  
 Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAATNRRGEDLDYK 600  
 QY 600 TFXTVGFTTTPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 Db 601 TFRVTGFTTTPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 8  
 AAE36272  
 ID AAE36272 standard; protein; 719 AA.  
 XX AC AAE36272;  
 XX AC AAE36272;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX

OS *Bacillus thuringiensis*.  
 XX WC200298911-A2.  
 XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PS Claim 12; Page 44-47; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is *Bacillus thuringiensis* insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.3%; Score 3722.5; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 8.9e-294;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVSASTI 60  
 Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDKGLDALAVYHDSLESWGNRNTRARSVVKSQVIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDKGLDALAVYHDSLESWGNRNTRARSVVKSQVIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
 QY 301 GTVHPHPSFTSTTYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLLNISTQSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVN-VPR 419  
 Db 361 GGHKLEFRITGGTLLNISTQSTNTSINPVTLPFTSRDVRYESLAGLNFLTQPVN-VPR 420  
 QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
 Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540

QY 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
 DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 QY 600 TFXTVGFTTFFSLDVOSTFTTICAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 DB 601 TFRVGVFTTFFSLDVOSTFTTICAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719

RESULT 9

AAE36274  
 ID AAE36274 standard; protein; 719 AA.

XX AAE36274;

AC AAE36274;

DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIa4.

DE Insecticide; transgenic plant; insect-resistance.

XX Insecticide; transgenic plant; insect-resistance.

OS Paecilomyces sp.

XX WO200100841-A1.

PN 04-JAN-2001.

PD 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

XX (ZENE) ZENECA LTD.

PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee MD;

PI WPI; 2001-123015/13.

DR Novel insecticidal protein obtained from species of Paecilomyces for

XX controlling insects, and for insect-resistant transgenic plant

PT production.

XX Claim 14; Page 60-62; 72pp; English.

PS The present invention relates to novel insecticidal proteins obtained

XX from Paecilomyces sp. (see AAB66901 and AAB66913). The

CC insecticidal proteins can be used to produce transgenic plants, which are

CC insect-resistant. Also, the insecticidal proteins are useful for

CC controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

SQ Query Match 99.2%; Score 3718.5; DB 4; Length 719;

XX Best Local Similarity 99.3%; Pred. No. 1.9e-293;

XX Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

XX 1 MLKNQDQKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDECLKXSEVENVEPVFVSASTI 60

DB 1 MLKNQDQKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDECLKXSEVENVEPVFVSASTI 60

QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFIILGELWPKGNQWEIIFMEHVVEEIIINQKISTYA 120

DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFIILGELWPKGNQWEIIFMEHVVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLALAVHDSLESWGNRNTRARSVKSOYIAELMFPVKLPSPFVSG 180

DB 121 RNKALTDLKGDLALAVHDSLESWGNRNTRARSVKSOYIAELMFPVKLPSPFVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYCHCVKWS 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYCHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDVTOMYPIKTAQLTREVYTDAL 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDVTOMYPIKTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTTWTWYNNAPSPSAIAAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMNW 360  
 DB 301 GTVHPHPSFTTWTWYNNAPSPSAIAAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419  
 DB 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 420  
 QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQOPNYESYSHRLSHIGLIS 479  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQOPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIIRRTN 539  
 DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIIRRTN 540  
 QY 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
 DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 QY 600 TFXTVGFTTFFSLDVOSTFTTICAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 DB 601 TFRVGVFTTFFSLDVOSTFTTICAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVYKAKQLHIERNM 719

RESULT 10

AAE36274  
 ID AAE36274 standard; protein; 719 AA.

XX AAE36274;

AC AAE36274;

DT 26-JUN-2003 (first entry)

XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.

DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

XX WO200298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN) SYNGENTA LTD.

XX Vincent JL, Viner R;

XX WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-

XX terminus, useful as an active ingredient of a pesticide.

XX Claim 12; Page 50-53; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine

XX motif at the amino-terminus. Polynucleotide or DNA constructs of the

XX invention are useful for producing plants or plant parts that are

CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify  
 CC other proteins with insecticidal activity. The present sequence is  
 CC *Bacillus thuringiensis* insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.2%; Score 3718.5; DB 6; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-293;  
 Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60  
 D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120  
 QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S Y H C V K W Y S 240  
 D b 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S Y H C V K W Y S 240  
 QY 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P S P S T T T W Y N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P S P S T T T W Y N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 QY 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419  
 D b 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419  
 QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479  
 D b 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479  
 QY 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 539  
 D b 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 539  
 QY 540 T G T F G D I R V N I N P P A Q R Y R I R Y A S T T D L O F H T S I N G K A I N Q N F S A T M N R G B D L D Y K 599  
 D b 540 T G T F G D I R V N I N P P A Q R Y R I R Y A S T T D L O F H T S I N G K A I N Q N F S A T M N R G B D L D Y K 599  
 QY 599 T F X T V G F T P F S L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E V D F E K A Q E K V 659  
 D b 599 T F X T V G F T P F S L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E V D F E K A Q E K V 659  
 QY 660 T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 718  
 D b 660 T A L F T S T N P R G L K T D V K Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q L H I E R N M 718

RESULT 11

AAB66911 ID AAB66911 standard; protein; 719 AA.

XX AC AAB66911;

XX DT 12-APR-2001 (first entry)

XX DE Insecticidal protein cryIIa5.

XX KW Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.  
 OS WO200100841-A1.  
 PN 04-JAN-2001.  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PT Claim 14; Page 62-64; 72pp; English.  
 PS The present invention relates to novel insecticidal proteins obtained  
 XX from Paecilomyces sp. (see AAB6699 to AAB6901 and AAB6913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ Query Match 99.0%; Score 3711.5; DB 4; Length 719;  
 Best Local Similarity 99.0%; Pred. No. 7e-293;  
 Matches 712; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60  
 D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120  
 QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S Y H C V K W Y S 240  
 D b 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S Y H C V K W Y S 240  
 QY 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P S P S T T T W Y N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P S P S T T T W Y N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 QY 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419  
 D b 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N - V P R 419  
 QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479  
 D b 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479  
 QY 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 539  
 D b 480 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 539

QY 540 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599  
 DB 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 600 TTXVGTTPPSLLDVQSTFTIGANFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQKV 659  
 DB 601 TRFTVGTTPPSFLDVQSTFTIGANFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQKV 660  
 QY 660 TALFTSNPRGLKTDVKDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYAKOLHIERNM 718  
 DB 661 TALFTSNPRGLKTDVKDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYANELHIERNM 719

RESULT 12  
 AAE36275  
 ID AAE36275 standard; protein; 719 AA.  
 XX  
 AC AAE36275;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO200298911-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN) SYNGENTA LTD.  
 XX  
 PI Vincent JL, Viner R;  
 XX  
 WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX  
 PS Claim 12; Page 53-56; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 SQ Sequence 719 AA;

Query Match 99.0%; Score 3711.5; DB 6; Length 719;  
 Best Local Similarity 99.0%; Pred. No. 7e-293;  
 Matches 712; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  
 QY 1 MLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCMKSEVENVEPVSASTI 60  
 DB 1 MLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCMKSEVENVEPVSASTI 60  
 QY 61 QTGIGIACKILGTGVFPAGQVASYLSYFILGELWPKGNQWEIEMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIACKILGTGVFPAGQVASYLSYFILGELWPKGNQWEIEMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGLDALAYHDSLSWVGNRNTRASVRSQYIAELMFVQKLPSPFAVSG 180  
 DB 121 RNKALTDLKLGLDALAYHDSLSWVGNRNTRASVRSQYIAELMFVQKLPSPFAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNRQVERAGDYSYHCVKWYS 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSISITFYNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFSDYDQMPYIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFSDYDQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPSPSTSTTYNNNAPSFAIAAIVRNPHLLDLEQVTIYSLLSWSNTQYMNW 360  
 DB 301 GTVHPSPSTSTTYNNNAPSFAIAAIVRNPHLLDLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEPRTIGGTINISTOGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTPQVNV-VP 419  
 DB 361 GGHKLEPRTIGGTINISTOGSTNTSINPVTLPFTSRDVYRTESLAGNLFLTPQVNVGPR 420  
 QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539  
 DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 540 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599  
 DB 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 600 TTXVGTTPPSLLDVQSTFTIGANFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQKV 659  
 DB 601 TRFTVGTTPPSFLDVQSTFTIGANFSSGNEVYIDRIEFPVVEVTEAEYDFEKAQKV 660  
 QY 660 TALFTSNPRGLKTDVKDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYAKOLHIERNM 718  
 DB 661 TALFTSNPRGLKTDVKDYHIDQVSNLVESLSDYFYLDEKRELFEIVKYANELHIERNM 719

RESULT 13  
 ADM74717  
 ID ADM74717 standard; protein; 719 AA.  
 XX  
 AC ADM74717;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE B. thuringiensis cryIIel SEQ ID NO:2.  
 XX  
 KW cryI; toxicity; lepidoptera; cryIaB; cryIa; coleoptera; diptera; cryIIel.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN CN1401772-A.  
 PD 12-MAR-2003.  
 PF 20-AUG-2001; 2001CN-00124163.  
 PR 20-AUG-2001; 2001CN-00124163.  
 PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
 PI Song F, Zhang J, Huang D;  
 XX WPI; 2003-442339/42.  
 DR N-PSDB; ADM74716.  
 XX  
 PT Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence with high-toxicity to lepidoptera pests, encoded protein, primer sequences and the shuttle vector pSXY422b, useful as a pesticide.  
 XX  
 PS Example 3; SEQ ID NO 2; 29pp; Chinese.

XX The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
 CC combination, expression vector, nucleotide sequence of the B  
 CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
 CC amino acid sequence of the protein encoded by it, cooperative use of the  
 CC cryI gene with the expression product of cryIaB or cryIaC, primer  
 CC sequences for expressing the genes, and the constructed shuttle vector  
 CC pSV422b. The gene in combination with the cryIaB or cryIaC genes  
 CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
 CC The present sequence represents the cryIaC protein.

XX  
 SQ Sequence 719 AA;

Query Match 93.7%; Score 3513.5; DB 7; Length 719;  
 Best Local Similarity 93.0%; Pred. No. 9.2e-277;  
 Matches 669; Conservative 26; Mismatches 23; Indels 1; Gaps 1;

QY 1 MRLKNDKQHSFSSNAKVDKISTDSLKNETDIELQNHEDCLMSEYENVEPVSASTI 60  
 DB 1 MRLKNDKQHSFSSNAKVDKISTDSLKNETDIELQNHEDCLMSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVAVSLYFSGILGELWPKGKQWEIEMFHEVBEIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVAVSLYFSGILGELWPKGKQWEIEMFHEVBEIINOKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTARSVVKQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTARSVVKQYIALELMFVQKLPFAVSG 180

QY 181 EVELLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSYHCVKWS 240  
 DB 181 EVELLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRVYQFRDNTLMVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
 DB 241 TGLNLRGTNAESWVRVYQFRDNTLMVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300

QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFEQVTIYSLSRWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFEQVTIYSLSRWSNTQYMNW 360

QY 361 GGHKLEFRFTIGTINISTQGSNTSINPVTLPFTSRDVRVYTESLAGNLFLOPVN-VPR 419  
 DB 361 GGHKLEFRFTIGTINISTQGSNTSINPVTLPFTSRDVRVYTESLAGNLFLOPVN-VPR 419

QY 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQLOQDSNELPPEATGQPNYESYSHRSLHIGLIS 479  
 DB 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQLOQDSNELPPEATGQPNYESYSHRSLHIGLIS 479

QY 480 ASHVKALVSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 539  
 DB 480 ASHVKALVSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 539

QY 540 TGTFGDIRVNIINPPFAQYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNGEDLDYK 599  
 DB 540 TGTFGDIRVNIINPPFAQYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNGEDLDYK 599

QY 600 TFXVTGFTTFFSLDDVQSTFTTGAMFSSNGNEVYIDRIEFVPEVTEYAEYDEKAQSKV 659  
 DB 600 TFXVTGFTTFFSLDDVQSTFTTGAMFSSNGNEVYIDRIEFVPEVTEYAEYDEKAQSKV 659

QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLDSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLDSDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 14  
 ID AAB66912 standard; protein; 719 AA.  
 XX  
 AC AAB66912;  
 XX  
 DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIb1.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.  
 XX  
 OS Paecilomyces sp.  
 XX  
 PN WO200100841-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-GB002457.  
 XX  
 PR 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX  
 DR WPI; 2001-123015/13.  
 XX  
 PT Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX  
 PS Claim 14; Page 64-66; 72pp; English.  
 XX  
 CC The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66912 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;

Query Match 92.9%; Score 3482.5; DB 4; Length 719;  
 Best Local Similarity 92.4%; Pred. No. 3.1e-274;  
 Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;

QY 1 MRLKNDKQHSFSSNAKVDKISTDSLKNETDIELQNHEDCLMSEYENVEPVSASTI 60  
 DB 1 MRLKNDKQHSFSSNAKVDKISTDSLKNETDIELQNHEDCLMSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVAVSLYFSGILGELWPKGKQWEIEMFHEVBEIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVAVSLYFSGILGELWPKGKQWEIEMFHEVBEIINOKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTARSVVKQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTARSVVKQYIALELMFVQKLPFAVSG 180

QY 181 EVELLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSYHCVKWS 240  
 DB 181 EVELLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRVYQFRDNTLMVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
 DB 241 TGLNLRGTNAESWVRVYQFRDNTLMVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300

QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFEQVTIYSLSRWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFEQVTIYSLSRWSNTQYMNW 360

QY 361 GGHKLEFRFTIGTINISTQGSNTSINPVTLPFTSRDVRVYTESLAGNLFLOPVN-VPR 419  
 DB 361 GGHKLEFRFTIGTINISTQGSNTSINPVTLPFTSRDVRVYTESLAGNLFLOPVN-VPR 419

QY 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQLOQDSNELPPEATGQPNYESYSHRSLHIGLIS 479  
 DB 420 VDFHWKFTVTHPIASDNFYYPGAGIGTQLOQDSNELPPEATGQPNYESYSHRSLHIGLIS 479

QY 480 ASHVKALVSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 539  
 DB 480 ASHVKALVSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 539

QY 540 TGTFGDIRVNIINPPFAQYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNGEDLDYK 599  
 DB 540 TGTFGDIRVNIINPPFAQYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNGEDLDYK 599

QY 600 TFXVTGFTTFFSLDDVQSTFTTGAMFSSNGNEVYIDRIEFVPEVTEYAEYDEKAQSKV 659  
 DB 600 TFXVTGFTTFFSLDDVQSTFTTGAMFSSNGNEVYIDRIEFVPEVTEYAEYDEKAQSKV 659

QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLDSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLDSDEFYLDKRELFEIVKYAKQLHIERNM 718

QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 540 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 599  
DB 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 600 TFXTVGTTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFEKAQEKV 659  
DB 601 TRTIGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFEKAQEKV 660  
QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 718  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 15  
AAE36276  
ID AAE36276 standard; protein; 719 AA.  
XX AAE36276;  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX  
OS Bacillus thuringiensis.  
PN W0200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-GB002666.  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX  
PI Vincent JL, Viner R;  
XX  
DR WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
PS Claim 12; Page 56-58; 67pp; English.  
XX  
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 719 AA;

Query Match 92.9%; Score 3482.5; DB 6; Length 719;  
Best Local Similarity 92.4%; Pred. No. 3.1e-274;  
Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;  
QY 1 MKLKNQDKHQSPSSNAKYDKISTDSLNKNETDIELQVINHEDCLKMSEYENVEPVSASTI 60  
DB 1 MKLKNPDQHQSLSSNAKYDKIATDSLNKNETDIELKNMNEEDYLRMSEHESIDPVSASTI 60  
QY 61 QTGTGIAGKILGTGVPAGQVASYLSYFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGTGIAGKILGTGVPAGQVASYLSYFILGELWPKGKQWEIFMEHVEEIIINOKILTYA 120

QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVKLPFAVSG 180  
DB 121 RNKALSDLRGLGDALAVYHDSLESWGNRNNTARSVVKQYIALELMFVKLPFAVSG 180  
QY 181 EEVPLLPYIAQAANLHLLLRDASIFCKEWGLSSSEISITFNNRQVERAGDYSYHCVKWYS 240  
DB 181 EEVPLLPYIAQAANLHLLLRDASIFCKEWGLSASEISITFNNRQVERTRDYSDHCIKWYN 240  
QY 241 TGLNNLRGTNAESWVRVYQFRDMDLMLVLDLVALFPSYDTOMYPIKTTAQLTREYVTDAL 300  
DB 241 TGLNNLRGTNAESWVRVYQFRDMDLMLVLDLVALFPSYDILVYPIKTTSQLTREYVTDAL 300  
QY 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360  
DB 301 GTVHPNQAFASTTWNNNAPSFAIEAAVIRSPHLLDLEKVTIYSLLSRWSNTQYMNW 360  
QY 361 GGHKLEFRTIGTILNISTGGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTPQVYV-VP 419  
DB 361 GGHLESREFIGGALNTSTGGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTPQVNGVPR 420  
QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
DB 421 VDFHWKFTPLPIASDNFYYPGYAGVGTQLODSENELPPEATTGQPNYESYSHRLSHIGLIS 480  
QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 540 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 599  
DB 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 600 TFXTVGTTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFEKAQEKV 659  
DB 601 TRTIGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFEKAQEKV 660  
QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 718  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Search completed: October 28, 2004, 18:19:45  
Job time : 91.5697 secs



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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.1643 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MCLKNQDKHQSFSSNAKVDK.....KRELFIVKYAKQLHIERNM 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3732.5	99.6	719	2 S25383	parasporal crystal
2	3724.5	99.3	719	2 I39814	insecticidal prote
3	3722.5	99.3	719	2 I39815	insecticidal prote
4	3482.5	92.9	719	2 I40590	crv465 protein -
5	2248	60.0	1228	2 S00873	parasporal crystal
6	1891	50.4	380	2 B42459	hypothetical prote
7	1480.5	39.5	1157	1 S49247	parasporal crystal
8	1462	39.0	1166	2 S32645	parasporal crystal
9	1455.5	38.8	1174	2 S32649	parasporal crystal
10	1448.5	38.6	1155	2 A26513	parasporal crystal
11	1441.5	38.5	1155	2 JD0002	parasporal crystal
12	1441.5	38.5	1156	2 A2125	parasporal crystal
13	1433	38.2	934	2 A22798	parasporal crystal
14	1432	38.2	1176	2 JT0241	parasporal crystal
15	1426	38.0	1176	2 JC2219	parasporal crystal
16	1424.5	38.0	1155	2 S02134	parasporal crystal
17	1424	38.0	1181	2 A41052	parasporal crystal
18	1422	37.9	1176	2 A22617	parasporal crystal
19	1422	37.9	1176	2 S02215	parasporal crystal
20	1420.5	37.9	1155	2 I39838	parasporal crystal
21	1354.5	36.1	1174	2 A42459	parasporal crystal
22	1340.5	35.8	1138	2 A48944	parasporal crystal
23	1319	35.2	1156	2 A29838	parasporal crystal
24	1310	34.9	823	2 S04181	parasporal crystal
25	1298	34.6	1189	2 S00944	parasporal crystal
26	1288.5	34.4	1154	2 S39536	parasporal crystal
27	1257.5	33.5	1171	2 I40572	parasporal crystal
28	1257.5	33.5	1171	2 A37829	parasporal crystal
29	1248.5	33.3	1176	2 A48970	parasporal crystal

30 1205.5 32.2 1160 2 S32647 parasporal crystal  
31 1197 31.9 1165 2 S11446 parasporal crystal  
32 1185 31.6 655 2 JC7140 protoxin - Bacillu  
33 1184.5 31.6 1172 2 S32689 parasporal crystal  
34 1179.5 31.5 1160 2 I40589 parasporal crystal  
35 1149.5 30.7 1177 2 A49785 parasporal crystal  
36 1146 30.6 1178 1 USBXKH parasporal crystal  
37 1136.5 30.3 652 2 A27323 parasporal crystal  
38 1114.5 29.7 659 2 S10228 parasporal crystal  
39 1082 28.9 652 2 I39811 parasporal crystal  
40 977.5 26.1 649 1 JH0261 parasporal crystal  
41 921.5 24.6 618 2 S11445 parasporal crystal  
42 875.5 23.4 1156 2 S19306 parasporal crystal  
43 818.5 21.8 1136 1 USB89I parasporal crystal  
44 686 18.3 934 2 B29838 parasporal crystal  
45 658.5 17.6 1180 2 I39870 parasporal crystal

ALIGNMENTS

RESULT 1

S25383

parasporal crystal protein cryllal - Bacillus thuringiensis

N;Alternate names: delta-endotoxin; parasporal crystal protein cryV

C;Species: Bacillus thuringiensis

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C;Accession: S25383

R;Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.

Mol. Microbiol. 6, 1211-1217, 1992

A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end

A;Reference number: S25383; MUID:92269582; PMID:1598820

A;Accession: S25383

A;Molecule type: DNA

A;Residues: 1-719 <TAI>

A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PIDN:CAA44633.1; PID:G40290

C;Genetics:

A;Gene: cryV

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 99.6%; Score 3732.5; DB 2; Length 719;  
Best Local Similarity 99.6%; Pred. No. 2.2e-250;  
Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy	1	MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIEQLONINHEDCLKMEYENVEPFVSA	60
Db	1	MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIEQLONINHEDCLKMEYENVEPFVSA	60
Qy	61	QTGIGIAGKILGTLCVPPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEINQKISTYA	120
Db	61	QTGIGIAGKILGTLCVPPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEINQKISTYA	120
Qy	121	RNKALTDLKGDLAVYHDSLESWGNRNTFARSVVKSQYIALELMFVQKLPFAVSG	180
Db	121	RNKALTDLKGDLAVYHDSLESWGNRNTFARSVVKSQYIALELMFVQKLPFAVSG	180
Qy	181	BEVPLLIPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS	240
Db	181	BEVPLLIPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS	240
Qy	241	TGLNLRGTNAESWVRYNQFRDRTLMDLVALFPSYDTQWYPIKTTAQLTREVTYDAI	300
Db	241	TGLNLRGTNAESWVRYNQFRDRTLMDLVALFPSYDTQWYPIKTTAQLTREVTYDAI	300
Qy	301	GTVHEHPSTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW	360
Db	301	GTVHEHPSTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW	360
Qy	361	GGHKLFRITGGTGLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNFLTQPVN-VPR	419
Db	361	GGHKLFRITGGTGLNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNFLTQPVN-VPR	420

QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLSHIGLIS 479  
 DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 QY 480 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 539  
 DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540  
 QY 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQPHSTINGKAINQGNFSAATNRGDDLDYK 599  
 DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQPHSTINGKAINQGNFSAATNRGDDLDYK 600  
 QY 600 TFXTVGFTTFFSLDVSQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 659  
 DB 601 TFRTVGFTTFFSLDVSQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2

I39814  
 insecticidal protein cryV1 - Bacillus thuringiensis  
 C;Species: Bacillus thuringiensis  
 C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
 C;Accession: I39814  
 R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
 Appl. Environ. Microbiol. 61, 2402-2407, 1995  
 A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
 tomoscidus.  
 A;Reference number: I39814; MUID:95314293; PMID:7793960  
 A;Accession: I39814  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-719 <RES>  
 A;Cross-references: GB:I36338; NID:G540281; PIDN:AAC36999.1; PID:G540282  
 C;Genetics:  
 A;Gene: cryV1  
 C;Superfamily: parasporal crystal protein

Query Match 99.3%; Score 3724.5; DB 2; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 7.8e-250;  
 Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 DB 1 MKLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLXGLGDALAVYHDSLSWGNRNTRARSVVKVQSYIALELMFYQKLPFAVSG 180  
 DB 121 RNKALTDLXGLGDALAVYHDSLSWGNRNTRARSVVKVQSYIALELMFYQKLPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFNNQVERAGDYSYHCVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFNNQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQYPIKTTAQLTREYVTDAL 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQYPIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVN-VPR 419  
 DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVN-VPR 420

QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLSHIGLIS 479  
 DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 QY 480 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 539  
 DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540  
 QY 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQPHSTINGKAINQGNFSAATNRGDDLDYK 599  
 DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQPHSTINGKAINQGNFSAATNRGDDLDYK 600  
 QY 600 TFXTVGFTTFFSLDVSQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 659  
 DB 601 TFRTVGFTTFFSLDVSQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3

I39815  
 insecticidal protein cryV - Bacillus thuringiensis  
 C;Species: Bacillus thuringiensis  
 C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I39815  
 R;Gleave, A.P.; Williams, R.; Hedges, R.J.  
 Appl. Environ. Microbiol. 59, 1683-1687, 1993  
 A;Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for t  
 iensis subsp. kurstaki.  
 A;Reference number: I39815; MUID:93298009; PMID:8517758  
 A;Accession: I39815  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-719 <RES>  
 A;Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PIDN:AAA22354.1; PID:G142768  
 C;Genetics:  
 A;Gene: cryV  
 C;Superfamily: parasporal crystal protein

Query Match 99.3%; Score 3722.5; DB 2; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.1e-249;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 DB 1 MKLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLXGLGDALAVYHDSLSWGNRNTRARSVVKVQSYIALELMFYQKLPFAVSG 180  
 DB 121 RNKALTDLXGLGDALAVYHDSLSWGNRNTRARSVVKVQSYIALELMFYQKLPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFNNQVERAGDYSYHCVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFNNQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQYPIKTTAQLTREYVTDAL 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQYPIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVN-VPR 419  
 DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVN-VPR 420

QY 420 VDFHMKFVTHPIASDNFYYPGYAGICTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGICTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
 DB 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599  
 DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 600 TFXTVGFTTFFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 DB 601 TFXTVGFTTFFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLDSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLDSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4  
 I40590  
 cryV465 protein - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: I40590  
 R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
 Appl. Environ. Microbiol. 61, 2402-2407, 1995  
 A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
 tomocidus.  
 A:Reference number: I39814; MUID:95314293; PMID:7793960  
 A:Accession: I40590  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-719 <RES>  
 A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:9467234; PIDN:AAA82114.1; PID:94672  
 C:Genetics:  
 A:Gene: cryV465  
 C:Superfamily: parasporal crystal protein

Query Match 92.9%; Score 3482.5; DB 2; Length 719;  
 Best Local Similarity 92.4%; Pred. No. 4.5e-233;  
 Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSPSSNAKVDKISTDSLNKNETDIELQNHEDCLMKSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSPSSNAKVDKISTDSLNKNETDIELQNHEDCLMKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVPAGQVASYLGFILGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPAGQVASYLGFILGELWPKGKNQWEIFMEHVEEIIINOKILTYA 120  
 QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALSDRLGLDALAVYHDSLESWGNRNNTARSVVKQYIALELMFVQKLPFAVSG 180  
 QY 181 EEPVLLPIYAQAANHLHLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANHLHLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
 DB 241 TGLNLRGTNAESWVRNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYMNW 360  
 DB 301 GTVHPNQAFSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYMNW 360  
 QY 361 GGHLKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRYESLAGNLF--LTQPVN--VPR 419  
 DB 361 GGHLKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRYESLAGNLF--LTQPVN--VPR 420

QY 420 VDFHMKFVTHPIASDNFYYPGYAGICTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGICTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
 DB 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599  
 DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 600 TFXTVGFTTFFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659  
 DB 601 TFXTVGFTTFFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLDSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLDSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5  
 S00873  
 parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
 N:Alternate names: parasporal crystal protein cryA4  
 C:Species: Bacillus thuringiensis subsp. thuringiensis  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C:Accession: S00873  
 R:Brizzard, B.L.; Whiteley, H.R.  
 Nucleic Acids Res. 16, 2723-2724, 1988  
 A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
 A:Reference number: S00873; MUID:88203216; PMID:3362680  
 A:Accession: S00873  
 A:Molecule type: DNA  
 A:Residues: 1-1228 <BRI>  
 A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:940264; PIDN:CAA29898.1; PID:958094;  
 C:Genetics:  
 A:Gene: cryA4  
 A:Start codon: TTG  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 60.0%; Score 2248; DB 2; Length 1228;  
 Best Local Similarity 62.3%; Pred. No. 3.2e-147;  
 Matches 446; Conservative 80; Mismatches 154; Indels 26; Gaps 7;

QY 23 TDSLKNETDIELQNH-----EDCLMKSEYENVEPVSASTIQTGIGIAGKI 70  
 DB 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVASTVQTGINIAGRI 61  
 QY 71 LGTLGVPPAGQVASYLGFILGELWPKGKNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130  
 DB 62 LGVLGVPPAGQVASYLGFILGELWPKGKNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 121  
 QY 131 LGDALAVYHDSLESWGNRNNTARSVVKQYIALELMFVQKLPFAVSGEVPPLPIYA 190  
 DB 122 LGDSFRAYQQSLEDWLENRDDARTSVLYTQYIALELDLFLNAMPLEFAIRNQEVPLLMVYA 181  
 QY 191 QAANHLHLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWSYSGTGLNLRGTN 250  
 DB 182 QAANHLHLLRDASIFGSEFGLTSQEIQYRYERQVTRDYSYCVWEWYNTGLNSLRGTN 241  
 QY 251 AESWRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREVYTDALGTVHPHPSFT 310  
 DB 242 AASWRYNQFRDMLMVLVALFPSYDTQMPYIKTTAQLTREVYTDALGTVHPHPSFT 299  
 QY 311 STTWNNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYMNWGHKLEFRIT 370  
 DB 300 SMNWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYMNWGHKLEFRIT 359  
 QY 371 GGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLF--LTQPVN--VPRVDFHMKFV 427  
 DB 360 GGGLNTSTHGTATNTSINPVTLPFTSRDVRYESLAGNLF--LTQPVN--VPRVDFHMKFV 416



Db 722 AAKLSRERNL 732

RESULT 8

S32645  
parasporal crystal protein cryIgal - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S32645  
R;Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A;Reference number: S32645  
A;Accession: S32645  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1166 <LAM>  
A;Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:G295861; PIDN:CAA80233.1; PID:G2958  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 39.0%; Score 1462; DB 2; Length 1166;  
Best Local Similarity 45.7%; Pred. No. 7.9e-93;  
Matches 322; Conservative 101; Mismatches 207; Indels 74; Gaps 17;

QY	41	DCLKMEYE----	NVEPVSASTIQIGIGIAGKILGTGVPPAGQVASYSLFELGELWPK	96
Db	13	NCLNPESEIFNARNSNFGLVQVSSGL---	TRFLEAAVPEAGPALGFLDIWGA---	66
QY	97	GKQWEIPMEHVEEII	NQKISTYARKKALTDKLGCDALAVYHDSLESWGNRRARS	156
Db	67	GVDQWSFLRQLEQLIQEITELERNEATALTGLSSSYNLYVEALREWDNDPNNPAQOE	126	
QY	157	VKXSYIALELMFVQKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKWLSSSE	216	
Db	127	RVTFRFLTDALVTGLPTLAIRNLEVNLVSVYTOAANLHLSLLRDADVFGERRGLTQAN	186	
QY	217	ISTFYNRQVERAGDYSYHCVKMYSTGLNNLRGTNAESWRYNQFRDRMTLWLDLVALFP	276	
Db	187	IEDLYTRLTNSIQEYSDHCARWYNOGLNEIGGISR----	RYLDFQRLDTISVLIDIVALFP	242
QY	277	SYDTQMYPIKTTAQLTREYVTDAL--	GTVHPHSFTSTTWYNNNAPSFAIAEAAVVRPH	334
Db	243	NYDRTYPTIPTQSLTREIYTSFVAVAGNI-----	NFGLSIANVLRAPI	285
QY	335	LLDFLEQVITYLLSRVSNQYMMWGGHKLFRITG-GLTN-----	ISTQGSTNTS	385
Db	286	LMDFDIRIVYITNSVR--STPY--	WAGHEVISRRTGQGGNEIRPPLYGVAANAEPVPT	340
QY	386	INPVTLPFTSRDVRYES-----	LAGLNLFQTQPNVPRVDFHMKFVTHPIASDNFYYP	439
Db	341	IRTGFTDEQRYRARSRVVSFRSSGQDFSLVDVG-----	FLT-IFSAVSIYRN	390
QY	440	GYAGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLISAS-----	HVKALVYSWTHRS	494
Db	391	GF-GFNT---DTIDEIPIEGTDP--	FTGYSHRLCHVGFLLASSPFIQYARAPIFSWTHRS	444
QY	495	ADRTNTIPENSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGTGFDIRVNIINPPF	554	
Db	445	ATLTNTIAPDVITQIPLVKAFNLSHGATIKVGPFTGGDILRRNTVSGFGDMRVNITAPL	504	
QY	555	AQRYVRIRYASTDLQFHTSINGKAINQGNFSAITWNRGDDLDYKFTXTVGTTPFSLDD	614	
Db	505	SQRYVRIRYASTDLQFYTNINGTTINIGNFSSTMDSGDDLOQYGRFRVAGFTTPFTFSD	564	
QY	615	VQSTFTIGAWNFSNGNEVIDRIEFVPEVTEYAEYDFEAKQEKVTALETSTNPRGLKTD	674	
Db	565	ANSTFTIGAFGSPNNEVIDRIEFVPAEVTFAEYDLEAKQAVNALFTSSNQIGLKTD	624	
QY	675	VKDYHIDQVSNLVESLDEFYLDKEKRELFEIVKYAKQLHIERNM	718	
Db	625	VTDYHIDQVSNLVESLDEFYLDKEKRELSEKVKHAKRLSDERNL	668	

RESULT 9

S32649  
parasporal crystal protein cryIFa3 - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S32649  
R;Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A;Reference number: S32649  
A;Accession: S32649  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1174 <LAM>  
A;Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295865; PIDN:CAA80235.1; PID:G2958  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 38.8%; Score 1455.5; DB 2; Length 1174;  
Best Local Similarity 44.7%; Pred. No. 2.3e-92;  
Matches 324; Conservative 101; Mismatches 205; Indels 95; Gaps 17;

QY	36	NINHE----	DCLKMEYENVEPVSASTIQIGIGIA-GKILGTGVPPAGQVASYSLFIL	90
Db	4	NIQNCQVYNCLSNPEVEILSEERSTGRPLDLSLSTRFLSEFPVGVGVAFLGLFDLIW	63	
QY	91	GELWPKGKQWEIPMEHVEEII	NQKISTYARKKALTDKLGCDALAVYHDSLESWGNRN	150
Db	64	GFITP---SWSLFILQLEQLIQEITELERNAITTLRGLADSYEYVLEALREWEENPN	120	
QY	151	NTRARSVKXSYIALELMFVQKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEW	210	
Db	121	NAQLREDRVIRFANTDDALITAINNFTLTSFEIPLLSVYQAAANLHLSLLRDADVSGQGW	180	
QY	211	GLSSSEISTFYNRQVERAGDYSYHCVKMYSTGLNNLRGTNAESWRYNQFRDRMTLWLD	270	
Db	181	GLDIATVNNHYNRNLINLTHRYTECHLDTYNQGLNLEGTNRQWRSFNQFRRLTITVLD	240	
QY	271	LVALPESYDTQMYPIKTTAQLTREYVTDALGTVHPHSFTSTTWYNNNAPS-FAIAEAAV	329	
Db	241	IVALFPYDARAYPIQTSQSLTREIYTSV--	IEDSP-----VSANIPNGFNRAEFG-	290
QY	330	VRNPHLLDFLEQVITYLLSRVSNQYMMWGGHKLFRITGGLTNISTQGSTNTSINPV	389	
Db	291	VRPPLHMDFMN----	SLFVTAETVRSQTVWGGHLV-----SSRNTAGNPI	331
QY	390	TLFP-----	TSRDVYRTESLAGLNLFQTQPNVPRVDFHMKFVTHPIASD	434
Db	332	NFYIYGFNPGGAIWAIEDPREFYRT-----	LSDPVFV-RGGP-----GN	371
QY	435	NFYYPGYAGIGTQLQ-----	DSENELPPEATQPNYESYSHRLSHI-----	475
Db	372	PHYVLGLRGVAFQOTGTNHTRTFRNSGTIDSLEIIPQDNGAPMNDYSHVLNHTVFRW	431	
QY	476	-GLISASHV-KALVYSWTHRSADRTNTIPENSITQIPLVKAFNLSGAAVVRGPGFTGGD	533	
Db	432	PGEIAGSDSWRAPMFSWTHRSADRTNTIINPNIITQIPAVKARNLHSGSTVVRGPGFTGGD	491	
QY	534	ILRRNTGTGFDIRVNIINPPFAQRYVRIRYASTDLQFHTSINGKAINQGNFSAITWNRG	593	
Db	492	LLRRNTGTGFDIRVNIINPPFAQRYVRIRYASTDLQFHTSINGKAINQGNFSAITWNRG	551	
QY	594	BDLYKFTXTVGTTPFSLDDVQSTFTIGAWNFSNGNEVIDRIEFVPEVTEYAEYDFE	653	
Db	552	GNLESGNFRTAGTPTFPFSNAOSTFTLGTQAFSN-QEVYIDRIEFVPAEVTFAESDLE	610	
QY	654	KAQEKVTALETSTNPRGLKTDVKDYHIDQVSNLVESLDEFYLDKEKRELFEIVKYAKQLH	713	
Db	611	RAQKAVNALFTSTISQLGLKTNVTGYHIDQVSNLVESLDEFYLDKEKRELSEKVKHAKRLS	670	
QY	714	IERNM	718	
Db	671	DKRNL	675	

RESULT 10

A26513  
 parasporal crystal protein - Bacillus thuringiensis (strain aizawai)  
 C;Species: Bacillus thuringiensis  
 C;Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
 C;Accession: A26513  
 R;Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.  
 Gene 53, 113-119, 1987  
 A;Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
 A;Reference number: A26513; MUID:87248103; PMID:3297927  
 A;Accession: A26513  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1155 <OED>  
 A;Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099  
 A;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 38.6%; Score 1448.5; DB 2; Length 1155;  
 Best Local Similarity 44.1%; Pred. No. 6.7e-92;  
 Matches 313; Conservative 112; Mismatches 229; Indels 55; Gaps 13;  
 36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGVPPAGQVASLYS 87  
 4 NPNINECIPYCNLSNPEVEVLGGERIEGTYPIDISLSLTQFLLEF-VPGAGFVLGLVD 62  
 88 FILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKLGLDALAVYHDSLESWG 147  
 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLYQIYAESFWEA 119  
 148 NRNNTARSVVVKSQYIAELMFVQKLPSPFAVSGEEVPLPIYAAQANLHLLLRDASIFG 207  
 120 DPTNPALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSVYVQAANLHLSVLDSVFG 179  
 208 KEWGSSSEISTFYNRQVERAGYSYHCVKYSTGLNNLRGTNAESVVRVYQFRDWTLM 267  
 180 QRWGFDAATNSRNDLRLIGNYTHAVRWNTGLERWGPDSRDWIRYQFRRLTIT 239  
 268 VLDLVALFSDYDTQMPYIKTTAQLTREYVTDAGTVHPHPSFTSTWYNNAPGSAIEA 327  
 240 VLDIVSLFNYDSTYPTPTVTSQLTREIYTNV-----LENFDGSPRALAQ 285  
 328 AV---VRNPHLLDLEQVITYLSLR---WSNTQYNNM---WGGHKLERTIGTGLNIS 377  
 286 GIEGIRSPHLMIDLNSITTYTDAHREYVYSGHQINASPVGSGPEFTTPLYGTMGNA 345  
 378 TQGSINTSINPVLTPFTSRDVRVTESLAGLNLFLTPQVNV-PRVDFHKEVTHPIASDNF 436  
 346 PQQRIVAGLQGGVYRTLSSTLYRRPFNIGIN---NOQLSVLDGTGFAYG-----TSSNL 396  
 437 YYPGYAGITQLODSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVYS 489  
 397 PSAYVRKSGT-VDSLDEIPQNNVPPRQGFSLHLSHVSFERSGFSNSVSIIIRAPMS 454  
 490 WTHRSADRTNTIENSITQIPLVKAFNLSSGAAVRGGPGFTGGDILRRTWTGTDIRVN 549  
 455 WIHRSAEFNNIIPSSQITQIPLTAKSTNLGSGTVSVKGGPGFTGGDILRRTSPGQISTLRVN 514  
 550 INPPFAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAVMNRGDLDYKTFXTVGTFTTP 609  
 515 ITAPLSQRVVRIRYASTNLQFHTSIDGRPNQGNFSAVMNRGDLDYKTFXTVGTFTTP 574  
 610 FSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEAEYDFEKAQEKVTAFTSTNPR 669  
 575 FNFSNGSVPTLSAHVFNNGNEVYIDRIEFVPAEVTEYAEAEYDFEKAQEKVTAFTSTNPR 634  
 670 GLKTDVVDYHIDQVSNLVSLSDFYLDKRELFEIVKYAKQLHTERNM 718  
 635 GLKTDVTDYHIDQVSNLVSLSDFYLDKRELFEIVKYAKQLHTERNM 683

RESULT 11

JD0002  
 parasporal crystal protein cryIIAb3 - Bacillus thuringiensis  
 N;Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot  
 C;Species: Bacillus thuringiensis  
 C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
 C;Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002  
 R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
 Agric. Biol. Chem. 51, 455-463, 1987  
 A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
 A;Reference number: A90025  
 A;Accession: A90025  
 A;Molecule type: mRNA  
 A;Residues: 1-1155 <KON>  
 A;Cross-references: UNIPROT:P06578  
 A;Experimental source: subsp. kurstaki  
 R;Geiser, M.; Schweitzer, S.; Grimm, C.  
 Gene 48, 109-118, 1986  
 A;Title: The hypervariable region in the genes coding for entomopathogenic crystal protei  
 A;Reference number: A91560; MUID:87163505; PMID:3557124  
 A;Accession: A91560  
 A;Molecule type: DNA  
 A;Residues: 1-1155 <GEI>  
 A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124  
 A;Experimental source: subsp. kurstaki  
 R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
 DNA 5, 305-314, 1986  
 A;Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal  
 A;Reference number: A90955; MUID:86300092; PMID:3743328  
 A;Accession: A90955  
 A;Molecule type: DNA  
 A;Residues: 1-1155 <WAB>  
 A;Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720  
 A;Experimental source: subsp. berliner  
 R;Chak, K.F.; Jen, J.C.  
 submitted to the EMBL Data Library, October 1990  
 A;Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
 A;Reference number: S14555  
 A;Accession: S14555  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1155 <CHA>  
 A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273  
 R;Hofte, H.; de Greve, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerck  
 Eur. J. Biochem. 161, 273-280, 1986  
 A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri  
 A;Reference number: A26461; MUID:87054026; PMID:3023091  
 A;Accession: A26461  
 A;Molecule type: DNA  
 A;Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>  
 A;Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255  
 A;Experimental source: strain berliner 1715  
 C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
 C;Genetics:  
 A;Gene: cry-1-2; bt2  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin  
 F;82-586/Product: toxic peptide #status predicted <TXP>  
 F;82-300/Region: toxic #status predicted  
 F;300-586/Region: insecticidal #status predicted

Query Match 38.5%; Score 1441.5; DB 2; Length 1155;  
 Best Local Similarity 44.2%; Pred. No. 2e-91;  
 Matches 314; Conservative 111; Mismatches 228; Indels 57; Gaps 14;

QY 36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGVPPAGQVASLYS 87  
 Db 4 NPNINECIPYCNLSNPEVEVLGGERIEGTYPIDISLSLTQFLLEF-VPGAGFVLGLVD 62  
 QY 88 FILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKLGLDALAVYHDSLESWG 147  
 Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLYQIYAESFWEA 119  
 QY 148 NRNNTARSVVVKSQYIAELMFVQKLPSPFAVSGEEVPLPIYAAQANLHLLLRDASIFG 207

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Db 120 DPTNPALREEMRIQFNDMSALTTPFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179
QY 208 KEWGLSSSEISTFYNQVERAGDYSYHCVKWTSTGLNLRGTAESWVRYNQFRDRTLM 267
Db 180 QRWGDAATINSRYNDLTRIGNYTDHVRWYNTGLERWGPDSRDWIRYNQFRRELTLT 239
QY 268 VLDLVALFPSTQMYPIKTAQLTREVYTDAGTVHPHPSFTSTTWYNNAPSF-----S 323
Db 240 VLDIVSLFPNDSTRTPIRTVSQLTRTYTNFV-----LENFDSFRGSAQ 285
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGGHKLERTIGTILNI 376
Db 286 GIEGS-IRSPHLMIDLNSITITDAHRGEYWSGHQIMASPVGSGPEFTFPPLGYTMGNA 344
QY 377 STQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNV-PRVDFHMKFVTHPIASDN 435
Db 345 APQQRIVAGLQGGVYRTLSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395
QY 436 FYYPGYAGIGTQLODSNELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 488
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQCFSHRLSHVSMFRSFGSNSSVSIIRAPMF 453
QY 489 SWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRV 548
Db 454 SWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRSPGOISTLRV 513
QY 549 NINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYKTXVTGFTT 608
Db 514 NITAPLSQRYRIRYASTTDLQFHTSIDGRPINQGNFSAATMSSGNSFRVTGFTT 573
QY 609 PFSLLDVQSTFTTICAMNFGSSGNEVYIDRIEFVPEVTEAEYDPEKAQKVTALFTSTNP 668
Db 574 PFNFGSSVFTLSAHVFNFGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQ 633
QY 669 RGLKTDVKYHIDQVSNLVESLDEFLDEKRELFEIVKYAKQLHIERNM 718
Db 634 IGLKTDVTDYHIDQVSNLVESLDEFLDEKRELFEIVKYAKQLHIERNM 683

RESULT 12
A29125
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29125
R:Rifischhoff, D.A.; Bowdish, K.S.; Perlak, P.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/Technology 5, 807-813, 1987
A:Title: Insect tolerant transgenic tomato plants.
A:Reference number: A29125
A:Accession: A29125
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1156 <FIS>
A:Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.5%; Score 1441.5; DB 2; Length 1156;
Best Local Similarity 44.2%; Pred. No. 2.1e-91;
Matches 314; Conservative 111; Mismatches 228; Indels 57; Gaps 14;

QY 36 NINHEDECLMSEVENVE-PFVSASTIQTG-----IGIAGKILGTGLGVFFAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGKNQWEIEMEHVERIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFARNOAISRLGLSNLYQIYAESFREWEA 119
QY 148 NRNNTARSVVKSVQYIAELMFVQKLPFAVSGEVEPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMSALTTPFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179

RESULT 13
A22798
parasporal crystal protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: A22798
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.
Gene 34, 243-251, 1985
A:Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuring
A:Reference number: A22798; MUID:85232070; PMID:2989108
A:Accession: A22798
A:Molecule type: DNA
A:Residues: 1-934 <SHI>
A:Cross-references: UNIPROT:Q9S5V8; GB:M10917; NID:G143100; PIDN:AAA22552.1; PID:G551713
C:Comment: The authors translated the codon ACA for residue 264 as Ser.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 38.2%; Score 1433; DB 2; Length 934;
Best Local Similarity 43.1%; Pred. No. 5.7e-91;
Matches 308; Conservative 119; Mismatches 221; Indels 66; Gaps 13;

QY 36 NINHEDECLMSEVENVE-PFVSASTIQTG-----IGIAGKILGTGLGVFFAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGKNQWEIEMEHVERIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFARNOAISRLGLSNLYQIYAESFREWEA 119
QY 148 NRNNTARSVVKSVQYIAELMFVQKLPFAVSGEVEPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMSALTTPFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179
QY 208 KEWGLSSSEISTFYNQVERAGDYSYHCVKWTSTGLNLRGTAESWVRYNQFRDRTLM 267

```

Db 180 QRWGFDAAATNSRYNDLRLIGNYTDVAVRWYNTGLERVWGPDSRDWVYNQFRELTLT 239  
Qy 268 VLDLVALFSPYDQMPYIKTTAQLTRVYTDAGTVVHPHPSFTSTTWYNNAPSFSAIEA 327  
Db 240 VLDLVALFSPYDQMPYIKTTAQLTRVYTDAGTVVHPHPSFTSTTWYNNAPSFSAIEA 327  
Qy 328 AV---VRNPHLLDFLEQVITYSLLSRWSNTQYMMWGGHKLFRIGT---LNISTQGS 381  
Db 286 RIEQNIRQHLMIDLNRITVYTDVHRG-----FNYWSGHQITASPVGSGPEFAPFLFGN 340  
Qy 382 TNSINPVTLPFTSRDVRVYTESL-----AGLN---LFLTQPVNVPRVDFHKKFVTH 429  
Db 341 AGNAAPPVLSLTGLGIFRTLSPLRYRIILGSGPNNQELFV-----LDGTEFSFASLT 395  
Qy 430 PIASDNFFYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLISAS-----HVK 484  
Db 396 NLPSTIYRQGTV-----DSLVDVIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLR 448  
Qy 485 ALVYSWTHESADRTNTIENPNSITQIPLVKAENLSGAAVVGPGFTGGDILRRNTGTGFG 544  
Db 449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKPGFTGGDILRRNTGTGFG 508  
Qy 545 DIRVNIAPPQRYRVRIRYASTTDQFHTSINGKAINQGNFSATMNRGDDLYKTFVTV 604  
Db 509 TLRVNIITAPLSQRYRVRIRYASTTDQFHTSINGKAINQGNFSATMNRGDDLYKTFVTV 604  
Qy 605 GFTTFPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFKAQKVTALFT 664  
Db 569 GFTTFPSNGSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFT 628  
Qy 665 STNPRGLKTDVVDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 718  
Db 629 SSNQIGLKTDTVDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 682

## RESULT 14

JT0241  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
N;Alternate names: 135K insecticidal protein  
C;Species: Bacillus thuringiensis  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: JT0241  
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
Agric. Biol. Chem. 52, 1565-1573, 1988  
A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein  
A;Reference number: JT0241  
A;Accession: JT0241  
A;Molecule type: DNA  
A;Residues: 1-1176 <SHI>  
A;Cross-references: UNIPROT:P02965  
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein  
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 38.2%; Score 1432; DB 2; Length 1176;  
Best Local Similarity 43.1%; Pred. No. 9.6e-91;  
Matches 308; Conservative 118; Mismatches 222; Indels 66; Gaps 13;  
Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLVPPFAGQVASLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELWPKGKNQWEIFMEHVEIINQKISTYARNKALTDLKGLDALAVYHDSLESWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFPARNOAISRLGSLNLYQIYAESFREWEA 119  
Qy 148 NRNNTARSVVKSQYIALELMFVQKLPSPFVSAGEEVPPLPIYAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREMRIQFNDNMNSALTATPILFAVQNYQVPLLSVYVQAANLHLSVLDRVSFVG 179  
Qy 208 KEWGLSSSISITFYNRQVERAGDYSYHCVKYSTGLNNLRGTNAESWVRYNQFRDWTLM 267

Db 180 QRWGFDAAATNSRYNDLRLIGNYTDVAVRWYNTGLERVWGPDSRDWVYNQFRELTLT 239  
Qy 268 VLDLVALFSPYDQMPYIKTTAQLTRVYTDAGTVVHPHPSFTSTTWYNNAPSFSAIEA 327  
Db 240 VLDLVALFSPYDQMPYIKTTAQLTRVYTDAGTVVHPHPSFTSTTWYNNAPSFSAIEA 327  
Qy 328 AV---VRNPHLLDFLEQVITYSLLSRWSNTQYMMWGGHKLFRIGT---LNISTQGS 381  
Db 286 RIEQNIRQHLMIDLNRITVYTDVHRG-----FNYWSGHQITASPVGSGPEFAPFLFGN 340  
Qy 382 TNSINPVTLPFTSRDVRVYTESL-----AGLN---LFLTQPVNVPRVDFHKKFVTH 429  
Db 341 AGNAAPPVLSLTGLGIFRTLSPLRYRIILGSGPNNQELFV-----LDGTEFSFASLT 395  
Qy 430 PIASDNFFYPGYAGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLISAS-----HVK 484  
Db 396 NLPSTIYRQGTV-----DSLVDVIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLR 448  
Qy 485 ALVYSWTHESADRTNTIENPNSITQIPLVKAENLSGAAVVGPGFTGGDILRRNTGTGFG 544  
Db 449 APTFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKPGFTGGDILRRNTGTGFG 508  
Qy 545 DIRVNIAPPQRYRVRIRYASTTDQFHTSINGKAINQGNFSATMNRGDDLYKTFVTV 604  
Db 509 TLRVNIITAPLSQRYRVRIRYASTTDQFHTSINGKAINQGNFSATMNRGDDLYKTFVTV 604  
Qy 605 GFTTFPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFKAQKVTALFT 664  
Db 569 GFTTFPSNGSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFT 628  
Qy 665 STNPRGLKTDVVDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 718  
Db 629 SSNQIGLKTDTVDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 682

## RESULT 15

JC2219  
parasporal crystal protein cryIAa - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C;Accession: JC2219  
R;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.  
Biosci. Biotechnol. Biochem. 58, 830-835, 1994  
A;Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an  
A;Reference number: JC2219; MUID:94289859; PMID:7764972  
A;Accession: JC2219  
A;Molecule type: DNA  
A;Residues: 1-1176 <UDA>  
A;Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:G506190; PIDN:BAA04468.1; PID:G53578  
C;Genetics:  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1426; DB 2; Length 1176;  
Best Local Similarity 43.0%; Pred. No. 2.5e-90;  
Matches 307; Conservative 118; Mismatches 223; Indels 66; Gaps 13;  
Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLVPPFAGQVASLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELWPKGKNQWEIFMEHVEIINQKISTYARNKALTDLKGLDALAVYHDSLESWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFPARNOAISRLGSLNLYQIYAESFREWEA 119  
Qy 148 NRNNTARSVVKSQYIALELMFVQKLPSPFVSAGEEVPPLPIYAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREMRIQFNDNMNSALTATPILFAVQNYQVPLLSVYVQAANLHLSVLDRVSFVG 179  
Qy 208 KEWGLSSSISITFYNRQVERAGDYSYHCVKYSTGLNNLRGTNAESWVRYNQFRDWTLM 267

Db 180 QRWGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVMGPDSDRDWVRYNQFRRELTLT 239  
QY 268 VLDLVALFPSTQMTPIKTAQLTREVYTDAGTVHPHPSFTSTTWNNAAPSFAIEA 327  
Db 240 VLDLVALFNSVDSRRYPRTVSQLTREIYNPV-----LENFDGSRGMAQ 285  
QY 328 AV---VRNPHLLDFEQVTIYSLLSRWSTQYMMNWGGHKLERTIGCT---LNISTQGS 381  
Db 286 RIEQNIHQPHLMDILNSITITVDVHRG-----FNYWSGHQITASPVGSGPEAFPLFGN 340  
QY 382 TMTSINPVTLPFTSRDVRTESL-----AGLN---LFLTQPVNVPRVDFHWKFVTH 429  
Db 341 AGNAAPPVLVSLTGLGIFRTLSPLRYRIILGSGPNNQELFV-----LDGTEFSFSLTT 395  
QY 430 PIASDNEYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVX 484  
Db 396 NLPSTIYRQGTV-----DSLVDIPPQNSVPPRAGFSHRLSHVTLMSQAAGAVYTLR 448  
QY 485 ALVYSWTHRSADRTNTEPNISITQIPLVKAFLSSGAAVVRGCGFTGGDILRRTNTGTFG 544  
Db 449 APTFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRTSPQIS 508  
QY 545 DIRVINPPFAQRYRYRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTXTV 604  
Db 509 TLRVNITAPLSQRYRVRIYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFTV 568  
QY 605 GTTPFSLLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTAFT 664  
Db 569 GTTPFNFSGSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFT 628  
QY 665 STNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
Db 629 SSNIQIGLXTDVTDYHIDQVSNLVECLSDFECLDEKQELSEKVKHAKRLSDERNL 682

Search completed: October 28, 2004, 18:31:47  
Job time : 21.1643 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.5881 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-54

Perfect score: 3749

Sequence: 1 MLLKNQDKHQSFSSNAKVDK.....KRELFIVKAYQLHIERNM 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3722.5	99.3	719	17	US-10-782-020-10
2	3722.5	99.3	719	17	US-10-782-141-8
3	3722.5	99.3	719	17	US-10-782-096-10
4	3722.5	99.3	719	17	US-10-782-570-7
5	3439	91.7	710	14	US-10-428-961-42
6	2249	60.0	1228	16	US-10-809-953-10
7	2236	59.6	1207	10	US-09-988-462-7
8	2156	57.5	1227	14	US-10-428-961-63
9	2141	57.1	1186	9	US-09-826-660-23
10	2085.5	55.6	1228	14	US-10-428-961-38
11	2085.5	55.6	1228	15	US-10-614-524-2
12	1902	50.7	643	9	US-09-826-660-25
13	1708	45.6	1167	14	US-10-089-678-1

14	1658	44.2	653	14	US-10-428-961-6	Sequence 6, Appli
15	1652	44.1	1157	17	US-10-782-141-16	Sequence 16, Appl
16	1652	44.1	1157	17	US-10-782-096-17	Sequence 17, Appl
17	1652	44.1	1157	17	US-10-782-570-13	Sequence 13, Appl
18	1500.5	40.0	1206	13	US-10-032-717-2	Sequence 2, Appli
19	1500.5	40.0	1206	14	US-10-414-637-2	Sequence 2, Appli
20	1500.5	40.0	1206	15	US-10-606-320-2	Sequence 2, Appli
21	1500.5	40.0	1206	17	US-10-746-914-2	Sequence 2, Appli
22	1477.5	39.4	1210	13	US-10-032-717-4	Sequence 4, Appli
23	1477.5	39.4	1210	14	US-10-414-637-4	Sequence 4, Appli
24	1477.5	39.4	1210	15	US-10-606-320-4	Sequence 4, Appli
25	1477.5	39.4	1210	17	US-10-746-914-4	Sequence 4, Appli
26	1474	39.3	1156	14	US-10-099-285-72	Sequence 72, Appl
27	1474	39.3	1156	14	US-10-428-961-28	Sequence 28, Appl
28	1441.5	38.5	1155	9	US-09-756-643-2	Sequence 2, Appli
29	1441.5	38.5	1155	10	US-09-988-462-9	Sequence 9, Appli
30	1441.5	38.5	1155	14	US-10-136-998A-2	Sequence 2, Appli
31	1441.5	38.5	1177	14	US-10-035-060-6	Sequence 6, Appli
32	1441.5	38.5	1181	10	US-09-988-462-11	Sequence 11, Appl
33	1441.5	38.5	1181	10	US-09-988-462-13	Sequence 13, Appl
34	1441.5	38.5	1181	10	US-09-988-462-15	Sequence 15, Appl
35	1441.5	38.5	1181	10	US-09-988-462-17	Sequence 17, Appl
36	1441.5	38.5	1181	10	US-09-988-462-28	Sequence 28, Appl
37	1441.5	38.5	1181	14	US-10-136-998A-4	Sequence 4, Appli
38	1441.5	38.5	1181	14	US-10-136-998A-8	Sequence 8, Appli
39	1441.5	38.5	1181	14	US-10-136-998A-10	Sequence 10, Appl
40	1441.5	38.5	1181	14	US-10-136-998A-12	Sequence 12, Appl
41	1436.5	38.3	1177	14	US-10-035-060-2	Sequence 2, Appli
42	1434.5	38.3	1177	14	US-10-035-060-8	Sequence 8, Appli
43	1433.5	38.2	1177	14	US-10-102-469-24	Sequence 24, Appl
44	1422	37.9	1176	17	US-10-782-141-6	Sequence 6, Appli
45	1422	37.9	1176	17	US-10-782-036-7	Sequence 7, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMT-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 99.3%; Score 3722.5; DB 17; Length 719;  
Best Local Similarity 99.4%; Pred. No. 1.7e-302;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy	1	MLKNQDKHQSFSSNAKVDKISTDLSKNETDIELQININHEDCLKMSEYENVEPFSASTI 60
Db	1	MLKNQDKHQSFSSNAKVDKISTDLSKNETDIELQININHEDCLKMSEYENVEPFSASTI 60
Qy	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVVEIINQKISTYA 120
Db	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGKNQWEIFMEHVVEIINQKISTYA 120

QY	121	RNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVKSYIAELMFPVKLPSPFAVSG	180
Db	121	RNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVKSYIAELMFPVKLPSPFAVSG	180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS	240
Db	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS	240
QY	241	TGLNNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREVTDAI	300
Db	241	TGLNNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREVTDAI	300
QY	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW	360
Db	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW	360
QY	361	GGHKLFPRTIGGTINISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR	419
Db	361	GGHKLFPRTIGGTINISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR	420
QY	420	VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS	479
Db	421	VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS	480
QY	480	ASHVKALVSWTHRSADRTNTIEPNSTIQIPLVKAPNLSSGAAVVRGPGFTGGDILRRTN	539
Db	481	ASHVKALVSWTHRSADRTNTIEPNSTIQIPLVKAPNLSSGAAVVRGPGFTGGDILRRTN	540
QY	540	TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	599
Db	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK	600
QY	600	TFXTVGTFTPFSLDDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	659
Db	601	TFRTVGTFTPFSLDDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	660
QY	660	TALFTSTNPRGLKTDVQYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM	718
Db	661	TALFTSTNPRGLKTDVQYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQLHIERNM	719
RESULT 2			
US-10-782-141-8			
; Sequence 8, Application US/10782141			
; Publication No. US20040197917A1			
; GENERAL INFORMATION:			
; APPLICANT: Carozzi, Nadine			
; APPLICANT: Hargiss, Tracy			
; APPLICANT: Koziel, Michael G.			
; APPLICANT: Duck, Nicholas B.			
; APPLICANT: Carr, Brian			
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and			
; TITLE OF INVENTION: Methods for Its Use			
; FILE REFERENCE: 045600/274143			
; CURRENT APPLICATION NUMBER: US/10782,141			
; CURRENT FILING DATE: 2004-02-20			
; PRIOR APPLICATION NUMBER: 60/448,632			
; PRIOR FILING DATE: 2003-02-20			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Bacillus thuringiensis			
US-10-782-141-8			
Query Match			
Best Local Similarity			
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			
99.3%; Score 3722.5; DB 17; Length 719;			
QY	1	MLKKNQDKHQSFSNAKVDKISTDSLKNETDIELQNNHEDCLKSEYENVEPVSASTI	60

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Best Local Similarity 99.4%; Pred. No. 1.7e-302;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPFSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPFSASTI 60
QY 61 QTGIGIACKILGTGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIACKILGTGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNNTRARSVVKSYQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWGNNRNNTRARSVVKSYQYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWYS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMDTLMVLDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMDTLMVLDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
QY 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419
DB 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 420
QY 420 VDFHWKVFTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 479
DB 420 VDFHWKVFTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 539
DB 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
QY 540 TGTFGDIRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 599
DB 540 TGTFGDIRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600
QY 600 TFXTVGTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 659
DB 600 TFXTVGTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQLHIERNM 718
DB 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQLHIERNM 719

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RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719

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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 99.3%; Score 3722.5; DB 17; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.7e-302;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPFSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPFSASTI 60
QY 61 QTGIGIACKILGTGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIACKILGTGVFPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNNTRARSVVKSYQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWGNNRNNTRARSVVKSYQYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWYS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMDTLMVLDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMDTLMVLDLVALPFSYDTQMYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360
QY 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 419
DB 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVN-VPR 420
QY 420 VDFHWKVFTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 479
DB 420 VDFHWKVFTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 539
DB 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540
QY 540 TGTFGDIRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 599
DB 540 TGTFGDIRVINPFPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600
QY 600 TFXTVGTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 659
DB 600 TFXTVGTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQLHIERNM 718
DB 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELIVKYAKQLHIERNM 719

```

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RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

```

; PRIOR FILING DATE: 2000-09-13		; APPLICANT: Van Mellaert, Herman	
; PRIOR APPLICATION NUMBER: 60/153,995		; APPLICANT: Botterman, Johan	
; PRIOR FILING DATE: 1999-09-15		; APPLICANT: Van Rie, Jeroen	
; NUMBER OF SEQ ID NOS: 63		; APPLICANT: Joos, Henk	
; SOFTWARE: PatentIn version 3.2		; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC	
; SEQ ID NO 42		; TITLE OF INVENTION: CRYSTAL PROTEINS	
; LENGTH: 710		; FILE REFERENCE: 021565-078	
; TYPE: PRT		; CURRENT APPLICATION NUMBER: US/10/809,953	
; ORGANISM: Bacillus thuringiensis		; CURRENT FILING DATE: 2004-03-26	
; NAME/KEY: misc feature		; PRIOR APPLICATION NUMBER: US/09/661,016	
; LOCATION: (200) (200)		; PRIOR FILING DATE: 2000-09-13	
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid		; PRIOR APPLICATION NUMBER: PCT/EP90/00905	
US-10-428-961-42		; PRIOR FILING DATE: 1990-05-30	
		; PRIOR APPLICATION NUMBER: GB 89401499.2	
		; PRIOR FILING DATE: 1989-05-31	
		; NUMBER OF SEQ ID NOS: 10	
		; SOFTWARE: PatentIn Ver. 2.0	
		; SEQ ID NO 10	
		; LENGTH: 1228	
		; TYPE: PRT	
		; ORGANISM: Bacillus thuringiensis	
		US-10-809-953-10	
Query Match		60.0%; Score 2249; DB 16; Length 1228;	
Best Local Similarity		62.3%; Pred. No. 9.9e-179;	
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;		Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;	
QY	1	MKLKQDKHQSPSSNAKVDKIDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60	
DB	1	MKSKQNMHQSLNNATVDKNTGSLNNTNTELQNFH-----EGIEPFSVSTI 51	
QY	61	QTGIGIAGKILGLVPFAGQVASYLFIIGELWPKGKQWEIFMEHVEEIIINQKISTYA 120	
DB	52	QTGIGIAGKILGNLGVFAGQVASYLFIIGELWPKGKQWEIFMEHVEEIIINQKISTYA 111	
QY	121	RNKALTDLKLGLDALAVYHDSLESWGNRNTRRSVKSQYIALELMFVQKLPSFAVSG 180	
DB	112	RNKALDLKGLDALAVYHDSLESWGNRNTRRSVKSQYIILELMFVQKLPSFAVSG 171	
QY	181	EEVPLPIYAQAANLHLLLRDASI FGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240	
DB	172	EEVPLPIYAQAANLHLLLRDASI FGKXWGLSDSEISTFYNRQSGKSEYSDHCVRWYN 231	
QY	241	TGLNLRGTNAESWVRNQFRDMLVLDVALFSPYDTQMPYIKTTAQLTREVYTDAL 300	
DB	232	TGLNLRGMNNAESWVRNQFRDMLVLDVALFSPYDTQMPYIKTTAQLTREVYTDAL 291	
QY	301	GTVHPHPSSTTWNNAAPSIAEAAVVRNPHLLDFLEQVITYSLLSRWSTQYNNMW 360	
DB	292	GTVHPHPSSTTWNNAAPSSTIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYNNMW 351	
QY	361	GGHLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNV 419	
DB	352	GGHLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNV 411	
QY	420	VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479	
DB	412	VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471	
QY	480	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539	
DB	472	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531	
QY	540	TGTGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 599	
DB	532	TGTGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 591	
QY	600	TEXTVGTTPFSLDDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 659	
DB	592	TEXTVGTTPFSLDDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 651	
QY	660	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFVLDKRELFEIVKYAKQLHIERNM 718	
DB	652	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDYFVLDKRELFEIVKYAKQLHIERNM 710	
RESULT 6			
US-10-809-953-10			
; Sequence 10, Application US/10809953			
; Publication No. US2004018125A1			
; GENERAL INFORMATION:			

Db 656 FTNPNRLKTDVTDYHIDQVSNLVACLSDFFCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7

; Sequence 7, Application US/09988462  
; Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-No. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 59.6%; Score 2236; DB 10; Length 1207;  
Best Local Similarity 63.9%; Pred. No. 1.2e-177;  
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;

Qy 40 EDCMKSEYENVEPPFVSASTIQTGTGKILGTLGVPPAGQVAVSLYSFILGELWPKGKN 99

Db 10 EDSLCAEGNIDPFPVSASTYQTGTGKILGTLGVPPAGQVAVSLYSFILGELWPKGRD 69

Qy 100 QWEIFMEHVEELINQISTYARNKALTDLKGDLALAVYHDSLESVWGNRNNTARSVKV 159

Db 70 QWEIFLEHVEQLINQITENARNALRLQGLGDSFRAYQQSLEDWLENRDDARTRSVLY 129

Qy 160 SQYTALELMFVQKLPFAVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEIST 219  
Db 130 TOYIALELDFLNAMPLFAIRNQEVPLMLVYQAANLHLLLRDASIFGSEFGLTSEIQIR 189  
Qy 220 FYNROVERAGDYSYHCVKMYSTGLNNLRGTNAESWRYNQRRDMLMVLVALPPSYD 279  
Db 190 YEROVERTRDYSYCVWEYNTGLNSURGTNAASWRYNQRRDMLMVLVALPPSYD 249  
Qy 280 TQMPDKTTAQLTREYVYDAIGTVHPHPSFTTWTWNNNAPSFAIEAAVVRNPHLLDEL 339  
Db 250 TRTPINTSAQLTREYVYDAIGAT--GVNMAWNNWNNNAPSFAIEAAARSPHLLDEL 307  
Qy 340 EQVTIYSLSRWSNTQYMNMGCHKLERTIGTGLNISTQGSTNTSINPVTLPTFSRDVY 399  
Db 308 EQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGLTSTHGATNTSINPVTLRFASRDVY 367  
Qy 400 RTESLAGLNLF--LTQPVN-VPRVDFHWKFTVTHP-----IASDNFYYPGYAGIGTQLQDS 451  
Db 368 RTESYAGVLLWGIYLEPIHGVPTRFNF--TNPQNISDRGTANYSQP-YESPGQLQKDS 423  
Qy 452 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 511  
Db 424 ETELPPETTERPNYESYSHRLSHIGLILQSRVNVVPYVSWTHRSADRTNTIGPNRITQIPM 483  
Qy 512 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTFGDIRVNIINPPFAQRYRIRYASTDLQ 571  
Db 484 VKASELPQGTTVVRGPGFTGGDILRRNTGTGGPIRVTVNGPLTORIGRIRYASTVDFD 543  
Qy 572 FHTSINGKAINQGNFSAWNRGDDLDYKFTXVTGFTTFFSLDDVOSTFTTIGAWNFSSGNE 631  
Db 544 FVSRGGTTVNNRFLRTMNSGDELKYNFVRRRAFTTFTTQIQDIIRTSIQGLSGNGE 603  
Qy 632 VIIDRIEFVVEVTEAEYDFEKAQEKVTALFTSTNPRGLKTDVXDYHIDQVSNLVESLS 691  
Db 604 VIIDKIEIFVTATFEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACL 663  
Qy 692 DEFYLDKRELFELVKYAKQLHIERNM 718  
Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63

; Sequence 63, Application US/10428961

; Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Donovan, William P.

APPLICANT: Gilmer, Amy J.

APPLICANT: Ruper, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECO201--1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patent in version 3.2

SEQ ID NO 63

LENGTH: 1227

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 57.5%; Score 2156; DB 14; Length 1227;  
Best Local Similarity 58.8%; Pred. No. 6.1e-171;  
Matches 420; Conservative 105; Mismatches 175; Indels 14; Gaps 4;

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QY 13 SSNAKVDKISTSLKN-----ETDIELQNHINHEDECKMSEYENVEPVFSASTIQTGIG 65
Db 7 NENEIINALSIPAVSNHSAQNLSTDAI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGKILGTGVPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 121
QY 126 TDLKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFYQKLPFSFAYSGEEVPL 185
Db 122 ARLOGLGNSFRAYQQSLEDWLENRRDARTSVLYTQYIALELDFLNAMPLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWTSTGLNN 245
Db 182 LMYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWTSTGLNN 241
QY 246 LRGNAESWVRNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREYVYTDAGTVHP 305
Db 242 LRGNAESWVRNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREYVYTDAGTVHP 301
QY 306 HPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWGGHKL 365
Db 302 PSGFASTWNNFNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWGGHKL 361
QY 366 EFRITGGTILNISTQSTNTSINPVTLPFTSRDVRYESHRLSHIGLISASHVK 484
Db 362 ESRTIRGSLSTWTHGNTNTSINPVTLPFTSRDVRYESHRLSHIGLISASHVK 481
QY 425 KFTVTHPIASDNFYYPYAGIGTQDSSENELPPEATGQPNYESYHRLSHIGLISASHVK 484
Db 422 RNPLNSLRGSLTYIGYGVGTQDFSETELPETTERPNYESYHRLSHIGLISASHVK 481
QY 485 ALVYSWTHRSADRTNTEIPNSITQIPLVKAENLSGAAVVRGPGTGGDILRRNTGTGFG 544
Db 482 APVYSWTHRSADRTNTEIPNSITQIPLVKAENLSGAAVVRGPGTGGDILRRNTGTGFG 541
QY 605 GFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYFKAQEKVTAFT 664
Db 602 EFPVGISASGSQ-TAGISISNAGROQTFHDKIEFIPITATFEAYDLERAQAVNALFT 660
QY 665 STNPRGLKTDVYDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 NTNPRRLKTVGYDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 714

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RESULT 9
US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

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Query Match 57.1%; Score 2141; DB 9; Length 1186;
Best Local Similarity 58.5%; Pred. No. 1e-169;
Matches 418; Conservative 108; Mismatches 174; Indels 14; Gaps 4;

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QY 13 SSNAKVDKISTSLKN-----ETDIELQNHINHEDECKMSEYENVEPVFSASTIQTGIG 65
Db 7 NENEIINALSIPAVSNHSAQNLSTDAI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGKILGTGVPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 121
QY 126 TDLKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFYQKLPFSFAYSGEEVPL 185
Db 122 ARLOGLGNSFRAYQQSLEDWLENRRDARTSVLYTQYIALELDFLNAMPLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWTSTGLNN 245
Db 182 LMYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWTSTGLNN 241
QY 246 LRGNAESWVRNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREYVYTDAGTVHP 305
Db 242 LRGNAESWVRNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREYVYTDAGTVHP 301
QY 306 HPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWGGHKL 365
Db 302 PSGFASTWNNFNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWGGHKL 361
QY 366 EFRITGGTILNISTQSTNTSINPVTLPFTSRDVRYESHRLSHIGLISASHVK 484
Db 362 ESRTIRGSLSTWTHGNTNTSINPVTLPFTSRDVRYESHRLSHIGLISASHVK 481
QY 425 KFTVTHPIASDNFYYPYAGIGTQDSSENELPPEATGQPNYESYHRLSHIGLISASHVK 484
Db 422 RNPLNSLRGSLTYIGYGVGTQDFSETELPETTERPNYESYHRLSHIGLISASHVK 481
QY 485 ALVYSWTHRSADRTNTEIPNSITQIPLVKAENLSGAAVVRGPGTGGDILRRNTGTGFG 544
Db 482 APVYSWTHRSADRTNTEIPNSITQIPLVKAENLSGAAVVRGPGTGGDILRRNTGTGFG 541
QY 545 DIRVNINPPFAQYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDDLDYKTFXTV 604
Db 542 SMGLNFNNTSLQYRVRVRYAASQTMVLRVTGSGTTFDQGFPTMSANESLTSQSFRFA 601
QY 605 GFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYFKAQEKVTAFT 664
Db 602 EFPVGISASGSQ-TAGISISNAGROQTFHDKIEFIPITATFEAYDLERAQAVNALFT 660
QY 665 STNPRGLKTDVYDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 SSNQLGKTDVYDHYDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 714

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```

RESULT 10
US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201-1
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

```

; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 38  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-428-961-38

Query Match 55.6%; Score 2085.5; DB 14; Length 1228;  
 Best Local Similarity 59.0%; Pred. No. 4.9e-165;  
 Matches 421; Conservative 98; Mismatches 183; Indels 11; Gaps 8;

QY	13	SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPVSASTIQTGIGIAGKI	70
Db	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI	66
QY	71	LGTGVFPAGQVAVSLYFIFELGKPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG	130
Db	67	LGVLGVFPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLNQITENARNTALARLOG	126
QY	131	LGDAVAVHDSLESWGNRNTRARSVVKSOYIALELMFVKQLPSPAVSGEEVPLPIYA	190
Db	127	LGDSFRAYQOQSLDWNLRDARTSRVLYTQYIALELDFLNAFLFAIRNQEVPLLMVYA	186
QY	191	QAANLHLLLRDASIFGKEWGLSSSBIETFYNRQVERAGDYSYHCVKWYSTGLNLRGTN	250
Db	187	QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVWEYNTGLNSLRGTN	246
QY	251	AESWRYNQFRDMDTLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDATGTVHPHSFT	310
Db	247	AASWRYNQFRDLTLGLVLDLVALFPSYDTRTYPINTSAQLTREVYTDATGAT--GVNMA	304
QY	311	STTWYNNAPPSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTQYMMWGGHKLERTI	370
Db	305	SMWYNNAPPSAIEATAVIRSPHLLDFLEQLTIFSTSSRSASATHMYWRGHTIQSRPI	364
QY	371	GGTLNISTQGSTNTSINPVLTPFTSRDYRTESLAGLNF--LTQPVN-VPRVDFHWKFV	427
Db	365	GGGLNTSTHGSTNTSINPVLSPFSDVDVYTESYAGVLWGIYLEPIHGVPVTRFNRNP	424
QY	428	--THPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLISASHVKA	485
Db	425	QNTFERGTANYSQP--YESPGLQKDSSETLPPETTERPNYESYSHRLSHIGLISQSRVHV	483
QY	486	LVYSWTHRSADRTNTIEPNSITQIPLVKAFLNSGAAVVRGPGTGGDILRRNTGTFGD	545
Db	484	PVYSWTHRSADRTNTISSDSITQIPLVKSFLNSGTSVVSFGPGTGGDIIRTNVNGSVLS	543
QY	546	IRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNMGEDLDYKTFXTVG	605
Db	544	MGLNFNTSLQRYRVRVRYAASQTMVLRVTVGSTTFDQGFPSMTSANEISLTSQSRFAE	603
QY	606	FTTFFSLDVGSTFTTIGAWNFSSGNEVIIDRIEFVPEVVEYAEYDFEKAQKVTALFTS	665
Db	604	FPVGISASGSO--TAGISISNAGROTFHFKEIFIPITATFEAEYDLERAQEAVALFTN	662
QY	666	TNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEPVYKAKQLHIERNM	718
Db	663	TNPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDEKRELEKVKYAKRLSDERNL	715

RESULT 11

US-10-614-524-2  
 ; Sequence 2, Application US/10614524  
 ; Publication No. US20040016020A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arnaut, Greta  
 ; APPLICANT: Boets, Annemie  
 ; APPLICANT: Damme, Nicole  
 ; APPLICANT: Mathieu, Eva

; APPLICANT: Vanneste, Stijn  
 ; APPLICANT: Van Rie, Jeroen  
 ; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.  
 ; FILE REFERENCE: NEWBTSUS2  
 ; CURRENT APPLICATION NUMBER: US/10/614,524  
 ; CURRENT FILING DATE: 2003-07-08  
 ; PRIOR APPLICATION NUMBER: US/09/739,243  
 ; PRIOR FILING DATE: 2000-12-19  
 ; PRIOR APPLICATION NUMBER: 60/173387  
 ; PRIOR FILING DATE: 1999-12-28  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-614-524-2

Query Match 55.6%; Score 2085.5; DB 15; Length 1228;  
 Best Local Similarity 59.0%; Pred. No. 4.9e-165;  
 Matches 421; Conservative 98; Mismatches 183; Indels 11; Gaps 8;

QY	13	SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPVSASTIQTGIGIAGKI	70
Db	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI	66
QY	71	LGTGVFPAGQVAVSLYFIFELGKPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG	130
Db	67	LGVLGVFPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLNQITENARNTALARLOG	126
QY	131	LGDAVAVHDSLESWGNRNTRARSVVKSOYIALELMFVKQLPSPAVSGEEVPLPIYA	190
Db	127	LGDSFRAYQOQSLDWNLRDARTSRVLYTQYIALELDFLNAFLFAIRNQEVPLLMVYA	186
QY	191	QAANLHLLLRDASIFGKEWGLSSSBIETFYNRQVERAGDYSYHCVKWYSTGLNLRGTN	250
Db	187	QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVWEYNTGLNSLRGTN	246
QY	251	AESWRYNQFRDMDTLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDATGTVHPHSFT	310
Db	247	AASWRYNQFRDLTLGLVLDLVALFPSYDTRTYPINTSAQLTREVYTDATGAT--GVNMA	304
QY	311	STTWYNNAPPSAIEAAVVRNPHLLDFLEQVTIYSLLRWSNTQYMMWGGHKLERTI	370
Db	305	SMWYNNAPPSAIEATAVIRSPHLLDFLEQLTIFSTSSRSASATHMYWRGHTIQSRPI	364
QY	371	GGTLNISTQGSTNTSINPVLTPFTSRDYRTESLAGLNF--LTQPVN-VPRVDFHWKFV	427
Db	365	GGGLNTSTHGSTNTSINPVLSPFSDVDVYTESYAGVLWGIYLEPIHGVPVTRFNRNP	424
QY	428	--THPIASDNFYYPGAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLISASHVKA	485
Db	425	QNTFERGTANYSQP--YESPGLQKDSSETLPPETTERPNYESYSHRLSHIGLISQSRVHV	483
QY	486	LVYSWTHRSADRTNTIEPNSITQIPLVKAFLNSGAAVVRGPGTGGDILRRNTGTFGD	545
Db	484	PVYSWTHRSADRTNTISSDSITQIPLVKSFLNSGTSVVSFGPGTGGDIIRTNVNGSVLS	543
QY	546	IRVNIINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATNMGEDLDYKTFXTVG	605
Db	544	MGLNFNTSLQRYRVRVRYAASQTMVLRVTVGSTTFDQGFPSMTSANEISLTSQSRFAE	603
QY	606	FTTFFSLDVGSTFTTIGAWNFSSGNEVIIDRIEFVPEVVEYAEYDFEKAQKVTALFTS	665
Db	604	FPVGISASGSO--TAGISISNAGROTFHFKEIFIPITATFEAEYDLERAQEAVALFTN	662
QY	666	TNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEPVYKAKQLHIERNM	718
Db	663	TNPRRLKTDVTDYHIDQVSNLVACLSDDEFCLDEKRELEKVKYAKRLSDERNL	715

RESULT 12

US-09-826-660-25

Sequence 25, Application US/09826660  
Patent No. US20010026940A1  
GENERAL INFORMATION:  
APPLICANT: Cardineau, Guy A.  
APPLICANT: Stelman, Steven J.  
APPLICANT: Narva, Kenneth E.  
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
FILE REFERENCE: MA-714XC2D1  
CURRENT APPLICATION NUMBER: US/09/826,660  
CURRENT FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 09/178,252  
PRIOR FILING DATE: 1998-10-23  
PRIOR APPLICATION NUMBER: 60/065,215  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/076,445  
PRIOR FILING DATE: 1998-03-02  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 25  
LENGTH: 643  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-09-826-660-25

Query Match 50.7%; Score 1902; DB 9; Length 643;  
Best Local Similarity 57.2%; Pred. No. 4.2e-150;  
Matches 369; Conservative 100; Mismatches 161; Indels 14; Gaps 4;  
QY 13 SSNAKVDKISTDSLN-----ETDELQNHEDCLMSEYENVEPVSASTIQTGIG 65  
DB 7 NENEIINALSIPAVNSHSAQNLSTDAI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61  
QY 66 IAGKILGTGVPAGQVASYLFIILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125  
DB 62 IAGRLGLVGVPPAGQVASYLFIILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 121  
QY 126 TDLKGLGDALAVYHDSLSWVGNRNTRARSVVKSYQVIALLELMFVQKLSFVSGEEVPL 185  
DB 122 ARLOGLGNFRVQOQSLDLEWLENDRTDARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPL 181  
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNQVERAGDYSHCVKWTSTGLNN 245  
DB 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYVERQVEKTRYSYDCARWNTGLNN 241  
QY 246 LRGTAESVRYNQFRDRTMLVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDAGTVP 305  
DB 242 LRGTAESVRYNQFRDRTMLVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDAGTVP 301  
QY 306 HPSFTSTTWNNAAPSFAIEAAVVRPHLLDFLEQVTIYLSLSWSNTQYMMNMGHKL 365  
DB 302 PSGFASNTNPNNAAPSFAIEAAVVRPHLLDFLEQVTIYLSLSWSNTQYMMNMGHKL 361  
QY 366 EFRITGGTINISTOGSTNTSINPVLPTSRDVRVRESLAGNLFLTPQVYV-VRVDPEW 424  
DB 362 ESRTIRGSLSTHGTNTSINPVLPTSRDVRVRESLAGNLFLTPQVYV-VRVDPEW 421  
QY 425 KFTVTHPIASDNFYPGYAGIGTQDSENELPPEATGQPNYESYHRLSHIGLISASHVK 484  
DB 422 RNPLNLSRGLLYTIGYGVGTQLFDSLETLPETTERPNYESYHRLSHIRLSGNTLR 481  
QY 485 ALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTWTFG 544  
DB 482 APVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTWTFG 541  
QY 545 DIRVNIINPPFAQRVRYRYASTTDLQPHTSINGKAINQGNFSAATNMRGDDLYKTFXTV 604  
DB 542 SMGLNFNTSLQRYRVRYRYASTTDLQPHTSINGKAINQGNFSAATNMRGDDLYKTFXTV 601  
QY 605 GFTTFFSLDDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYE 647  
DB 602 EFPVGTASGSQ-TAGISISNAGRQTFFHDKIEFIPITATLE 643

RESULT 13  
US-10-089-678-1  
Sequence 1, Application US/10089678  
Publication No. US20030017967A1  
GENERAL INFORMATION:  
APPLICANT: ASANO, Shinichiro  
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN  
FILE REFERENCE: Q68921  
CURRENT APPLICATION NUMBER: US/10/089,678  
CURRENT FILING DATE: 2002-05-02  
PRIOR APPLICATION NUMBER: JP 2000-236140  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: PCT/JP01/06660  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1167  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-10-089-678-1  
Query Match 45.6%; Score 1708; DB 14; Length 1167;  
Best Local Similarity 47.4%; Pred. No. 1.9e-133;  
Matches 357; Conservative 126; Mismatches 222; Indels 48; Gaps 11;  
QY 1 MKLKQDKHQ---SFSSNAKVDKISTDSLNKEDTIELQNHEDCLMSEYE-----NV 51  
DB 1 MSPNNQNEVEILDASSSTSVSDNSVRYPLANDQTTLLQNNMYKDYLRMSEGENPELFGNP 60  
QY 52 EPPVSASTIQTGIGIAGKILGTGVPAGQVASYLFIILGELWPKGNK-NOWEIFNEHVEE 110  
DB 61 ETFISSSTVQTGIGIAGKILGTGVPAGQVASYLFIILGELWPKGNK-NOWEIFNEHVEE 120  
QY 111 IINQKISTYARNKALTDLKGGLDALAVYHDSLSWVGNRNTRARSVVKSYQVIALLELMFV 170  
DB 121 LIDQKITDSVRKKTALAGLQGLDGLDYQKSLKQWLENRNDTRARSVVVYQYIALELDFV 180  
QY 171 QKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNQVERAGD 230  
DB 181 AKIPFAISQCEVEPLLSVYAQAANLHLLLRDASIFGAEWGTPTGEISTFYDRQVTRTAQ 240  
QY 231 YSYHCVKWTSTGLNLRGTAESVRYNQFRDRTMLVLDLVALFPSYDTQMPYPIKTTA 290  
DB 241 YSDYCVKWTSTGLNLRGTAESVRYNQFRDRTMLVLDLVALFPSYDTQMPYPIKTTA 300  
QY 291 LTREYVTDAGTVPHPSTSTTWNNAAPSFAIEAAVVRPHLLDFLEQVTIYLSLS- 349  
DB 301 LTREYVTDPIVNEETSGGFCRRWSLNSDISFSEVESAVIRSPHLPDILSEIEFYTRAG 360  
QY 350 -RWSNTQYMMNMGHKLERTIGTGLNISTOGSTNTSINPVLPTSRDVRVRESLAGNL-AGL 407  
DB 361 LPLNTEYLFYVWGHISIKYKNTNASSALERNYGTITSNKIKYVDLANKDIFQVRSILGADL 420  
QY 408, NLFLTPVAVPRVDFHVKFVTHPIASDNFYPGYAGIG-----TQDQSEN 453  
DB 421 ANYYAQVYGPYASF-----TLDDKN---TGSGVGGFTYKPHHTMQVCTQNTVID 470  
QY 454 ELPPRATGQPNYESYHRLSHIGLIS-----ASHVKALVYSWTHRSADRTNTEPNS 505  
DB 471 EIPPE--NEPLSRGYSHRUSHITSYFSKKNASSPARTGNLPVFAWTHRSADRTNTEPNS 528  
QY 506 ITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGFGDIRVNIINPPFAQRVRYRYA 565  
DB 529 ITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGFGDIRVNIINPPFAQRVRYRYA 588  
QY 566 STTDLOFHTSINGKAINQGNFSAATNMRGDDLYKTFXTVFTTTPPSLDDVQSTFTIGAWN 625  
DB 589 STTNLRFLVTSIGTRIYSINVNKTMKGGDLTFTFLATIGTAFTSNYSDSLTVGADS 648

QY 626 FSSGNEVYIDRIEFVPEVYEAEDFEKAQEKVYALFTSTNPRGLKTDVYKHIDQVSN 685  
 Db 649 FASGGEVYVDKPELIPNATPEAEEDLDVAKAVNGLFSTSKD-ALQTSVTDYQVQAAAN 707  
 QY 686 LVESLSDEYFDLDEKRELPEIVKYAKOLHIERNM 718  
 Db 708 LVECLSDLYPNEKRLMLWDVAKELVQARNL 740

RESULT 14  
 US-10-428-961-6  
 ; Sequence 6, Application US/10428961  
 ; Publication No. US20030237111A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baum, James A.  
 ; APPLICANT: Chu, Chih-Rei  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Gilmer, Amy J.  
 ; APPLICANT: Ruper, Mark J.  
 ; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
 ; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
 ; FILE REFERENCE: MECO201-1  
 ; CURRENT APPLICATION NUMBER: US/10/428,961  
 ; CURRENT FILING DATE: 2003-05-02  
 ; PRIOR APPLICATION NUMBER: 09/661,322  
 ; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 6  
 ; LENGTH: 653  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-428-961-6

Query Match 44.2%; Score 1658; DB 14; Length 653;  
 Best Local Similarity 51.3%; Pred. No. 1.2e-129;  
 Matches 345; Conservative 104; Mismatches 175; Indels 48; Gaps 15;

QY 13 SNAKVDKISTSLKN---ETDIELQNIHEDCLKMSYENVEPVFSASTIQTGIGTAGK 69  
 Db 2 NENEIINALSIPAVNSHSAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINAGR 60  
 QY 70 ILGTLGVPPFAGVASYFVLGELWPKGNQWEIPMEHVVEIINQKISTYARNKALTDLK 129  
 Db 61 ILGVLGVPPFAGVASYFVLGELWPKGNQWEIPMEHVVEIINQKISTYARNKALTDLK 120  
 QY 130 GLGDALAVYHDSLEWYGNRNTRARSVVKSYIALELMFVQKLPFAVSGEVPVLLPIY 189  
 Db 121 GLGRGYRSYQQALETWLDNRDARSIIILERYVALELDITTAIPLFIRNEEVPLLMVY 180  
 QY 190 AQAAHLHLLLRDASIPGKWLSSSEISTFYNROVERAGDYSYHCVKWSYSTGLNNLRGT 249  
 Db 181 AQAAHLHLLLRDASIPGKWLSSSEISTFYNROVERAGDYSYHCVKWSYSTGLNNLRGT 240  
 QY 250 NAEWVYRNOFRDMLVLDLVALPSPYDTOMYFIKTTAQLTEVYTDAGTVHPHPSF 309  
 Db 241 NAEWVYRNOFRDMLVLDLVALPSPYDTOMYFIKTTAQLTEVYTDAGTVHPHPSF 300  
 QY 310 TSTWYNNAPSFSAEAAVVRNPHLLDFLEQVTTISLRSWNTQYNNWNGHKLERT 369  
 Db 301 ASTWYNNAPSFSAEAAVVRNPHLLDFLEQVTTISLRSWNTQYNNWNGHKLERT 360  
 QY 370 IGTGLNSTQGST-NTSINPVTLPF-TSRDYRTESLAGNLFITQPVN-VPRVDFHMKF 426  
 Db 361 IGTGLNSTQGST-NTSINPVTLPF-TSRDYRTESLAGNLFITQPVN-VPRVDFHMKF 418  
 QY 427 VTHPIASDNFYYP-----GYAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIG-- 476  
 Db 419 IYLRIFMKEAPLPTVNRIRLGFNVLIOKLNHYHQK-----QQNDQIMNHIVIDISYR 470  
 QY 477 LISASHVKALVYSWTHRSADRTNTIENPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILR 536

Db 471 LIIGNTLRAPVYSWTHRSADRTNTIGNRIITQIPAVKGRFLFNG-SVISGFGFTGDDVVR 529  
 QY 537 -RTWGTGF---GDIRVNIN-PFPAQVRVRIRYASTIDLOHTSINGKALNQCNSATWVN 591  
 Db 530 LNRNNGNIQNRGYEIVPIQFTSTSTRYVRVRYASVTSIELNVNLGNSSTFTNTLPATAA 589  
 QY 592 RGEDLDYKTFXTVGFTTTPFSLLDVQSTFT-----IGANFSSNGNEVYIDRIEFVPEVT 645  
 Db 590 SLNLIQ-----SGDFGYVEINNAFTSATGNIVGARNFSANAEEVIIDRFEFIPVTAT 640  
 QY 646 YEAEYDFEKAQE 657  
 Db 641 FEVEYDLERAQK 652

RESULT 15  
 US-10-782-141-16  
 ; Sequence 16, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10/782,141  
 ; CURRENT FILING DATE: 2004-02-20  
 ; PRIOR APPLICATION NUMBER: 60/448,632  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16  
 ; LENGTH: 1157  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-16

Query Match 44.1%; Score 1652; DB 17; Length 1157;  
 Best Local Similarity 48.8%; Pred. No. 9e-129;  
 Matches 369; Conservative 100; Mismatches 229; Indels 58; Gaps 19;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDS----LKNETDIELQNIHEDCLKMSYE-----N 50  
 Db 1 MSPNNQNEYIIDIATPST-SVSSDSNRYPFANEPTDALQNNYKDYLMKSGGENPELFGN 59  
 QY 51 VEPFVSASTIQTGIGIAGKILGTGVPPFAGVASYFVLGELWP-KGKNQWEIPMEHVE 109  
 Db 60 PETPISSTIQTGIGIAGKILGTGVPPFAGVASYFVLGELWP-KGKNQWEIPMEHVE 119  
 QY 110 EITNQKISTYARNKALTDLKGLGDALAVYHDSLEWYGNRNTRARSVVKSYIALELMF 169  
 Db 120 ELVDQKIEKVYKDKALAEKGLGNALDVYQOSLEDWLENRDARTSRVSVNQFIADLNF 179  
 QY 170 VQKLPSFAVSGEVPVLLPIYAAQANLHLLLRDASIFGKWLSSSEISTFYNROVERAG 229  
 Db 180 VSSIPFSAVSGHEVLLLAQVAVNHLHLLLRDASIFGKWLSSSEISTFYNROVERAG 239  
 QY 230 DYSYHCVKWSYSTGLNNLRGTNAESWYRNYNQFRDMLVLDLVALPSPYDTOMYFIKTTA 289  
 Db 240 EYSDYCVKWSYKIGLDKLGTTSKSWLNHYHQFRREMTLLVLDLVALFPNYTHMYPETTA 299  
 QY 290 QLTREYVYTDAGTVHPHPSFTST---TWYNNAPSFSAEAAVVRNPHLLDFLEQVTTIY 345  
 Db 300 QLTREYVYTDAGTVHPHPSFTST---TWYNNAPSFSAEAAVVRNPHLLDFLEQVTTIY 355  
 QY 346 SLLSR-----WSNTQYNNWNGHKLERT-----TIGTGLNSTQGSTNTSINPVTLPFTSR 396  
 Db 356 T--SRGGITLNDAYINYSWGHSLTKYRTADSTVITYTANYGRITSEKNS-----FALEDR 408



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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3033 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MKLKNQDHQSPSSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 68318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCRTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3718.5	99.2	719	3	US-08-286-870A-8
2	3439	91.7	710	4	US-09-661-322A-42
3	3360.5	89.6	648	3	US-08-286-870A-4
4	3358.5	89.6	719	2	US-09-003-217-2
5	3356.5	89.5	719	3	US-09-218-942-2
6	2778.5	74.1	535	3	US-08-286-870A-6
7	2415	64.4	1229	1	US-08-100-709-4
8	2415	64.4	1229	1	US-08-176-865-4
9	2415	64.4	1229	1	US-08-474-038-4
10	2415	64.4	1229	2	US-08-779-046-4
11	2415	64.4	1229	2	US-08-881-340-4
12	2319	61.9	488	1	US-08-448-170-10
13	2319	61.9	488	3	US-08-961-803-10
14	2236	59.6	1207	1	US-07-951-715A-7
15	2236	59.6	1207	2	US-08-459-448A-7
16	2236	59.6	1207	3	US-08-459-595A-7
17	2236	59.6	1207	3	US-08-459-504B-7
18	2236	59.6	1207	3	US-08-459-444-7
19	2236	59.6	1207	3	US-09-053-549-8
20	2236	59.6	1207	3	US-09-547-422-7
21	2236	59.6	1207	4	US-09-988-462-7
22	2235	59.6	1227	3	US-09-053-549-2
23	2165	57.7	1227	1	US-08-448-170-8
24	2165	57.7	1227	3	US-08-961-803-9
25	2156	57.5	1227	4	US-09-661-322A-63
26	2141	57.1	1186	3	US-09-178-252-23
27	2141	57.1	1186	4	US-09-826-660-23

28	2085.5	55.6	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1902	50.7	643	3	US-09-178-252-25	Sequence 25, Appl
30	1902	50.7	643	4	US-09-826-660-25	Sequence 25, Appl
31	1891	50.4	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1658	44.2	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1652	44.1	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1652	44.1	1157	1	US-07-812-180A-2	Sequence 2, Appl
35	1652	44.1	1157	1	US-08-315-468-2	Sequence 2, Appl
36	1652	44.1	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1482	39.5	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1480.5	39.5	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1480.5	39.5	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1480.5	39.5	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1480.5	39.5	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1480.5	39.5	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1480.5	39.5	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1474	39.3	1156	3	US-09-002-285-72	Sequence 72, Appl
45	1474	39.3	1156	4	US-09-589-477-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPEIT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 03-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

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Query Match      99.2%; Score 3718.5; DB 3; Length 719;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MCLKNODKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLMSEYENVEPVSASTI 60
DB 1 MCLKNODKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLMSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFVILGELWPKGKQWEIFMEHVBEIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFVILGELWPKGKQWEIFMEHVBEIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRVYQFRDMTLMVLDLVALPFSYDTQMPYPIKTTAQLTREYVTDI 300
DB 241 TGLNLRGTNAESWVRVYQFRDMTLMVLDLVALPFSYDTQMPYPIKTTAQLTREYVTDI 300

QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360

QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSDVYRTESLAGNLFQTQVNGVPR 419
DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSDVYRTESLAGNLFQTQVNGVPR 419

QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 479
DB 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 479

QY 480 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539
DB 480 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539

QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600

QY 600 TFXTVGFTTFFSLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659
DB 600 TFXTVGFTTFFSLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659

QY 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
DB 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

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RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compositions and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

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; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match      91.7%; Score 3439; DB 4; Length 710;
Best Local Similarity 91.9%; Pred. No. 1.1e-299;
Matches 661; Conservative 15; Mismatches 33; Indels 10; Gaps 2;

QY 1 MCLKNODKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLMSEYENVEPVSASTI 60
DB 1 MCLKNODKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLMSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFVILGELWPKGKQWEIFMEHVBEIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFVILGELWPKGKQWEIFMEHVBEIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRVYQFRDMTLMVLDLVALPFSYDTQMPYPIKTTAQLTREYVTDI 300
DB 241 TGLNLRGTNAESWVRVYQFRDMTLMVLDLVALPFSYDTQMPYPIKTTAQLTREYVTDI 300

QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360

QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSDVYRTESLAGNLFQTQVNGVPR 419
DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSDVYRTESLAGNLFQTQVNGVPR 419

QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 479
DB 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 479

QY 480 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539
DB 480 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539

QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 591
DB 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 591

QY 600 TFXTVGFTTFFSLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659
DB 600 TFXTVGFTTFFSLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659

QY 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718
DB 660 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718

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RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENN, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN

```

ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 89.6%; Score 3360.5; DB 3; Length 648;  
Best Local Similarity 99.4%; Pred. No. 1e-292;  
Matches 644; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K V S E Y E N V E F V S A S T I 60  
D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K V S E Y E N V E F V S A S T I 60  
QY 61 Q T G I G I A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120  
D b 61 Q T G I G I A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120  
QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
D b 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
QY 181 E E V P L L P I Y A Q A A N L H L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240  
D b 181 E E V P L L P I Y A Q A A N L H L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240  
QY 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D I V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
D b 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D I V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
QY 301 G T V H P H S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T T Y S L S R W S N T Q Y N M W 360  
D b 301 G T V H P H S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T T Y S L S R W S N T Q Y N M W 360  
QY 361 G G H K L E F T I G T L N I S T Q S T N T S I N P V T L P F T S R D V R T E S L A G L N L F L T O P V N - V P R 419  
D b 361 G G H K L E F T I G T L N I S T Q S T N T S I N P V T L P F T S R D V R T E S L A G L N L F L T O P V N G V P R 420  
QY 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q N Y E S Y S H R L S H I G L I S 479  
D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q N Y E S Y S H R L S H I G L I S 480

QY 480 A S H V K A L V T S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G F T G G D I L R R T N 539  
D b 481 A S H V K A L V T S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G F T G G D I L R R T N 540  
QY 540 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T N R G E D L D Y K 599  
D b 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T N R G E D L D Y K 600  
QY 600 T F X T V G F T T P F S L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E 647  
D b 601 T F R T V G F T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E 648  
RESULT 4  
US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5986177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,217  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 89.6%; Score 3358.5; DB 2; Length 719;  
Best Local Similarity 89.6%; Pred. No. 1.9e-292;  
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
D b 1 M K L K N P D K H Q T L S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H S I D P F V S A S T I 60  
QY 61 Q T G I G I A K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120  
D b 61 Q T G I G I A K I L G T L G V P P P G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E A I I N R K I S T Y A 120  
QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
D b 121 R N K A L T D L K G L G D A L A V Y H S L E S W G N R N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
QY 181 E E V P L L P I Y A Q A A N L H L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S H C V K W Y S 240

Db 181 EVVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNQVERTRDYSYHCVKWN 240  
Qy 241 TGLNLRGTNAESWVRNQFRDMTLMVLVALFSDYDQMPYPIKTTAQLTREVYTDI 300  
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Db 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVN - VPR 420  
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Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENEPPEATGQPNYESYSHRSHIGLIS 480  
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Db 541 SGTGHIRVNINPFPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600  
Qy 600 TFXTVGFTTFFSLLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659  
Db 601 TFRVTVGFTTFFSLLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
Qy 660 TALFTSTNPRGLKTDVQHYHIDQVSNLVSLSDELVDKRELFEIVKYAKQIHERNM 718  
Db 661 TALFTSTNPRGLKTDVQHYHIDQVSNLVSLSDELVDKRELFEIVKYAKQIHERNM 719

RESULT 5  
US-09-218-942-2  
; Sequence 2, Application US/09218942  
; Patent No. 6232439  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia  
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
; FILE REFERENCE: Crv11  
; CURRENT APPLICATION NUMBER: US/09/218,942  
; EARLIER FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/035,361  
; EARLIER FILING DATE: 1997-01-10  
; EARLIER APPLICATION NUMBER: 09/003,217  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-09-218-942-2

Query Match 89.5%; Score 3356.5; DB 3; Length 719;  
Best Local Similarity 89.6%; Pred. No. 2.8e-292;  
Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;  
Qy 1 MGLKNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLNKESEYENVEPVSASTI 60  
Db 1 MGLKNPDKHQTLSSNAKVDKIATDSLKNETDIELKNMNEVYLRNSESHEIDPVSASTI 60  
Qy 61 QTGIGIAGKILGTGVPAGQVSLYFGLGELWPKGNKOWEIFMEHVEIINOKISTYA 120  
Db 61 QTGIGIAGKILGTGVPAGQVSLYFGLGELWPKGNKOWEIFMEHVEIINOKISTYA 120  
Qy 121 RNKALTDLKGLDALAVYHDSLSWGNRNNTRARSVVKVSOYIALELMFVQKLPFAVSG 180  
Db 121 RNKALTDLKGLDALAVYHDSLSWGNRNNTRARSVVKVSOYIALELMFVQKLPFAVSG 180

Qy 181 EVVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNQVERAGDYSYHCVKWNYS 240  
Db 181 EVVPLPIYAQAANLHLLLRDASIFKNGGLSASEISTFYNQVERTRDYSYHCVKWN 240  
Qy 241 TGLNLRGTNAESWVRNQFRDMTLMVLVALFSDYDQMPYPIKTTAQLTREVYTDI 300  
Db 241 TGLNLRGTNAESWVRNQFRDMTLMVLVALFSDYDQMPYPIKTTAQLTREVYTDI 300  
Qy 301 GTVHPHPSSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMNW 360  
Db 301 GTVHPHPSSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMNW 360  
Qy 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPV - NVPR 419  
Db 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPV - NVPR 420  
Qy 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENEPPEATGQPNYESYSHRSHIGLIS 479  
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENEPPEATGQPNYESYSHRSHIGLIS 480  
Qy 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539  
Db 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTK 540  
Qy 540 TGFQDIRVNINPFPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 599  
Db 541 SGTGHIRVNINPFPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600  
Qy 600 TFXTVGFTTFFSLLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659  
Db 601 TFRVTVGFTTFFSLLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
Qy 660 TALFTSTNPRGLKTDVQHYHIDQVSNLVSLSDELVDKRELFEIVKYAKQIHERNM 718  
Db 661 TALFTSTNPRGLKTDVQHYHIDQVSNLVSLSDELVDKRELFEIVKYAKQIHERNM 719

RESULT 6  
US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENN, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-6

Query Match 74.1%; Score 2778.5; DB 3; Length 535;  
Best Local Similarity 99.6%; Pred. No. 1.4e-240;  
Matches 533; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKQKQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKQKQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVVKSYQYIALELMFVQKLPSPAVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLESWVGNNRNNTRARSVVKSYQYIALELMFVQKLPSPAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWS 240

QY 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPPSYDTQMPYIKTTAQLTREVYTDI 300  
DB 241 TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPPSYDTQMPYIKTTAQLTREVYTDI 300

QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMW 360

QY 361 GGHKLEPRTIGTNTSTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVN-VPR 419  
DB 361 GGHKLEPRTIGTNTSTQSTNTSINPVTLPFTSRDVRTESLAGNLFITQPVN-VPR 420

QY 420 VDFHKKFVTHPIASDNFYYPGVAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 479  
DB 421 VDFHKKFVTHPIASDNFYYPGVAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480

QY 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDI 534  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDI 535

RESULT 7  
US-08-100-709-4  
Sequence 4, Application US/08100709  
Patent No. 5323687  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CYVET4 AND CYVET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia

STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/100,709  
FILING DATE: 19930729  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-100-709-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDSLK-N-ETDIELQ-NINHEDECLKMSYENVEPVSASTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPTVSNPSTQMNLSPADIEDSLCAEVNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTGVFPAGQVASYLSFILGELWPKQKQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
DB 67 LGVLGVFPAGQVASYLSFILGELWPKQKQWEIFMEHVEEIIINQKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLESWVGNNRNNTRARSVVKSYQYIALELMFVQKLPSPAVSGEVPPLPIYA 190  
DB 127 LGRGVRSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLRIRNEEVPPLMVA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWSNTGLNLRGTN 250  
DB 187 QAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSYHCVKWSNTGLNLRGTN 246

QY 251 AESWRYNQFRDMLVLDLVALFPPSYDTQMPYIKTTAQLTREVYTDIQTGIGIAGKI 310  
DB 247 AESWRYNQFRDMLVLDLVALFPPSYDTQMPYIKTTAQLTREVYTDIQTGIGIAGKI 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMWGCHKLEFRTI 370  
DB 307 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYNNMWGCHKLEFRTI 366

QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVN-VPRVDFHKKFVT 428  
DB 367 GGTINISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFITQPVN-VPRVDFHKKFVT 422

QY 429 HPIASDNFYYPG-----YAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 481  
DB 423 --INPQNIYERGATTYSQYQGVIGIQLFDSSETLPETTERPNYESYSHRSLHIGLIS 480

QY 482 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRRNTG 541  
DB 481 TLRAPIVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRRNTG 540

QY 542 TFGDIRVINPPTAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSAATNRRGEDLDYKTF 601  
DB 541 TFGDIRVINPPTAQRVRYRIRYASTTDLQPHTSINGKAINQGNFSAATNRRGEDLDYKTF 600

QY 602 XTVCFTTTPSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTA 661  
DB 601 RTAGFSTPFLNAQSTFTLGAQSFSN-QEVYIDRIEFVPEVTEAEYDFEKAQKVTA 659

QY 662 LFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVVKYAKQLHIERNM 718  
DB 660 LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDFCLEKRELFVVKYAKRLSDERNL 716

RESULT 8  
US-08-176-865-4  
; Sequence 4, Application US/08176865  
; Patent No. 5616319  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/176,865  
; FILING DATE: 30-DEC-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egoif, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-176-865-4

Query Match 54.4%; Score 2415; DB 1; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPVSNPSTQNLSPDARIEDSLCAEVANNIDPFSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
DB 67 LGVLGVFPAGQLASFSYFLVGLNWPGRDPWEIFLEHVEQLRQVVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLSRSGVNRNTRARSVVKSOYIALELMFVQKLPSFAVSGEEVPLLPPIYA 190  
DB 127 LGRGYRSYQQALETWLDNRNDARSRIILERYVALELDITTAIFLRIRNEEVPLLMVYA 186

QY 191 QAAHLHLRLDRASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYSTGLNLRGTN 250  
DB 187 QAAHLHLRLDRASLFGSEWGMASSDVNYQYQEQIRYTEYSNHCVCWYNTGLNLRGTN 246

QY 251 AESWVRYNQFRDRLTGLVLDLVALFPSPDYDTQMPYIKTTAQITREYVTDALGTGVHPSPFT 310

DB 247 AESWLRYNQFRDRLTGLVLDLVALFPSPDYDTQMPYIKTTAQITREYVTDALGTGVHPSPFT 306

QY 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYISLLSRWSNTQYMMNWGGHKLFRPI 370  
DB 307 STWNFNNAAPSFAIEAIFRPPHLLDFPEQVTIYISASRWSSTQHMNTVWVGHRLNFRPI 366

QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVTESLAGLNLFLETPVN-VPRVDFHWKFTV 428  
DB 367 GGTLNISTQGLTNNTSINPVTLPFTSRDVTESLAGLNLFLETPVN-VPRVDFHWKFTV 422

QY 429 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLISAS 481  
DB 423 --INPQNIYERGATTYSQPYQGVGIQFDSETELPETTERPNYESYSHRLSHIGLIGN 480

QY 482 HVKALVYSWTHRSADRTNTIBPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTNTG 541  
DB 481 TLRAPVYSWTHRSADRTNTIBPNSITQIPLVKALNLHSGVTVVGGPGFTGGDIILRTNTG 540

QY 542 TFGDIRVNIINPPFAQRYRIRYASVTTDLQFHTSINGKAINQGNFSATVNRGDELDTYKTF 601  
DB 541 TFGDIRVNIINPPFAQRYRIRYASVTTDLQFHTSINGKAINQGNFSATVNRGDELDTYKTF 600

QY 602 XTGVGTTTPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTA 661  
DB 601 RTAGESTPFPFLNAQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTA 659

QY 662 LFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVVKYAKQLHIERNM 718  
DB 660 LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDFCLEKRELFVVKYAKRLSDERNL 716

RESULT 9  
US-08-474-038-4  
; Sequence 4, Application US/08474038  
; Patent No. 5679343  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,038  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/176,865  
; FILING DATE: 30-DEC-1993  
; APPLICATION NUMBER: US 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egoif, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-038-4

Query Match 64.4%; Score 2415; DB 1; Length 1229;  
Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTQTGTGIGIAGKI 70  
Db 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCVAEVNNDPFSVASTVGTGINIAGRI 66  
QY 71 LGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
Db 67 LGVLGVPPAGQLASFYSLVGLWPGSDPWEIFLEHVEQLIRQVVTENTRTAIARLEG 126  
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSGEVEPLPIYA 190  
Db 127 LGRGYRSYQOALETWLDRNDARSILERYVALELDITTAIPLRIRNEEVPLLMVA 186  
QY 191 QAAHLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSYHCVKMYSTGLNNLRGTN 250  
Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCQVQWYNTGLNNLRGTN 246  
QY 251 AESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTQAQLTREYVTDAGTVHPHPSFT 310  
Db 247 AESWLRYNQFRDLTLGLVDLVALFPSYDTQMPYIKTQAQLTREYVTDAGTVHPHPSFT 306  
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMWGGHKLFRPTI 370  
Db 307 STWYNNAPSFSAIEAIFRPPHLLDFPEQLTIYSSASSRWSSTQHMNVVGHRLNFRPI 366  
QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLEQVNT-VPVRVDFHWKFVT 428  
Db 367 GGTINISTQGLTNTSINPVTLOFTSRDVRVYTESNAGTNILFTTPVNGVWARFNF- 422  
QY 429 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGPQNYESYSHRSLHIGLISAS 481  
Db 423 --INPQNIYERGATTYSQPYQGVIGLQFDSSETLPETTERPNYESYSHRSLHIGLIGN 480  
QY 482 HVKALVYSWTHRSADRNTIENSIQTQPLVKAFNLSSGAADVGGPFGTGGDILRRNTG 541  
Db 481 TLRAPVYSWTHRSADRNTIGPNRITQIPLVKALNLHSGVTVVGGPFGTGGDILRRNTG 540  
QY 542 TFGDIRVNPFPFAQRVVRIRYASTDLOFHTSNGKAINQGNFSATNWRGDELDTYKTF 601  
Db 541 TFGDIRLNVNPLSQRVVRIRYASTDLOFTRINGTTVYNGFSTRWNRGDNLEYSF 600  
QY 602 XTGVFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 661  
Db 601 RTAGFSTFENFLNAQSTFTLGAQSFN-QEYVIDRVEFVPAEVTFEAEYDLERACKAVNA 659  
QY 662 LFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
Db 660 LFTSTNPRRLKTDVTDYHIDQVSNMVACLSDDEFCLDEKRELFEKVKYAKRLSDERNL 716

## RESULT 10

US-08-779-046-4  
Sequence 4, Application US/08779046  
Patent No. 5854053

## GENERAL INFORMATION:

APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,046  
FILING DATE: 06-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/100,709  
FILING DATE: 29-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-779-046-4

Query Match 64.4%; Score 2415; DB 2; Length 1229;

Best Local Similarity 65.1%; Pred. No. 2.3e-207;

Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTQTGTGIGIAGKI 70  
Db 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCVAEVNNDPFSVASTVGTGINIAGRI 66  
QY 71 LGTLGVPPAGQVASYLFGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
Db 67 LGVLGVPPAGQLASFYSLVGLWPGSDPWEIFLEHVEQLIRQVVTENTRTAIARLEG 126  
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSGEVEPLPIYA 190  
Db 127 LGRGYRSYQOALETWLDRNDARSILERYVALELDITTAIPLRIRNEEVPLLMVA 186  
QY 191 QAAHLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSYHCVKMYSTGLNNLRGTN 250  
Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCQVQWYNTGLNNLRGTN 246  
QY 251 AESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTQAQLTREYVTDAGTVHPHPSFT 310  
Db 247 AESWLRYNQFRDLTLGLVDLVALFPSYDTQMPYIKTQAQLTREYVTDAGTVHPHPSFT 306  
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMWGGHKLFRPTI 370  
Db 307 STWYNNAPSFSAIEAIFRPPHLLDFPEQLTIYSSASSRWSSTQHMNVVGHRLNFRPI 366  
QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLEQVNT-VPVRVDFHWKFVT 428  
Db 367 GGTINISTQGLTNTSINPVTLOFTSRDVRVYTESNAGTNILFTTPVNGVWARFNF- 422  
QY 429 HPIASDNFYYPG-----YAGIGTQLQDSNELPPEATGPQNYESYSHRSLHIGLISAS 481  
Db 423 --INPQNIYERGATTYSQPYQGVIGLQFDSSETLPETTERPNYESYSHRSLHIGLIGN 480  
QY 482 HVKALVYSWTHRSADRNTIENSIQTQPLVKAFNLSSGAADVGGPFGTGGDILRRNTG 541  
Db 481 TLRAPVYSWTHRSADRNTIGPNRITQIPLVKALNLHSGVTVVGGPFGTGGDILRRNTG 540

QY 542 TFGDIRVNPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF 601  
 DB 541 TFGDIRLNVPLSQRVVRIRYASTTDLQFTRINGTTWIGNFSRTWNRGDNLEYSF 600  
 QY 602 XTGVFTTSPSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTA 661  
 DB 601 RTAGFSTPFNFNAQSTFTLGAQSFN-QEYVIDRVEFVPAEVTPEAEYDLERAKAVNA 659  
 QY 662 LFTSNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIKVYAKOLHIERNM 718  
 DB 660 LFTSNPRGLKTDVYHIDQVSNMVACLSDEFCLDEKRELFEIKVYAKRLSDERNL 716

RESULT 11  
 US-08-881-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-881-340-4

Query Match 64.4%; Score 2415; DB 2; Length 1229;  
 Best Local Similarity 65.1%; Pred. No. 2.3e-207;  
 Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCIKMEYENVEPFSASTIQTGTGIAGKI 70  
 DB 7 NENEINALSIPTVSNPSTQMNLSDPDARIEDSLCVAEWNIDPFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 130  
 DB 67 LGVLGVPPFAGQLASFYSFLVGLWPSGRDPWEIFLHVEQLIRQQVTENTTAIRLEG 126  
 QY 131 LGDALAVYHDSLSWVGNRNTRARSVVKVSYIALELMFVKLPSPFAVSGEEVPLPIYA 190

DB 127 LGRVRSYQOALETWLDRNDARSRIILERVVALELDITTAIPLFRIRNEEVPLLMVYA 186  
 QY 191 QAANLEHLLLRDASIFGKXEWGLSSSEISTFYNRQVERAGDYSHYCVKYSTGLNLRGTN 250  
 DB 187 QAANLEHLLLRDASLFGSEWGMASDVNQYQEQIRYTESYHNCVQWYNTGLNLRGTN 246  
 QY 251 AESWRYNQFRDNTLMVLDLVALFPSTOMYPIKTTAQLTREVYTDAGTGVHPPSFT 310  
 DB 247 AESWRYNQFRDNTLMVLDLVALFPSTOMYPIKTTAQLTREVYTDAGTGVHPPSFT 306  
 QY 311 STTWANNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRVSNTOYMMWGHKLEFRTI 370  
 DB 307 STTWANNAPSFSAIEAAVVRNPHLLDFLEQVITYSLLSRVSNTOYMMWGHKLEFRTI 366  
 QY 371 GGTNLNISTQST-NTSINPVTLPFTSRDVTRESLGLNLFITQPVN-VPRVDFHWKFTV 428  
 DB 367 GGTNLNISTQST-NTSINPVTLPFTSRDVTRESLGLNLFITQPVN-VPRVDFHWKFTV 422  
 QY 429 HPIASDNFYYPG-----YAGIGTQDQSENELPPPEATGQPNYESYSHRLSHIGLISAS 481  
 DB 423 --INPQNIYERGATYSQYQGVIGLQFDSSETLPPETTERPNYESYSHRLSHIGLIGN 480  
 QY 482 HVKALVYSWTHRSADRTNTEPNSTIQLPLVKAFNLSSGAAVVRGPGFTGGDILERTNTG 541  
 DB 481 TLRAVYSWTHRSADRTNTEPNSTIQLPLVKAFNLSSGAAVVRGPGFTGGDILERTNTG 540  
 QY 542 TFGDIRVNPFPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTF 601  
 DB 541 TFGDIRLNVPLSQRVVRIRYASTTDLQFTRINGTTWIGNFSRTWNRGDNLEYSF 600  
 QY 602 XTGVFTTSPSLDQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTA 661  
 DB 601 RTAGFSTPFNFNAQSTFTLGAQSFN-QEYVIDRVEFVPAEVTPEAEYDLERAKAVNA 659  
 QY 662 LFTSNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIKVYAKOLHIERNM 718  
 DB 660 LFTSNPRGLKTDVYHIDQVSNMVACLSDEFCLDEKRELFEIKVYAKRLSDERNL 716

RESULT 12  
 US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Stelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. P9158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA: US 07/759,247  
;; APPLICATION NUMBER: 13-SEPT-1991  
;; FILING DATE: 424  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Salwanchik, David R.  
;; REGISTRATION NUMBER: 31,794  
;; REFERENCE/DOCKET NUMBER: M/S 102D.C1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (904) 375-8100  
;; TELEFAX: (904) 372-5800  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-448-170-10

Query Match 61.9%; Score 2319; DB 1; Length 488;  
Best Local Similarity 89.3%; Pred. No. 2.1e-199;  
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
Db 1 MKSKQNMHQSLSNATVDKNTGSLNNTNTELQNFH-----EGIEPFVSASTI 51

QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 111

QY 121 RNKALTDKGLDALAVYHDSLESWGNRNNTNRASVVKSQYIALELMFVQKLPSPFVSG 180  
Db 112 RNKALADLKGDLALAVYHDSLESWGNRNNTNRASVVKSQYIALELMFVQKLPSPFVSG 171

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
Db 172 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 231

QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDI 300  
Db 232 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDI 291

QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
Db 292 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 351

QY 361 GGHKLEFRTIGTLNTSTQSTNTSINPVLPTFSRDVYRTESLAGLNLFLTPQVN-VPR 419  
Db 352 GGHKLEFRTIGTLNTSTQSTNTSINPVLPTFSRDVYRTESLAGLNLFLTPQVNGVPR 411

QY 420 VDFHWKFTHTPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
Db 412 VDFHWKFTHTPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471

QY 480 ASHVKALVYSWTHRSAD 496  
Db 472 ASHVKALVYSWTHRSAD 488

## RESULT 13

US-08-961-803-10  
; Sequence 10, Application US/08961803  
; Patent No. 6150589  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted  
; ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

;; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Jay M. Sanders  
;; STREET: 2421 N.W. 41st Street, Suite A-1  
;; CITY: Gainesville  
;; STATE: Florida  
;; COUNTRY: USA  
;; ZIP: 32606  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/961,803  
;; FILING DATE: 31-OCT-1997  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/069,902  
;; FILING DATE: 01-JUNE-1993  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/759,247  
;; FILING DATE: 13-SEPT-1991  
;; CLASSIFICATION: 800  
;; APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/448,170  
;; FILING DATE: 23-MAY-1995  
;; CLASSIFICATION: 800  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sanders, Jay M.  
;; REGISTRATION NUMBER: 39,355  
;; REFERENCE/DOCKET NUMBER: M/S 102DCD1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (352) 375-8100  
;; TELEFAX: (352) 372-5800  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 488 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-961-803-10

Query Match 61.9%; Score 2319; DB 3; Length 488;  
Best Local Similarity 89.3%; Pred. No. 2.1e-199;  
Matches 444; Conservative 13; Mismatches 30; Indels 10; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
Db 1 MKSKQNMHQSLSNATVDKNTGSLNNTNTELQNFH-----EGIEPFVSASTI 51

QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLSFILGELWPKGKQWEIFMEHVEEIIINQKISTYA 111

QY 121 RNKALTDKGLDALAVYHDSLESWGNRNNTNRASVVKSQYIALELMFVQKLPSPFVSG 180  
Db 112 RNKALADLKGDLALAVYHDSLESWGNRNNTNRASVVKSQYIALELMFVQKLPSPFVSG 171

QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
Db 172 BEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 231

QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDI 300  
Db 232 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDI 291

QY 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
Db 292 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 351

QY 361 GGHKLEFRITGGTINISQGSTNTSINPVTLPFTSDVYRTESLAGLNLFLTPQVN-VPR 419  
DB 352 GGHKLEFRITGGTINTSTQGSTNTSINPVTLPFTSDVYRTESLAGLNLFLTPQVNGVPR 411  
QY 420 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENEIPPEATGQPNYESYSHRSLSHIGLIS 479  
DB 412 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENEIPPEATGQPNYESYSHRSLSHIGLIS 471  
QY 480 ASHVKALVYSWTHRSAD 496  
DB 472 ASHVKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7

Query Match 59.6%; Score 2236; DB 1; Length 1207;

Best Local Similarity 63.9%; Pred. No. 2.6e-191;  
Matches 439; Conservative 78; Mismatches 156; Indels 14; Gaps 6;  
QY 40 EDCLKQSEVENVEPVSASTIQTGIGIAGKILGTLPVFPAGQVASYLSFELGELWPKGN 99  
DB 10 EDSCIAEGNNIDPVSASTVQTGINIAGRIILGVLGVFPAGQVASYLSFELGELWPKGRD 69  
QY 100 QWEIFMEHVEEIIQKISTYARNKALTDKLGLDALAYHDSLESWGNRNNTARSVVK 159  
DB 70 QWEIFLEHVEQLNQIITENARNATALAELQGLGDSFRAYQOSLEDWLENRDDARTSVLY 129  
QY 160 SQYIALELMFVQKLPSPFAVSGSEVPLPIYAQAANLHLLLRDASIFGKRWGLSSSEIST 219  
DB 130 TOYIALELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIOR 189  
QY 220 FYNROVERAGDYSYHCKWYSTGLNNLRGTNAESWVRYNQFRRDMLVLDLVALFPSSYD 279  
DB 190 YERQVTRTDYSDYCVEMYNITGLNSURGTNAASWVRYNQFRRDMLVLDLVALFPSSYD 249  
QY 280 TOMYPIKTTAQLTREVTDAIGTVHPHPSFTTWTYNNNAPSFSAEAAVVRNPHLLDFL 339  
DB 250 TRTYPINTSAQLTREVTDAIGAT--GYNMASMNWYNNNAPSFSAEAAAIRSPHLLDFL 307  
QY 340 EQVTIYSLRSWNTQYNNMWGCHKLBFTTIGTLNISTQGSTNTSINPVTLPFTSRDYY 399  
DB 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDYY 367  
QY 400 RTESLAGLNLF--LTQPVN-VPRVDFHWKFVTHP-----IASDNFYYPGAGIGTQLODS 451  
DB 368 RTESYAGVLLWGIYLEPHGVPTVRFNF--TNPQNTSDRGATANYSQP-YESPGQLKDS 423  
QY 452 ENELPPEATGQPNYESYSHRSLSHIGLISASHVKALVYSWTHRSADRTNTEPNSTQIPL 511  
DB 424 ETELPPEPPERPNYESYSHRSLSHIGLISQSRVNVVYVSWTHRSADRTNTEPNSTQIPL 483  
QY 512 VKAFNLSSGAAVVRGPGTGGDILRRNTGTGDIRVNVNPPFAQRYRVRIRYASTTDLQ 571  
DB 484 VKASELPQGTTVVRGPGTGGDILRRNTGTGDIRVNVNPPFAQRYRVRIRYASTTDLQ 543  
QY 572 PHTSINGKAINQGNFSATMNRGSDLDYKTXVGTFTPFSLDDVQSTFTIGAMNPFSSGNE 631  
DB 544 FVSRGGTTVNNFRFLRTMNSGDELKYNFVRRRAFTTPTFTQIODIIRTSIQGLSGNGE 603  
QY 632 VYIDRIEFPVVEVYEAEDYDFAEYDLEAQAQVKTALSTNPRGLKTDVKDYHIDQVSNLVESLS 691  
DB 604 VYIDKIEIIPVTATFEAEYDLEAQAQVKTALSTNPRGLKTDVKDYHIDQVSNLVESLS 663  
QY 692 DEFYLDKRELFEIVKYAKQLHIERNM 718  
DB 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-55

Perfect score: 3760

Sequence: 1 MKLKNQDKHQSPSSNAKVDK.....KRELFVIVKAYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3760	100.0	719	1 C1IA_BACTK	Q45752 bacillus th
2	3760	100.0	719	2 Q6X181	Q6X181 bacillus th
3	3760	100.0	719	2 AAP86782	AAP86782 bacillus
4	3755	99.9	719	2 Q3N3J5	Q9n3j5 bacillus th
5	3754	99.8	719	2 O85796	O85796 bacillus th
6	3752	99.8	719	2 CAC85964	CAC85964 bacillus
7	3625	96.4	719	2 Q8KY61	Q8KY61 bacillus th
8	3551	94.4	719	2 Q9F0P8	Q9F0P8 bacillus th
9	3520	93.6	719	1 C1IB_BACTE	Q45709 bacillus th
10	3397	90.3	719	1 C1ID_BACTU	Q9Xdl1 bacillus th
11	3377	89.8	719	1 C1IC_BACTU	O87404 bacillus th
12	2446.5	65.1	1229	1 C1BB_BACTU	Q45739 bacillus th
13	2446.5	65.1	1233	1 C1BC_BACTM	Q45774 bacillus th
14	2278.5	60.6	1228	2 Q33T75	Q93c75 bacillus th
15	2277.5	60.6	1228	1 C1BA_BACTK	P05517 bacillus th
16	2269.5	60.4	1228	2 Q93NM5	Q93nm5 bacillus th
17	2195.5	58.4	849	2 Q8PYW8	Q6pyw8 bacillus th
18	2195.5	58.4	849	2 AAS93797	AAS93797 bacillus
19	2195.5	58.4	1227	1 C1BE_BACTU	O85805 bacillus th
20	2112.5	56.2	1231	2 Q8KNY2	Q8kny2 bacillus th
21	2107.5	56.1	1231	1 C1BD_BACTZ	Q9zaz5 bacillus th
22	1988.5	52.9	1215	1 C1KA_BACTM	Q45715 bacillus th
23	1904	50.6	381	2 Q45740	Q45740 bacillus th
24	1670.5	44.4	1157	1 C8AA_BACUK	Q45704 bacillus th
25	1658	44.1	1144	2 Q8KZL7	Q8kz17 bacillus th
26	1492	39.7	1157	2 Q9CA_BACTO	Q45733 bacillus th
27	1486.5	39.5	1169	1 C8BA_BACUK	Q45705 bacillus th
28	1482.5	39.4	1166	1 C1GA_BACTU	Q45746 bacillus th
29	1478	39.3	1167	1 C1JA_BACTU	Q45738 bacillus th
30	1477	39.3	1169	1 C1FB_BACTM	O66377 bacillus th
31	1471	39.1	1174	2 Q45749	Q45749 bacillus th

32	1467	39.0	1155	1 C1AB_BACTK	P06578 bacillus th
33	1467	39.0	1155	2 Q7BE98	Q7be98 bacillus th
34	1467	39.0	1155	2 Q9F296	Q9f296 bacillus th
35	1467	39.0	1155	2 AAN76494	Aan76494 bacillus
36	1467	39.0	1155	2 AAO13302	Aao13302 bacillus
37	1465	39.0	1118	2 Q9AM83	Q9am83 bacillus th
38	1462	38.9	1156	2 Q6GUA7	Q6gua7 bacillus th
39	1457	38.8	1177	2 Q6EIX3	Q6eix3 bacillus th
40	1455	38.7	1155	2 Q93T21	Q93t21 bacillus th
41	1454.5	38.7	793	2 Q6PYW7	Q6pyw7 bacillus th
42	1454.5	38.7	793	2 AAS93798	Aas93798 bacillus
43	1454.5	38.7	1180	2 Q9SSV8	Q9ssv8 bacillus th
44	1453.5	38.7	1176	2 Q7WZT9	Q7wzt9 bacillus th
45	1449.5	38.6	1181	1 C1AE_BACTL	Q03748 bacillus th

#### ALIGNMENTS

RESULT 1  
C1IA\_BACTK STANDARD; PRT; 719 AA.  
AC Q45752; P71092; Q45750; Q45751; Q45756;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin  
CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIIa; Synonyms=cryII(a), cryV, cryV1, CGCryV;  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSIR732;  
RX MEDLINE=93298009; PubMed=8517758;  
RA Gleave A.P., Williams R., Hedges R.J.;  
RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
serotypes for the presence of cryV-like insecticidal protein genes and  
characterization of a cryV gene cloned from B. thuringiensis subsp.  
kurstaki.";  
RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JHCC4835;  
RX MEDLINE=92269582; PubMed=1588820;  
RA Tailor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
RT "Identification and characterization of a novel Bacillus thuringiensis  
delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";  
RL Mol. Microbiol. 61:1211-1217(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD-1;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
thuringiensis and cloning of cryV-type genes from Bacillus  
thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
entomocidus.";  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB88;  
RX MEDLINE=96178985; PubMed=8606196;  
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.;  
RA Craig J.A., Koziel M.G., Estruch J.J.;  
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
thuringiensis; the cryV-encoded protein is expressed early in  
stationary phase.";  
RL J. Bacteriol. 178:2141-2144(1996).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=61;

RA Selvapandian A., Bhatnagar R.K.;  
RT "Isolation, cloning and expression of cryV gene."  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Promotes colloidomeric lysis by binding to the midgut  
CC epithelial cells of certain coleopteran and lepidopteran species.  
CC Active on Plutella xylostella and Bombyx mori.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; M98544; AAA22354.1; -  
CC EMBL; X62821; CAA44633.1; -  
CC EMBL; L36338; AAC36999.1; -  
CC EMBL; L49391; AAB00958.1; -  
CC EMBL; Y08920; CAA70124.1; -  
CC PIR; I39815; I39815.  
CC PIR; S25383; S25383.  
CC HSP; P02965; ICIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal\_bind\_Like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
CC Sporulation; Toxin.  
KW VARIANT 159 159 K -> R (in strain 61).  
FT VARIAT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
FT 1).  
FT VARIAT 443 443 A -> V (in strain AB88).  
FT VARIAT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;  
  
Query Match 100.0%; Score 3760; DB 1; Length 719;  
Best Local Similarity 100.0%; Pred. No. 2.6e-253;  
Matches 719; Conservative -0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MRLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
  
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Db 61 QTGIGIAGKILGTLGVPAGQVAVSLYSFILGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120  
  
QY 121 RNKALTDLKGLDALAVYHDSLESWGNNRNNRARSVVKVQSYIALELMFVKLPSPFVAVSG 180  
Db 121 RNKALTDLKGLDALAVYHDSLESWGNNRNNRARSVVKVQSYIALELMFVKLPSPFVAVSG 180  
  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGDYSCHCVKWS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGDYSCHCVKWS 240  
  
QY 241 TGLNLRGTNAESWVRVYNOFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
Db 241 TGLNLRGTNAESWVRVYNOFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
  
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Db 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMNW 360  
  
QY 361 GGKLEFRITGGTILNISTQGSTNTSINPVTLPFTSRDVTSTESLAGLNLFTQPVNGVPR 420

Db 361 GGKLEFRITGGTILNISTQGSTNTSINPVTLPFTSRDVTSTESLAGLNLFTQPVNGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQGPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQDSENELPPEATQGPNYESYSHRLSHIGLIS 480  
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Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGTGGDILRRTN 540  
QY 541 TGTGDIRVNNINPPFAQRYRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLVYK 600  
Db 541 TGTGDIRVNNINPPFAQRYRVIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLVYK 600  
QY 601 TFRVGTFTPFSLDVQSTFTTGAMNFGSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
Db 601 TFRVGTFTPFSLDVQSTFTTGAMNFGSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFIIVKAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFIIVKAKQLHIERNM 719  
  
RESULT 2  
Q6X181 PRELIMINARY; PRT; 719 AA.  
AC Q6X181;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE CryII.  
GN Name=cryII;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY262167; AAP86782.1; -  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;  
  
Query Match 100.0%; Score 3760; DB 2; Length 719;  
Best Local Similarity 100.0%; Pred. No. 2.6e-253;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
Db 1 MRLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTLGVPAGQVAVSLYSFILGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120  
Db 61 QTGIGIAGKILGTLGVPAGQVAVSLYSFILGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120  
  
QY 121 RNKALTDLKGLDALAVYHDSLESWGNNRNNRARSVVKVQSYIALELMFVKLPSPFVAVSG 180  
Db 121 RNKALTDLKGLDALAVYHDSLESWGNNRNNRARSVVKVQSYIALELMFVKLPSPFVAVSG 180  
  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGDYSCHCVKWS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGDYSCHCVKWS 240  
  
QY 241 TGLNLRGTNAESWVRVYNOFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300  
Db 241 TGLNLRGTNAESWVRVYNOFRDWTMLVLDLVALFPSYDTQMPYIKTTAQLTREYITDAI 300

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QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMW 360
QY 361 GGHKLEPRTIGTTLNSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEPRTIGTTLNSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVGTTPPFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
DB 601 TFRVGTTPPFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719

RESULT 3
AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE CryII.
GN CryII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T01 328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RT "Complete sequence of cryII gene of isolate T01 328 from Bacillus
RT thuringiensis from Cubatao (SP - Brazil) soil."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 100.0%; Score 3760; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 2.6e-253;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHCLKXSEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHCLKXSEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVVEIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVVEIINOKISTYA 120
QY 121 RNKALTDLKGLDALAVYHDSLESWGVRNTRARSVVKSQYIALELMFVQKLPSPFVSG 180
DB 121 RNKALTDLKGLDALAVYHDSLESWGVRNTRARSVVKSQYIALELMFVQKLPSPFVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYFNQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTYFNQVERAGDYSCHVKWYS 240
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QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMW 360
QY 361 GGHKLEPRTIGTTLNSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEPRTIGTTLNSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
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QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQLHIERNM 719

RESULT 4
Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CryIIa.
GN Name=cryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; ICIV.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.9%; Score 3755; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 5.8e-253;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHCLKXSEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHCLKXSEYENVEPFSASTI 60
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Db 61 QTGIGIAGKILGTLGVPFAGQVASYLFIIGELWPKGKNQWEIFMEHVBEIIINQKISTYA 120  
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 Db 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVQKLPFAVSG 180  
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 Db 241 TGLNLRGTNAESWVRVYQNFRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVIYDAI 300  
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 Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYAGICTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGYAGICTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
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 Db 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDLIRRTN 540  
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 Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
 QY 601 TFRVGTFTPFSLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVGTFTPFSLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5

O85796 PRELIMINARY; PRT; 719 AA.  
 ID O85796  
 AC O85796;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Insecticidal protein.  
 GN Name=crv101;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OG Plasmid large plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SI01;  
 RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF076953; AAC26910.1; -  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.

KW Plasmid. 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
 SQ SEQUENCE  
 Query Match 99.8%; Score 3754; DB 2; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 6.8e-253;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHNEDCLKSEYENVEPVASATI 60  
 Db 1 MKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHNEDCLKSEYENVEPVASATI 60  
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 Db 61 QTGIGIAGKILGTLGVPFAGQVASYLFIIGELWPKGKNQWEIFMEHVBEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVQKLPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRVYQNFRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVIYDAI 300  
 Db 241 TGLNLRGTNAESWVRVYQNFRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVIYDAI 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTOPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYAGICTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGYAGICTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
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 Db 481 ASHKALVYSWTHRSADRTNTEPNSTIQIPLVKAFLNLSGAAVVRGPGFTGGDLIRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
 Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
 QY 601 TFRVGTFTPFSLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVGTFTPFSLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6

CAC85964 PRELIMINARY; PRT; 719 AA.  
 ID CAC85964  
 AC CAC85964;  
 DT 02-MAR-2004 (TREMBlrel. 27, Created)  
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
 DE Delta-endotoxin.  
 GN CRYIIA.  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group; Bacillus thuringiensis.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BNS3;  
 RA Tounsi S., Zouari N., Jacoua S.;

RT "Cloning and study of the expression of a novel cryIIa-type gene from  
 RT Bacillus thuringiensis subsp. kurstaki.";  
 RL J. Appl. Microbiol. 95:23-28 (2003).  
 DR EMBL; AJ315121; CAC85964.1; -;  
 SQ SEQUENCE 719 AA; 81203 MW; 867655A6C25DAFE8 CRC64;

Query Match 99.8%; Score 3752; DB 2; Length 719;  
 Best Local Similarity 99.7%; Pred. No. 9.4e-253;  
 Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNNTRARSVVKSQYIALELMFVQKLPSPFVSG 180  
 Db 121 RNKALTDLKGDLALAVYHDSLESWGNNRNNTRARSVVKSQYIALELMFVQKLPSPFVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMDTLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMDTLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300

QY 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
 Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600

QY 601 TFRVTGFTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 Db 601 TFRVTGFTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 7  
 Q8KY61 PRELIMINARY; PRT; 719 AA.  
 ID Q8KY61  
 AC Q8KY61;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cyt.  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP Porcar M., Martinez C., Caballero P.;  
 RA SEQUENCE FROM N.A.

Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF278797; AAM73516.1; -;  
 PIR; B42459; B42459.  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF03945; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 96.4%; Score 3625; DB 2; Length 719;  
 Best Local Similarity 96.2%; Pred. No. 6.7e-244;  
 Matches 692; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGNNRNNTRARSVVKSQYIALELMFVQKLPSPFVSG 180  
 Db 121 RNKALTDLKGDLALAVYHDSLESWGNNRNNTRARSVVKSQYIALELMFVQKLPSPFVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMDTLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMDTLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300

QY 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600  
 Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDYK 600

QY 601 TFRVTGFTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 Db 601 TFRVTGFTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 8  
 Q9F0P8 PRELIMINARY; PRT; 719 AA.  
 ID Q9F0P8  
 AC Q9F0P8;

DT	01-MAR-2001 (TREMELrel. 16, Created)	QY	541	TGTEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGCDLDYK	600
DT	01-MAR-2001 (TREMELrel. 16, Last sequence update)	Db	541	TGTEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGCDLDYK	600
DT	01-MAR-2004 (TREMELrel. 26, Last annotation update)	QY	601	TFRVGVFTTFFSFLDVQSTFTIGANFNSSGNEVYIDRIEFVFPVETYEAEYDFEKAQEKV	660
GN	Name=cryII;	Db	601	TFRVGVFTTFFSFLDVQSTFTIGANFNSSGNEVYIDRIEFVFPVETYEAEYDFEKAQEKV	660
OS	Bacillus thuringiensis.	QY	661	TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM	719
OG	Plasmid pBTC19.	Db	661	TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM	719
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1428;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BTC007;				
RX	MEDLINE=22837682; PubMed=12957903;				
RA	Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,				
RA	Hu Y., Li G., Huang D.;				
RT	"Identification of cryII-type genes from Bacillus thuringiensis				
RT	strains and characterization of a novel cryII-type gene."				
RL	Appl. Environ. Microbiol. 69:5207-5211(2003).				
DR	EMBL; AF211190; AAG43526.1; --				
DR	HSSP; P02965; ICIY.				
DR	GO; GO:0005102; P:receptor binding; IEA.				
DR	GO; GO:0006952; P:defense response; IEA.				
DR	GO; GO:0009405; P:pathogenesis; IEA.				
DR	InterPro; IPR001178; Endotoxin_C.				
DR	InterPro; IPR005638; endotoxin_N.				
DR	InterPro; IPR008979; Gal_bind_Like.				
DR	Pfam; PF03944; Endotoxin_C; 1.				
DR	Pfam; PF00555; Endotoxin_M; 1.				
DR	Pfam; PF03945; Endotoxin_N; 1.				
KW	Plasmid.				
SQ	SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;				
	Query Match 94.4%; Score 3551; DB 2; Length 719;				
	Best Local Similarity 93.6%; Pred. No. 9.7e-239;				
	Matches 673; Conservative 26; Mismatches 20; Indels 0; Gaps 0;				
QY	1 MMLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLXMEYENVEPVSASTI	60			
Db	1 MMLKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNINHEDEFLNHEHSIDPVSASTI	60			
QY	61 QTGIGIAGKILGTLPVPPAGVAVSLYFELGELWPKGKNQWEIFMEHVEBIIINOKISTYA	120			
Db	61 QTGIGIAGKILGTLPVPPAGVAVSLYFELGELWPKGKNQWEIFMEHVEBIIINOKISTYA	120			
QY	121 RNKALTDLKLGLDALAVHDSLESWGNRNTRARSVKQYIALELMFVKLPSPFVSG	180			
Db	121 RNIALADLKLGLDALAVHDSLESWGNRNTRARSVKQYIALELMFVKLPSPFVSG	180			
QY	181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNQVERAGDYSDHCVKWYS	240			
Db	181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNQVERAGDYSDHCVKWYS	240			
QY	241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPSYDTQMPYIKTTAQLTREVYTDAI	300			
Db	241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPSYDTQMPYIKTTAQLTREVYTDAI	300			
QY	301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMNW	360			
Db	301 GTVHPNASTTWNNAAPSFAIESAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYMNW	360			
QY	361 GGHLEFRFTIGGLTINISTQGSTNTSINPVTLPFTSRDVTYTESLAGNLFLTPQVNGVPR	420			
Db	361 GGHLEFRFTIGGLTINISTQGSTNTSINPVTLPFTSRDVTYTESLAGNLFLTPQVNGVPR	420			
QY	421 VDFHWKFVTHPIASDNFFYPGAGIGTCLQDSENELPPEATGQPNYESYSHRLSHIGLIS	480			
Db	421 VDFHWKFATLPIASDNFFYLGAVGVTCLQDSENELPPEATGQPNYESYSHRLSHIGLIS	480			
QY	481 ASHVKALVSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGILRTN	540			
Db	481 ASHVKALVSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGILRTN	540			
	Query Match 93.6%; Score 3520; DB 1; Length 719;				
	Best Local Similarity 92.9%; Pred. No. 1.4e-236;				
	Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;				
QY	1 MMLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLXMEYENVEPVSASTI	60			

Db 1 MRLKNDKQKSSNAKVDKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSPFGLGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
Db 61 QTGIGIAGKILGTLPVFPAGQVASYLSPFGLGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKLGDALAVYHDSLESVGNRNTRARVSVKSYQYIALELMFVQKLPFAVSG 180  
Db 121 RNKALSDRLGLDALAVYHDSLESVGNRNTRARVSVKSYQYIALELMFVQKLPFAVSG 180  
QY 181 EEFVLLPIYAQAANLHLLLRDASIFGKWEGLSSSEISITFYNROVERAGDYSCHVKWYS 240  
Db 181 EEFVLLPIYAQAANLHLLLRDASIFGKWEGLSSSEISITFYNROVERAGDYSCHVKWYS 240  
QY 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAL 300  
Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAL 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
Db 301 GTVHPNQAFSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
QY 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFLTPVNGVPR 420  
Db 361 GGHKLESPICGALNTSTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFLTPVNGVPR 420  
QY 421 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHMKFPTLPASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
QY 541 TGTFTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
Db 541 TGTFTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 601 TFRVGTFTTTPFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAEKV 660  
Db 601 TFRVGTFTTTPFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAEKV 660  
QY 661 TALFTSNRGLKTDVKYHIDQVSNLVSLSDEFLDYKRELFVIVYAKQIHIERNM 719  
Db 661 TALFTSNRGLKTDVKYHIDQVSNLVSLSDEFLDYKRELFVIVYAKQIHIERNM 719

RESULT 10  
CLID\_BACTU STANDARD; PRT; 719 AA.  
ID AC Q9XDL1, 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryII(d) (Insecticidal delta-endotoxin  
DE CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIId; Synonyms=cryII(d), NRcryV;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BR30;  
RX MEDLINE=20374042; PubMed=10919402;  
RA Choi S.-K., Shin B.-S., Kong B.-M., Rho H.-M., Park S.-H.;  
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
RT gene.";  
RL Curr. Microbiol. 41:65-69(2000).  
CC -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut  
CC epithelial cells of many lepidopteran larvae. Active on Plutella  
CC xylostella and on Bombyx mori.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of

the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF047579; AAD4366.1; -;  
DR HSP; P02965; 1CIV.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;  
  
Query Match 90.3%; Score 3397; DB 1; Length 719;  
Best Local Similarity 89.8%; Pred. No. 5.3e-228;  
Matches 646; Conservative 35; Mismatches 38; Indels 0; Gaps 0;  
  
QY 1 MRLKNDKQKSSNAKVDKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTI 60  
Db 1 MRLKNDKQKSSNAKVDKIATDSLKNETDIELKMNNDYLRMSHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSPFGLGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
Db 61 QTGIGIAGKILGTLPVFPAGQVASYLSPFGLGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKLGDALAVYHDSLESVGNRNTRARVSVKSYQYIALELMFVQKLPFAVSG 180  
Db 121 RNKALADLKLGDALAVYHDSLESVGNRNTRARVSVKSYQYIALELMFVQKLPFAVSG 180  
QY 181 EEFVLLPIYAQAANLHLLLRDASIFGKWEGLSSSEISITFYNROVERAGDYSCHVKWYS 240  
Db 181 EEFVLLPIYAQAANLHLLLRDASIFGKWEGLSSSEISITFYNROVERAGDYSCHVKWYS 240  
QY 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAL 300  
Db 241 TGLNLRGTNAESWVRNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREYVTDAL 300  
QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
Db 301 GTVHPNASFASTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360  
QY 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFLTPVNGVPR 420  
Db 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRVTTESLAGLNLFLTPVNGVPR 420  
QY 421 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHMKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRTN 540  
QY 541 TGTFTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
Db 541 TGTFTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 601 TFRVGTFTTTPFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAEKV 660  
Db 601 TFRVGTFTTTPFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAEKV 660

```

QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFELFVYKAKQLHIERNM 719
DB 661 TAMFTSTNLRRLKTNVTDCHIDQVSNLVESLSEDFYLDKRELFELFVYKAKQLHIERNM 719

RESULT 11
CLIC_BACTU STANDARD; PRT; 719 AA.
ID C1CB_BACTU STANDARD; PRT; 1229 AA.
AC 087404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIc (insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OC Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF056933; AAC62933.1; -.
DR HSSP; P02965; LCIV.
DR InterPro; IPR001178; Endotoxin..
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Plasmid; Sporulation; Toxin.
KW SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;
SQ
Query Match 89.8%; Score 3377; DB 1; Length 719;
Best Local Similarity 89.8%; Pred. No. 1.3e-226;
Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVYDKISTLSLKNETDIELQNHEDCLNKEYENVEPVASATI 60
DB 1 MKLKNPDKHQTLSSNAKVYDKIATDSLKNETDIELKNNNEDYLRMSHESIDPVSASTI 60

QY 61 QTGIGIAGKILGTLGVPPAGVASLYSFIILGELWPKGKNQWEIFMEHVEEIIINOKISYVA 120
DB 61 QTGIGIAGKILGTLGVPPGQIASLYSFIILGELWPKGKSQWEIFMEHVEEAIINRKISYVA 120

QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNNTNRSVVKSQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGDLALAVYHDSLESWGNRNNTNRSVVKQYIALELMFVQKLPFAVSG 180

QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNNRQVERAGDYSCHVKWYS 240
DB 181 EEVPLLPYIAQAANLHLLLRDASIFGKNGGLSASEISTFTYNNRQVERTRDYSYHCWKNN 240

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QY 241 TGLNLRGTNAESWVRYNQFRDMDTLMVLDLVALPSPSYDTQMPYPIKTTAQLTRVYTDI 300
DB 241 TGLNLRATNGQSWVRYNQFRKDIEMVLDLVRVPSPSYDILVYPIKTTAQLTRVYTDI 300

QY 301 GTVHPHPSFTSTTWYNNAPSAEAAVVRNPHLLDFLEOVITYSLLSRWNSNTQYMNW 360
DB 301 GTVDPNQALRSTTWYNNAPSAEAAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYMNW 360

QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESTLAGLNLFTQPVNGVER 420
DB 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLQFTSRDFYRTESWAGLNLFTQPVNGVER 420

QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTPLPIASDNFYVLGYAGVGTQLQDSNELPPEATTGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRTN 540
DB 481 GSHVKALVYSWTHRSADRTNITPNSITQIPLVKAFNLSGAAVVRGPGTGGHILRRTK 540

QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
DB 541 SGTFGHIRVNIINPPFAQRYRVRMSYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600

QY 601 TFRVTGFTTFPESFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
DB 601 TFRVTGFTTFPESDVQSTFTIGAMNFSNGNEVYIGRIEFVPEVTEYAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFELFVYKAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFELFVYKAKQLHIERNM 719

RESULT 12
C1CB_BACTU STANDARD; PRT; 1229 AA.
ID C1CB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIBb (insecticidal delta-endotoxin
DE CryIB(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIBb; Synonyms=cryIB(b), cryET5;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; L32020; AAA22344.1; -.
DR HSSP; P02965; LCIV.
DR InterPro; IPR001178; Endotoxin.

```

OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX	NCBI_TaxID=1441;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Bishop A.H., Bone E.J., Ellar D.J.;
RT	"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC	-!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut epithelial cells of insects.
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	EMBL; Z46442; CAA86568.1; -.
DR	HSSP; P02965; 1CIV.
DR	InterPro; IPR001178; Endotoxin.
DR	InterPro; IPR005638; endotoxin_C.
DR	InterPro; IPR005639; endotoxin_N.
DR	InterPro; IPR008979; Gal bind like.
DR	Pfam; PF03944; Endotoxin_C; 1.
DR	Pfam; PF00555; Endotoxin_M; 1.
DR	Pfam; PF03945; Endotoxin_N; 1.
KW	Sporulation; Toxin.
SQ	SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;
Query Match 65.1%; Score 2446.5; DB 1; Length 1233;	
Best Local Similarity 65.6%; Pred. No. 2.2e-161;	
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;	
QY	13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDCLMSEYENVEPFVSASTIQTGIGIAGKI 70
DB	7 NENEINALSIPTVSNPSTQMLSPDARIEDSLCVAEWNIDPFVSASTVQTGINAGRI 66
QY	71 LGTLGVPPAGQVASYLFIKELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 130
DB	67 LGVLGVPPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLRQVTTENTRTAARLEG 126
QY	131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPFAVSGEEVPLPIYA 190
DB	127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIFLRINNEEVP LLMVYA 186
QY	191 QAAHLHLLLRDASIFGKELWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
DB	187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCQWYNTGLNNLRGTN 246
QY	251 AESWRYNQFRDMLTMDLVLPSPYDTQMYPIKTTAQLTREYVTDATGTVHPHPSFT 310
DB	247 AESWLRYNQFRDRLTLGLVDLVALFPSTYDTRTPINTSAQLTRIEYTDPIGRTNAPS GFA 306
QY	311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMNMGWGHKLEFRTI 370
DB	307 STWYNNNAPSFAIEAAIFRPPHLLDFPEQLTIYSSASSRWSSTQHMNYVWVGHRLNFRPI 366
QY	371 GGTNLNISTQGST-NTSINPVTLPFTSRDVRVRESLQNLNLFQTQPVNGVPRVDFHWKFVT 429
DB	367 GGTNLNISTQGLTNNTSINPVTLPFTSRDVRVRESNAGTNILFTTPVNGVPRVDFHWKFVT 422
QY	430 HPIASDNFYYPG-----YAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLISAS 482
DB	423 --INPQNIYERGATTYSQFYQGVGIQFDSETELPPTETTERPNYESYSHRLSHIGLIIGN 480
QY	483 HVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542
DB	481 TLRAPVYSWTHRSADRTNTEPNISITQIPLVKALNLHSGVTWVGPGFTGGDILRRTNTG 540
QY	543 TFGDIRVNINPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGEBLDYKTF 602
DB	541 TFGDIRLNINPVSQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDNLEYSRF 600
QY	603 RTVGFTTFPFLDVQSTFTIGAWNFGSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662
DB	601 RTAGFTTFPFLDVQSTFTIGAGSFSN-QEVYIDRVFVPAEVTFAEYDLERAKAVNA 659
QY	663 LFTSTNPRGLKTDVQKHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB	660 LFTSTNPRGLKTDVQKHIDQVSNMVACLSDEFCLDEKRELFEIVKYAKELSDERNL 716
RESULT 13	
CIBC_BACTM STANDARD; PRT; 1233 AA.	
ID	CIBC_BACTM
AC	Q45774;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin)
DE	CryIb(c) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN	Name=cryIbC; Synonyms=cryIb(c), cryIbC;
OS	Bacillus thuringiensis (subsp. morrisoni).

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Db 481 TLRAVYVSWTHRSADRTNTIGPNRITQIPLKALNLSGVTVVGGPGFTGGDILRRNTG 540
QY 543 TFGDIRVNIWPPFAQRVYRIRYASTTDLQFHTSINGKAINQGNFSAWNRGEGDLDYKTF 602
Db 541 TFGDIRVNIWPPFAQRVYRIRYASTTDLQFHTSINGKAINQGNFSAWNRGEGDLDYKTF 600
QY 603 RTVGFTTTPSFVLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVT 662
Db 601 RTAGFSTPFNLAQSTFTLGAQFSN-QEVYIDRVFVPAEVTFAEYDLERAKAVNA 659
QY 663 LFTSTNPRGLKTDVVDYHIDQVSNVLSLSEDFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 LFTSTNPRGLKTDVVDYHIDQVSNVLSLSEDFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 14
Q93775 PRELIMINARY; PRT; 1228 AA.
AC Q93775;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Delta-endotoxin Cry1Ba2.
GN Name=Cry1Ba2;
OS Bacillus thuringiensis (subsp. entomococcus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; A363025; AAK51084.1; -
DR HSP; P07130; IDLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.6%; Score 2278.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred. No. 1.1e-149;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLAKNETDIELQNIH-----EDCLKMSEYENVEPVSASTIQTGTGIAGKI 70
Db 2 TSNRKQNEIINAVSNHSAQMDLLPDARIEDSLCIAEGNIDPVSASTVQTGINAGRI 61
QY 71 LGTLGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFYSPLVGLWPRGRDQWEIFLEHVEQLINQITENARNTALARQOG 121
QY 131 LGDALAVYHDSLSWGNRNTRARSVYVKSOYIALELMFVQKLPSFAVSGEEVPLLPYIA 190
Db 122 LGDSFRAYQOOSLEDWLENRDDARTSVLHTQYIALEDLFLNAMPULFAIRNQEVPLLMVYA 181
QY 191 QAANLHLLLRDASIFGEGWGLSSSEISTFYNRQVERAGDYSDCHVKWYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVTRDYSDYCVWYNTGLNLRGTN 241
QY 251 AESWRYNQFRDMLTMDLVALFSPYDQYPIKTAQLTREYVYTDALGTGVHPHPSFT 310
Db 242 AASWRYNQFRDMLTMDLVALFSPYDQYPIKTAQLTREYVYTDALGTGVHPHPSFT 299
QY 311 STTWYNNAPSFSAIEAAVVRPHLLDFLEQTLTFSASSRWSNTRHMTYWRGHTTQSRPI 359

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Db 300 SMWYNNAPSFSAIEAAAIRSPHLLDFLEQTLTFSASSRWSNTRHMTYWRGHTTQSRPI 359
QY 371 GGTNLNISTOGSTNTSINPVTLPFTSRDVRYSLAGLNF--LTQPVNGVPRVDFHKKFV 428
Db 360 GGGLNTSTHGATNTSINPVTLPFTSRDVRYSLAGLNF--LTQPVNGVPRVDFHKKFV 416
QY 429 THP-----IASDNFYPGYAGICTQLODSENELPPEATQOPNYESYSHRLSHIGLISASH 483
Db 417 TNPQNSDRGTANTSQP-YESPGQLQKDSSETLPPETERENYESYSHRLSHIGLISASH 475
QY 484 VKALVYVSWTHRSADRTNTIGPNRITQIPLKALNLSGVTVVGGPGFTGGDILRRNTG 543
Db 476 VNPVYVSWTHRSADRTNTIGPNRITQIPLKALNLSGVTVVGGPGFTGGDILRRNTG 535
QY 544 FGDIRVNIWPPFAQRVYRIRYASTTDLQFHTSINGKAINQGNFSAWNRGEGDLDYKTF 603
Db 536 FGPVIRVTVNGPLTQRYRIGFRYASTVDFVFSRGGTGVANNFRFLRTMNSGDELKYGNFV 595
QY 604 TVGFTTTPSFVLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTAL 663
Db 596 RRAFTTPTFTQIDIIIRTSIQGLSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTAL 655
QY 664 FTSTNPRGLKTDVVDYHIDQVSNVLSLSEDFYLDKRELFEIVKYAKQLHIERNM 719
Db 656 FTNTNPRGLKTDVVDYHIDQVSNVLSLSEDFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 15
C1BA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1998 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin CryIIa) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=CryIIa; Synonyms=cryII(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis."
RL Nucleic Acids Res. 16:2723-2723 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomococcus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
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DR EMBL; X06711; CAA29898.1; -
DR EMBL; X95704; CAA65003.1; -

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DR PIR; S00873; S00873.
DR HSSP; P07130; 1DLG.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_N; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match      60.6%; Score 2277.5; DB 1; Length 1228;
Best Local Similarity 62.7%; Pred. No. 1.3e-149;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TSLKNETDIELQNIH-----EDCLKNSEYENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNESAQMDDLPPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

QY 71 LGTLGVPFAGQVASLYSIFLGELWPKGKNQWEIFMEHVEIINOKISTYARNKALTDLKG 130
Db 62 LGVLGVFPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINOQITENARNATALARLQG 121

QY 131 LGDALAVYHDSLESWGNRNNTARSVKSOYIALELMFVKLPFAVSAGEEVEPLLPPIYA 190
Db 122 LGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLAMPFLFAIRNQEVPELLMVYA 181

QY 191 QAAHLHLILLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKVYSTGLNNLRGTN 250
Db 182 QAAHLHLILLRDASLFGSEFGLTSQEIQRYYERQVTRDYCYCVEMWTGLNSLRGTN 241

QY 251 AESWVRNQFRDMTLMVLVDLVALFSDYDQMPYIKTTAQLTREYVYDAIGTVHPHPSFT 310
Db 242 AASWVRNQFRDRLTLGLVDLVALFSDYDRTYPINTSAQLTREYVYDAIGAT--GVNMA 299

QY 311 STTWYNNAPPSAIEAAVVRNPHLLDFLBQVTIYSLLSWSNTQYMMNWGGHKLERTI 370
Db 300 SNNWYNNAPPSAIEAAIRSPHLLDFLEQLTIFSSASRWSNTRHMTYRGHTIQSRPI 359

QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLF--LTQPVNGVPRVDFHWKFV 428
Db 360 GGGINTSTHGANTNTSINPVTLPFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRNF--- 416

QY 429 THP-----IASDNFYYPGYAGIGTQLQDSENELPPEATGPNVYESYSHLSHIGLISASH 483
Db 417 TNPQNISDRGTANYQP--YESPGLQKQSELPETTERENYESYSHLSHIGIILQSR 475

QY 484 VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGDDILRRTNTGT 543
Db 476 VNVFVYSWTHRSADRTNTIGPNRITQIPMKASLPQGTTVVRGPGFTGDDILRRTNTGG 535

QY 544 FGDIVNINPPFAQRYRIRYASTTDLQFTSTNGKAINQGNFSATMNRGEDLDYKTFR 603
Db 536 FGFIRVTNGLPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNFV 595

QY 604 TVGFTTPPSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTAL 663
Db 596 RRAFTTPTFTQIDIIRTSIQGLSGNGEYVIDKIEIIPVTATFEAYDLELRAQEAVAL 655

QY 664 FTSTNPRGLKTDVKDHIDQVSNLVSLSDEFYLDKRELFEIVKYAKOLHIERNM 719
Db 656 FTNTNPRKTDVTDYHIDQVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 711

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Search completed: October 28, 2004, 18:29:51  
Job time : 101.579 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-55

Perfect score: 3760

Sequence: 1 MKLNQDKHQSPSSNAKVXK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Genesecp1980s:\*  
2: Genesecp1990s:\*  
3: Genesecp2000s:\*  
4: Genesecp2001s:\*  
5: Genesecp2002s:\*  
6: Genesecp2003as:\*  
7: Genesecp2003bs:\*  
8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	4	AAB66908 Insectici
2	3760	100.0	719	6	AAB66908 Insectici
3	3756	99.9	719	4	AAB66910 Insectici
4	3756	99.9	719	6	AAB66910 Insectici
5	3751	99.8	719	4	AAB66911 Insectici
6	3749	99.7	719	4	AAB66911 Insectici
7	3749	99.7	719	6	AAB66911 Insectici
8	3743	99.5	719	4	AAB66909 Insectici
9	3743	99.5	719	6	AAB66910 Insectici
10	3739	99.4	719	2	AAR08041 81 kD end
11	3728.5	99.2	718	6	AAB66911 Insectici
12	3722.5	99.0	718	4	AAB66907 Insectici
13	3551	94.4	719	7	ADM74717 B. thurin
14	3520	93.6	719	4	AAB66912 Insectici
15	3520	93.6	719	6	AAB66912 Insectici
16	3476.5	92.5	710	4	AAB66911 Insectici
17	3397	90.3	719	3	AB07073 Bacillus
18	3377	89.8	719	2	AAW49089 Bacillus
19	3291	87.5	1217	4	AAU02092 Bacillus
20	2734	72.7	1208	4	AAU02093 Bacillus
21	2448	65.1	1230	8	ADK98484 B thuring
22	2448	65.1	1230	8	ADK98489 B thuring
23	2448	65.1	1230	8	ADK98481 B thuring
24	2448	65.1	1230	8	ADK98491 B thuring
25	2448	65.1	1230	8	ADK98487 B thuring

#### ALIGNMENTS

##### RESULT 1

AAB66908

ID AAB66908 standard; protein; 719 AA.

XX AC AAB66908;

XX 12-APR-2001 (first entry)

XX Insecticidal protein cryIIa2.

XX Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-GB002457.

XX 29-JUN-1999; 99GB-00015215.

XX 23-DEC-1999; 99GB-00030536.

XX (ZENEC) ZENEC LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

XX Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.

XX Claim 14; Page 55-57; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66908 to AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

XX Query Match 100.0%; Score 3760; DB 4; Length 719;

XX Best Local Similarity 100.0%; Pred. No. 1.1e-293;

XX Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVPPAGQVSLYFILGELWPKGKQWEIEMEVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVSLYFILGELWPKGKQWEIEMEVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRVYQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300  
 DB 241 TGLNNLRGTNAESWVRVYQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSIAEAAVVRNPHLLDFLEQVTIYSLRSWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWYNNNAPSIAEAAVVRNPHLLDFLEQVTIYSLRSWSNTQYMNW 360  
 QY 361 GGKLEFRITGTLNISTQGSNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGKLEFRITGTLNISTQGSNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYK 600  
 DB 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYK 600  
 QY 601 TFRVGFPTTFFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVGFPTTFFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2

AAE36272  
 ID AAE36272 standard; protein; 719 AA.  
 XX  
 AC AAE36272;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO200298911-A2.  
 XX  
 XX 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 XX  
 PS Claim 12; Page 44-47; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 SQ Sequence 719 AA;

Query Match 100.0%; Score 3760; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-293;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLGVPPAGQVSLYFILGELWPKGKQWEIEMEVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTLGVPPAGQVSLYFILGELWPKGKQWEIEMEVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEMGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRVYQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300  
 DB 241 TGLNNLRGTNAESWVRVYQFRDMDTLMVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSIAEAAVVRNPHLLDFLEQVTIYSLRSWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWYNNNAPSIAEAAVVRNPHLLDFLEQVTIYSLRSWSNTQYMNW 360  
 QY 361 GGKLEFRITGTLNISTQGSNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGKLEFRITGTLNISTQGSNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYK 600  
 DB 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYK 600  
 QY 601 TFRVGFPTTFFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVGFPTTFFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3  
 ID AAB66910 standard; protein; 719 AA.  
 XX AAB66910;  
 AC AAB66910;  
 XX AAB66910;  
 DT 12-APR-2001 (first entry)  
 XX Insecticidal protein cryIIa4.  
 DE Insecticide; transgenic plant; insect-resistance.  
 XX Paecilomyces sp.  
 OS Paecilomyces sp.  
 XX WO200100841-A1.  
 FN WO200100841-A1.  
 XX 04-JAN-2001.  
 PD 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE) ZENECA LTD.  
 PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PT Claim 14; Page 60-62; 72pp; English.  
 PS The present invention relates to novel insecticidal proteins obtained  
 XX from Paecilomyces sp. (see AAB66910 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;  
 SQ Query Match 99.9%; Score 3756; DB 4; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 2.3e-293;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQININHEDECLKMSYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKQWEIPMEHVEEIIQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGKQWEIPMEHVEEIIQKISTYA 120  
 QY 121 RNKALTDLKLGDALAVYHDSLESWVGNRNTRARSVKSQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKLGDALAVYHDSLESWVGNRNTRARSVKSQYIALELMFVQKLPFAVSG 180  
 QY 181 EEVPLLIYAQAANLHLLLRDASIFGKWLSSSEISITFYNRQVERAGDYSCHVKWYS 240  
 DB 181 EEVPLLIYAQAANLHLLLRDASIFGKWLSSSEISITFYNRQVERAGDYSCHVKWYS 240  
 QY 241 TGLNNLRGTNAESWRYNQPRDMLWLDLVALFPSPYDTQMYPIKTTAQLTREYVTDAL 300  
 DB 241 TGLNNLRGTNAESWRYNQPRDMLWLDLVALFPSPYDTQMYPIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNISTQGSNTSINPVTLPFTSRDVRVRESLAGLNLFITQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSNTSINPVTLPFTSRDVRVRESLAGLNLFITQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSSENELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTEGDIRVNIINPPFAQRYRIRYASTDLQFHTSINGKAINQGNFSATMNRGDLDDYK 600  
 DB 541 TGTEGDIRVNIINPPFAQRYRIRYASTDLQFHTSINGKAINQGNFSATMNRGDLDDYK 600  
 QY 601 TFRVTGFTTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFPEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFPEIVKYAKQLHIERNM 719  
 RESULT 4  
 ID AAE36274 standard; protein; 719 AA.  
 XX AAE36274;  
 AC AAE36274;  
 XX 26-JUN-2003 (first entry)  
 DT B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 OS Bacillus thuringiensis.  
 XX WO200298911-A2.  
 PN 12-DEC-2002.  
 PD 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN) SYNGENTA LTD.  
 XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Claim 12; Page 50-53; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 SQ Sequence 719 AA;  
 Query Match 99.9%; Score 3756; DB 6; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 2.3e-293;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60  
 D b 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E I I N Q K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E I I N Q K I S T Y A 120  
 QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
 D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
 QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P H P S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P H P S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 QY 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 D b 481 A S H V K A L V S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E W I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 D b 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E W I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L T D K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719  
 D b 661 T A L F T S T N P R G L T D K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719

RESULT 5  
 AAU02095  
 ID AAU02095 standard; protein; 719 AA.  
 XX  
 AC AAU02095;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Bacillus thuringiensis partial mutant CryIIa.  
 XX  
 KW Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;  
 XX mutant; mutein.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PH Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= signal\_peptide  
 FT Protein 20..719  
 FT /label= Mature\_CryIIa  
 XX  
 PN EP1099760-A1.  
 XX

PD 16-MAY-2001.  
 XX 09-NOV-1999; 99EP-00203723.  
 XX 09-NOV-1999; 99EP-00203723.  
 XX (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.  
 PA De Maagd RA, Bosch HJ;  
 PI WPI; 2001-337141/36.  
 XX N-PSDB; AAS04855.  
 DR  
 XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural  
 PT domains derived from at least 2 different crystal proteins, such as  
 PT CryIIa and CryIIb, and having insecticidal activity, useful for combating  
 PT insects.  
 XX Example; Page 30-32; 43pp; English.  
 PS The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA  
 XX encoding which was mutated to allow cloning of domain III or domains I  
 CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
 CC of the invention, having structural domains I, II and III in this order  
 CC starting from the N-terminal derived from at least 2 different crystal  
 CC proteins, are useful for protecting plants against pest insects, e.g.  
 CC moths, butterflies and Colorado potato beetle or for combating insects  
 XX  
 SQ Sequence 719 AA;  
 Query Match 99.8%; Score 3751; DB 4; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 5.8e-293;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60  
 D b 1 M L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E I I N Q K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E I I N Q K I S T Y A 120  
 QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
 D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S D H C V K W Y S 240  
 QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P H P S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P H P S F T S T T W Y N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 QY 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 D b 481 A S H V K A L V S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600

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QY 601 TFRVGTTPFSLDVQSTFTIGAMNFGSSGNEVYIDRIEVPVVEVYEAEDFEKAQEKV 660
DB 601 TFRVGTTPFSLDVQSTFTIGAMNFGSSGNEVYIDRIEVPVVEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 6
ID AAB66911 standard; protein; 719 AA.
XX
AC AAB66911;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa5.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
XX
PR 23-DEC-1999; 99GB-00030536.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
XX Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX
PS Claim 14; Page 62-64; 72pp; English.
XX
XX The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB6699 to AAB6691 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 719 AA;

Query Match 99.7%; Score 3749; DB 4; Length 719;
Best Local Similarity 99.6%; Pred. No. 8.4e-293;
Matches 716; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEVENVEPVSASTI 60
DB 1 MLKLNQDKHQSPSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEVENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIEMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKLGLDALAVYHDSLESWGNNRNNTRARSVVKSQYIALELMFVKLPSPFVSG 180
DB 121 RNKALTDLKLGLDALAVYHDSLESWGNNRNNTRARSVVKSQYIALELMFVKLPSPFVSG 180
QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFPYNRQVERAGDYSCHVKWYS 240
DB 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFPYNRQVERAGDYSCHVKWYS 240
```

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QY 241 TGLNNLRGTNAESWVRVYNOFRRDMTLMVLDLVALFFSYDTOMYPIKTAQTREYVTDAL 300
DB 241 TGLNNLRGTNAESWVRVYNOFRRDMTLMVLDLVALFFSYDTOMYPIKTAQTREYVTDAL 300
QY 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEOVTIYILLSRWSNTQVNNMW 360
DB 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEOVTIYILLSRWSNTQVNNMW 360
QY 361 GGHKLEFRTIGGTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFILTOPVNGVPR 420
DB 361 GGHKLEFRTIGGTLNISTOGSTNTSINPVTLPFTSRDVYRTESLAGLNLFILTOPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVININPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
DB 541 TGTGDIRVININPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLDYK 600
QY 601 TFRVGTTPFSLDVQSTFTIGAMNFGSSGNEVYIDRIEVPVVEVYEAEDFEKAQEKV 660
DB 601 TFRVGTTPFSLDVQSTFTIGAMNFGSSGNEVYIDRIEVPVVEVYEAEDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 7
ID AAE36275 standard; protein; 719 AA.
XX
AC AAE36275;
XX
DT 26-JUN-2003 (first entry)
XX
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.
XX
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX
OS Bacillus thuringiensis.
XX
PN WO200298911-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-GB002666.
XX
PR 07-JUN-2001; 2001GB-00013900.
XX
PA (SYGN ) SYNGENTA LTD.
XX
PI Vincent JL, Viner R;
XX
DR WPI; 2003-175137/17.
XX
PT New insecticidal protein comprising an X-glycine motif at the amino-
PT terminus, useful as an active ingredient of a pesticide.
XX
PS Claim 12; Page 53-56; 67pp; English.
XX
XX The invention relates to insecticidal protein comprising an X-glycine
CC motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC invention are useful for producing plants or plant parts that are
CC resistant to insects. The protein or synergistic combination is useful as
CC an active ingredient of a pesticide or for controlling insects.
CC Antibodies raised to the insecticidal proteins can be used to identify
```

CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.7%; Score 3749; DB 6; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 8.4e-293;  
 Matches 716; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKLKQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKXSEYENVEPVSASTI	60
DB	1	MKLKQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKXSEYENVEPVSASTI	60
QY	61	QTGIGIAGKILGTGVPFAGQVASYLSPILGELMPKGNQWEIFMEHVEIINQKISTYA	120
DB	61	QTGIGIAGKILGTGVPFAGQVASYLSPILGELMPKGNQWEIFMEHVEIINQKISTYA	120
QY	121	RNKALTDLKGGLDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVQKLPFAVSG	180
DB	121	RNKALTDLKGGLDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVQKLPFAVSG	180
QY	181	EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS	240
DB	181	EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS	240
QY	241	TGLNLRGNTAESWVRVYQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL	300
DB	241	TGLNLRGNTAESWVRVYQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL	300
QY	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPVHLLDFLEQVTIYSLLSRWSTQYMNW	360
DB	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPVHLLDFLEQVTIYSLLSRWSTQYMNW	360
QY	361	GGHKLFRITIGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR	420
DB	361	GGHKLFRITIGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR	420
QY	421	VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS	480
DB	421	VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN	540
DB	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK	600
DB	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK	600
QY	601	TFRVVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV	660
DB	601	TFRVVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV	660
QY	661	TALFTSTNPRGLTVDKDYHIDQVSNLVESLSDEFYLDKEKELFIVKAKQLHIERNM	719
DB	661	TALFTSTNPRGLTVDKDYHIDQVSNLVESLSDEFYLDKEKELFIVKAKQLHIERNM	719

RESULT 8  
 AAB66909  
 ID AAB66909 standard; protein; 719 AA.

AC AAB66909;  
 XX  
 DT 12-APR-2001 (first entry)  
 XX  
 DE Insecticidal protein cryIIa3.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.  
 XX  
 OS Paecilomyces sp.  
 XX

PN WO200100841-A1.  
 XX 04-JAN-2001.  
 PD  
 XX 23-JUN-2000; 2000WO-GB002457.  
 XX  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX  
 XX (ZENE ) ZENECA LTD.  
 PA  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 DR  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX  
 PS Claim 14; Page 57-59; 72pp; English.  
 XX  
 CC The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB6699 to AAB6691 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;

Query Match 99.5%; Score 3743; DB 4; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MKLKQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKXSEYENVEPVSASTI	60
DB	1	MKLKQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKXSEYENVEPVSASTI	60
QY	61	QTGIGIAGKILGTGVPFAGQVASYLSPILGELMPKGNQWEIFMEHVEIINQKISTYA	120
DB	61	QTGIGIAGKILGTGVPFAGQVASYLSPILGELMPKGNQWEIFMEHVEIINQKISTYA	120
QY	121	RNKALTDLKGGLDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVQKLPFAVSG	180
DB	121	RNKALTDLKGGLDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVQKLPFAVSG	180
QY	181	EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS	240
DB	181	EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS	240
QY	241	TGLNLRGNTAESWVRVYQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL	300
DB	241	TGLNLRGNTAESWVRVYQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL	300
QY	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPVHLLDFLEQVTIYSLLSRWSTQYMNW	360
DB	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPVHLLDFLEQVTIYSLLSRWSTQYMNW	360
QY	361	GGHKLFRITIGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR	420
DB	361	GGHKLFRITIGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR	420
QY	421	VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS	480
DB	421	VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN	540
DB	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK	600
DB	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK	600

QY 601 TTRVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TTRVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDFYLDKRELFELVYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDFYLDKRELFELVYAKQLHIERNM 719

RESULT 9  
 AAE36273  
 ID AAE36273 standard; protein; 719 AA.

AC AAE36273;  
 XX 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.  
 OS WO200298911-A2.

XX 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

XX Vincent JL, Viner R;  
 DR WPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Claim 12; Page 47-50; 67pp; English.

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

SQ Sequence 719 AA;

Query Match 99.5%; Score 3743; DB 6; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 2.5e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLQSEYENVEPVFVASTI 60

Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLQSEYENVEPVFVASTI 60

QY 61 QTGIGIACKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120

Db 61 QTGIGIACKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120

QY 121 RNKALTDLKLGDALAYHDSLESVWGNRNTRARSVVKSOYIALELMPVQKLPSFAVSG 180

Db 121 RNKALTDLKLGDALAYHDSLESVWGNRNTRARSVVKSOYIALELMPVQKLPSFAVSG 180

QY 181 EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMWYS 240

181 EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMWYS 240

Db 181 EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKMWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMDTLMVLVLPFSDYDQMPYIKTTAQLTREVYTDAL 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMDTLMVLVLPFSDYDQMPYIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLDLDFLEQVTIYSLLSWSNTQYMMW 360  
 Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLDLDFLEQVTIYSLLSWSNTQYMMW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLOQSENELPPEATQPNYESYSHRSLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLOQSENELPPEATQPNYESYSHRSLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDIQFHTSINGKAINQGNFSATMNRGDDLDYK 600  
 Db 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDIQFHTSINGKAINQGNFSATMNRGDDLDYK 600  
 QY 601 TFRVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TFRVGTTPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFPVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDFYLDKRELFELVYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDFYLDKRELFELVYAKQLHIERNM 719

RESULT 10

AA08041

ID AA08041 standard; protein; 719 AA.

XX AAR08041;

XX 24-OCT-2003 (revised)

XX 25-MAR-2003 (revised)

XX 27-FEB-1991 (first entry)

XX 81 kD endotoxin deduced from DNA carried on pJH12.

XX Crystal; insecticide; toxin; delta endotoxin.

XX Bacillus thuringiensis; JHCC 4353 and 4835.

XX WO9013651-A.

XX 15-NOV-1990.

XX 09-MAY-1989; 89GB-00010624.

XX 09-MAY-1989; 89GB-00010624.

XX (ICIL ) IMPERIAL CHEM IND PLC.

XX Blenk RG, Ely S, Tailor RH, Tippet JM;

XX WPI; 1990-361486/48.

XX N-PSDB; AAQ06636.

XX Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.

XX Claim 5; Fig 5-10; 66pp; English.

CC The sequence carried on pJH12 which was isolated from B. thuringiensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can

CC be used to produce transformants E. coli strain MCI2022/pJH12 (NCIB 40278,  
 CC or bacteriophage EMBL4 vector (NCIB 40279) or E. coli strain BL21/pJH11  
 CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be  
 CC used in formulations for combating Lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 2; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 5.3e-292;  
 Matches 716; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60  
 D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120

QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S H C V K W Y S 240  
 D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S T S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P H P S T S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

QY 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420

QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 D b 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540

QY 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M R G E D L Y K 600  
 D b 541 T G T F G D I R V N I N P P P A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M R G E D L Y K 600

QY 601 T F R V G F T P P F S L D V O S T F T I C A W N P S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 D b 601 T F R V G F T P P F S L D V O S T F T I C A W N P S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L P E I V K A Q L H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L P E I V K A Q L H I E R N M 719

RESULT 11

AAE36271  
 ID AAE36271 standard; protein; 718 AA.  
 XX  
 AC AAE36271;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIaI.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.  
 OS WC200298911-A2.  
 PN 12-DEC-2002.  
 XX 30-MAY-2002; 2002WO-GB002666.  
 PF 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 PA Vincent JL, Viner R;  
 PI WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 PS Claim 12; Page 42-44; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 XX Sequence 718 AA;

Query Match 99.2%; Score 3728.5; DB 6; Length 718;  
 Best Local Similarity 99.6%; Pred. No. 3.7e-291;  
 Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60  
 D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120

QY 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S H C V K W Y S 240  
 D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q R V E R A G D Y S H C V K W Y S 240

QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S T S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P H P S T S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

QY 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N V P R 419

QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 420 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 479

QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 D b 480 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 539

QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 540 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
QY 601 TFRVTGTTTFFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVETYEAEYDFEKAQEKV 660  
DB 600 TFRVTGTTTFFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVETYEAEYDFEKAQEKV 659  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDSEKRELFEIVKYAKQLHIERNM 719  
DB 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDSEKRELFEIVKYAKQLHIERNM 718

RESULT 12  
AAB66907  
ID AAB66907 standard; protein; 718 AA.  
XX  
AC AAB66907;  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa1.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-CB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX  
PS Claim 14; Page 53-55; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 718 AA;  
Query Match 99.0%; Score 3722.5; DB 4; Length 718;  
Best Local Similarity 99.4%; Pred. No. 1.1e-290;  
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLXQSEYENVEPFVSASTI 60  
DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLXQSEYENVEPFVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKLGDALAVYHDSLESWYGNRNTRARSVKRSQYIALELMFVQKLPSFAVSG 180  
DB 121 RNKALTDLKLGDALAVYHDSLESWYGNRNTRARSVKRSQYIALELMFVQKLPSFAVSG 180

QY 181 EEVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSCHCVKWYS 240  
DB 181 EEVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSCHCVKWYS 240  
QY 241 TGLNNLRGNAESWVRVYQFRDMTLMVLVALPFSYDTQMPYPIKTTAQLTREVYTDAL 300  
DB 241 TGLNNLRGNAESWVRVYQFRDMTLMVLVALPFSYDTQMPYPIKTTAQLTREVYTDAL 300  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMNM 360  
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMNM 360  
QY 361 GGHKLEFRITIGTLINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHKLEFRITIGTLINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVN-VPR 419  
QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
DB 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRSLSHIGLIS 479  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
DB 480 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 539  
QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 540 TGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
QY 601 TFRVTGTTTFFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVETYEAEYDFEKAQEKV 660  
DB 600 TFRVTGTTTFFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVETYEAEYDFEKAQEKV 659  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDSEKRELFEIVKYAKQLHIERNM 719  
DB 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDSEKRELFEIVKYAKQLHIERNM 718

RESULT 13  
ADM74717  
ID ADM74717 standard; protein; 719 AA.  
XX  
AC ADM74717;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE B. thuringiensis cryIIa1 SEQ ID NO:2.  
XX  
KW cryI; toxicity; lepidoptera; cryIaB; cryIaC; coleoptera; diptera;  
KW cryIIa1.  
XX  
OS Bacillus thuringiensis.  
XX  
PN CN1401772-A.  
XX  
PD 12-MAR-2003.  
XX  
PF 20-AUG-2001; 2001CN-00124163.  
XX  
PR 20-AUG-2001; 2001CN-00124163.  
XX  
PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
XX  
PI Song F, Zhang J, Huang D;  
XX  
DR WPI; 2003-442339/42.  
DR N-PSDB; ADM74716.  
XX  
PT Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
PT with high-toxicity to lepidoptera pests, encoded protein, primer  
PT sequences and the shuttle vector pSKV422b, useful as a pesticide.  
XX  
PS Example 3; SEQ ID NO 2; 29pp; Chinese.

XX The invention relates to a novel *Bacillus thuringiensis* cryI gene, gene  
 CC combination, expression vector, nucleotide sequence of the B  
 CC *thuringiensis* cryI gene with high-toxicity to lepidoptera pests and the  
 CC amino acid sequence of the protein encoded by it, cooperative use of the  
 CC cryI gene with the expression product of cryIaB or cryIaC, primer  
 CC sequences for expressing the genes, and the constructed shuttle vector  
 CC pSX422b. The gene in combination with the cryIaB or cryIaC genes  
 CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
 CC The present sequence represents the cryIaB protein.  
 XX  
 SQ Sequence 719 AA;

Query Match 94.4%; Score 3551; DB 7; Length 719;  
 Best Local Similarity 93.6%; Pred. No. 7.5e-277;  
 Matches 673; Conservative 26; Mismatches 20; Indels 0; Gaps 0;

QY 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
 D b 1 M K L N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K N I N H E D F L R M S E H S I D P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G O V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G O V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120  
 QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N I A L A D L K G L G D A L A V H S E S W I K N R A R S V V K S Q Y I A L E L L F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240  
 D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S V F G K E W G L S N S I S T F Y N R Q V E R T D S Y D H C V K W Y S 240  
 QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L I A L P S Y D T L V Y P I K T T S Q L T R E V Y T D A I 300  
 QY 301 G T V H P H P S T T T W Y N N N A P S F A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
 D b 301 G T V H P N A S P A S T T W Y N N N A P S F A I E S A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
 QY 361 G G H K L E F R T I G G L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H R L E F R T I G G V L N T S Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F V T H P I A S D N F Y Y L G V A G V G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F A T L P I A S D N F Y Y L G V A G V G T Q L Q D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A P N L S G A A V V R G P G T T G D I L R T N 540  
 D b 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A P N L S G A A V V R G P G T T G D I L R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L Y K 600  
 QY 601 T E R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 D b 601 T E R T V G F T T P F S F S D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S I S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S I S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719

RESULT 14  
 AAB66912  
 ID AAB66912 standard; protein; 719 AA.  
 XX  
 AC AAB66912;  
 XX  
 DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIb1.  
 DE  
 XX Insecticide; transgenic plant; insect-resistance.  
 KW  
 XX Paecilomyces sp.  
 OS  
 XX WO200100841-A1.  
 PN  
 XX 04-JAN-2001.  
 PD  
 XX 23-JUN-2000; 2000WO-GB002457.  
 PF  
 XX 29-JUN-1999; 99GB-00015215.  
 PR  
 XX 23-DEC-1999; 99GB-00030536.  
 PR  
 XX (ZENE ) ZENECA LTD.  
 PA  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 PI  
 XX WPI; 2001-123015/13.  
 DR  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PT  
 XX Claim 14; Page 64-66; 72pp; English.  
 PS  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 CC  
 XX Sequence 719 AA;

Query Match 93.6%; Score 3520; DB 4; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 2.4e-274;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
 D b 1 M K L N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K N N N E D Y L R M S E H S I D P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G O V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G O V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120  
 QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N K A L S D L R G L G D A L A V H S E S W E N R N N T R A R S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240  
 D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R Y S D H C I K W Y N 240  
 QY 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A K S W R Y N Q F R D M T L M V L D L V A L P S Y D T L V Y P I K T T S Q L T R E V Y T D A I 300  
 QY 301 G T V H P H P S T T T W Y N N N A P S F A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
 D b 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A V I R S P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
 QY 361 G G H K L E F R T I G G L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F V T H P I A S D N F Y Y L G V A G V G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F P T L P I A S D N F Y Y L G V A G V G T Q L Q D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQVRVRIYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQVRVRIYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600  
QY 601 TFRVGTTPPSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
DB 601 TFRVGTTPPSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 15  
AAE36276  
ID AAE36276 standard; protein; 719 AA.  
AC AAE36276;  
XX 26-JUN-2003 (first entry)  
DT  
XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.  
DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
KW  
XX Bacillus thuringiensis.  
OS  
XX WO200298911-A2.  
PN  
XX 12-DEC-2002.  
PD  
XX 30-MAY-2002; 2002WO-GB002666.  
PF  
XX 07-JUN-2001; 2001GB-00013900.  
PR  
XX (SYGN ) SYNGENTA LTD.  
XX Vincent JL, Viner R;  
PI WPI; 2003-175137/17.  
DR  
XX  
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
XX Claim 12; Page 56-58; 67pp; English.  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 719 AA;

Query Match 93.6%; Score 3520; DB 6; Length 719;  
Best Local Similarity 92.9%; Pred. No. 2.4e-274;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
QY 1 MLKNQDKHQSSNAKVDKISTDSLKNETDIELQINHEDECLXMEVENVEPVFVASTI 60  
DB 1 MLKNPDKHQSSNAKVDKISTDSLKNETDIELKNMNEDELYRSEHESIDPFVASTI 60  
QY 61 QTGIGIACKILGTGVFPAGQVASYLSFIILGELWPKGKQWEIFMEHVHEEIIINQKISTYA 120  
DB 61 QTGIGIACKILGTGVFPAGQIASLYSFIILGELWPKGKQWEIFMEHVHEEIIINQKILTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWVGNRNNTNRAESVVKSOYIALELMFVQKLPFAVSG 180  
DB 121 RNKALSDLRGLGDALAVYHDSLESWVGNRNNTNRAESVVKSOYIALELMFVQKLPFAVSG 180  
QY 181 EEVPLLPPIYAQAANLHLLLRDASIFGKENGSLSSSEISITFYNRQVERAGDYSRHCVKWYS 240  
DB 181 EEVPLLPPIYAQAANLHLLLRDASIFGKENGSLSSSEISITFYNRQVERAGDYSRHCVKWYN 240  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREVYTTDAI 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMYPIKTTAQLTREVYTTDAI 300  
QY 301 GTVHPHPSTTWTYNNNAPPSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMNW 360  
DB 301 GTVHPNQAFASWTYNNNAPPSAIEAAVVRNPHLLDFLEQVTTYSLLSRWSNTQYMNW 360  
QY 361 GGHKLEPRTIGTGLNISTQSTNTSINPVILPFTSRDVRVATESLAGNLFLTQPVNGVPR 420  
DB 361 GGHRLSPRIGGALNTSTQSTNTSINPVILQFTSRDVRVATESLAGNLFLTQPVNGVPR 420  
QY 421 VDFHMKFVTHPIASDNFVYPGYAGIGTQLOQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
DB 421 VDFHMKFPTLPIASDNFVYLGAGVGTQLOQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQVRVRIYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQVRVRIYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600  
QY 601 TFRVGTTPPSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
DB 601 TFRVGTTPPSFLDVQSTTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Search completed: October 28, 2004, 18:19:54  
Job time : 95.6903 secs



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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-55

Perfect score: 3760

Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3756	99.9	719	3	US-08-286-870A-8
2	3476.5	92.5	710	4	US-09-661-322A-42
3	3398	90.4	648	3	US-08-286-870A-4
4	3377	89.8	719	2	US-09-003-217-2
5	3372	89.7	719	3	US-09-218-942-2
6	2804	74.6	535	3	US-08-286-870A-6
7	2446.5	65.1	1229	1	US-08-100-709-4
8	2446.5	65.1	1229	1	US-08-176-865-4
9	2446.5	65.1	1229	1	US-08-474-038-4
10	2446.5	65.1	1229	2	US-08-779-046-4
11	2446.5	65.1	1229	2	US-08-881-340-4
12	2344.5	62.4	488	1	US-08-448-170-10
13	2344.5	62.4	488	3	US-08-961-803-10
14	2265.5	60.3	1207	1	US-07-951-715A-7
15	2265.5	60.3	1207	2	US-08-459-448A-7
16	2265.5	60.3	1207	3	US-08-459-595A-7
17	2265.5	60.3	1207	3	US-08-459-504B-7
18	2265.5	60.3	1207	3	US-08-459-444-7
19	2265.5	60.3	1207	3	US-09-053-549-8
20	2265.5	60.3	1207	3	US-09-547-422-7
21	2265.5	60.3	1207	4	US-09-988-462-7
22	2264.5	60.2	1227	3	US-09-053-549-2
23	2195.5	58.4	1227	1	US-08-448-170-8
24	2195.5	58.4	1227	3	US-08-961-803-9
25	2186.5	58.2	1227	4	US-09-661-322A-63
26	2171.5	57.8	1186	3	US-09-178-252-23
27	2171.5	57.8	1186	4	US-09-826-660-23

28 2116 56.3 1228 4 US-09-661-322A-38 Sequence 38, Appl  
29 1932.5 51.4 643 3 US-09-178-252-25 Sequence 25, Appl  
30 1932.5 51.4 643 4 US-09-826-660-25 Sequence 25, Appl  
31 1900 50.5 380 5 PCT-US91-02560-4 Sequence 4, Appl  
32 1681.5 44.7 653 4 US-09-661-322A-6 Sequence 6, Appl  
33 1670.5 44.4 1157 1 US-07-876-280-30 Sequence 30, Appl  
34 1670.5 44.4 1157 1 US-07-812-180A-2 Sequence 2, Appl  
35 1670.5 44.4 1157 1 US-08-315-468-2 Sequence 2, Appl  
36 1670.5 44.4 1157 3 US-07-941-650A-2 Sequence 2, Appl  
37 1507.5 40.1 1176 1 US-08-257-999-2 Sequence 2, Appl  
38 1492 39.7 1157 2 US-08-532-547-5 Sequence 5, Appl  
39 1492 39.7 1157 2 US-08-379-656B-5 Sequence 5, Appl  
40 1492 39.7 1157 3 US-08-455-838-5 Sequence 5, Appl  
41 1492 39.7 1157 3 US-09-019-809-5 Sequence 5, Appl  
42 1492 39.7 1157 4 US-09-471-177-5 Sequence 5, Appl  
43 1492 39.7 1157 4 US-09-220-806-5 Sequence 5, Appl  
44 1486.5 39.5 1169 1 US-08-315-468-4 Sequence 4, Appl  
45 1485.5 39.5 1156 3 US-09-002-285-72 Sequence 72, Appl

## ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES.  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Query Match 99.9%; Score 3756; DB 3; Length 719;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 718; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P P V S A S T I 60  
Db 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P P V S A S T I 60

Qy 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N K I S T Y A 120  
Db 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N K I S T Y A 120

Qy 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
Db 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240  
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240

Qy 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

Qy 301 G T V H P H P S T S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
Db 301 G T V H P H P S T S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

Qy 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V R T E S L A G L N L F L T Q P V N G V P R 420  
Db 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V R T E S L A G L N L F L T Q P V N G V P R 420

Qy 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

Qy 481 A S H V K A L V S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 540  
Db 481 A S H V K A L V S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 540

Qy 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
Db 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

Qy 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F P V P V E Y T Y E A Y D F E K A Q E K V 660  
Db 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F P V P V E Y T Y E A Y D F E K A Q E K V 660

Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719  
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719

RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (200)-(200)  
; OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 92.5%; Score 3476.5; DB 4; Length 710;  
Best Local Similarity 92.5%; Pred. No. 5.2e-303;  
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;

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Db 1 M K S K N Q N H Q S L S N N A T V D K N F T G S L E N N T N T E L Q N P N H -----EGIEPFPVSVTI 51

Qy 61 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N K I S T Y A 120  
Db 52 Q T G I G I A G K I L G T L G V P P A G V A S L Y S F I L G E L W P K G K S Q W E I F M E H V E E I I N K I S T Y A 111

Qy 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
Db 112 R N K A L A D L K G L G D A L A V Y H E S L E S W I E N R N N T R S V V K S Q Y I T L E L M F V Q S L P S F A V S G 171

Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S D H C V K W Y S 240  
Db 172 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S K S K E Y S D H C V K W Y N 231

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Qy 301 G T V H P H P S T S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
Db 292 G T V H P H P S T S T T W Y N N N A P S F T I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 351

Qy 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V R T E S L A G L N L F L T Q P V N G V P R 420  
Db 352 G G H K L E F R T I G G T L N T S T Q S T N T S I N P V T L P F T S R D V R T E S L A G L N L F L T Q P V N G V P R 411

Qy 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
Db 412 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 471

Qy 481 A S H V K A L V S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 540  
Db 472 A S H V K A L V S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R K N 531

Qy 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
Db 532 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 591

Qy 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F P V P V E Y T Y E A Y D F E K A Q E K V 660  
Db 592 T F R T V G T T P F S F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F P V P V E Y T Y E A Y D F E K A Q E E V 651

Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719  
Db 652 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D K F Y L D E K R E L F E I V K A Q L H I E R N M 710

RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of  
 ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/286,870A  
 FILING DATE: 05-AUG-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/520228  
 FILING DATE: 09-MAY-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 8910624.9  
 FILING DATE: 09-MAY-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PAUL N. KOKULIS  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 70608/220720  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 648 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-286-870A-4

Query Match 90.4%; Score 3398; DB 3; Length 648;  
 Best Local Similarity 100.0%; Pred. No. 5e-296;  
 Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYA 120  
 QY 121 RNKALTDKGLGDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDKGLGDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVQKLPSPFVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFTYNRQVERAGDYSCHVKWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFTYNRQVERAGDYSCHVKWYS 240  
 QY 241 TGLNLRGTNAESWVRNQFRDMLMVLVALPSSYDQMPYIKTTAQLTRVYTDAL 300  
 DB 241 TGLNLRGTNAESWVRNQFRDMLMVLVALPSSYDQMPYIKTTAQLTRVYTDAL 300  
 QY 301 GTVHPHPSTSTTYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNW 360  
 DB 301 GTVHPHPSTSTTYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNW 360  
 QY 361 GGHKLEFRITIGTGLNISTQGSNTSINPVTLPFTSRDVTYTESLAGNLFLOTQVNGVPR 420  
 DB 361 GGHKLEFRITIGTGLNISTQGSNTSINPVTLPFTSRDVTYTESLAGNLFLOTQVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNINPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 DB 541 TGTFGDIRVNINPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVTGFTTTPSFVLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVETYE 648  
 DB 601 TFRVTGFTTTPSFVLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVETYE 648

RESULT 4

US-09-003-217-2  
 Patent No. 5986177  
 GENERAL INFORMATION:  
 APPLICANT: Osman, Yehia A.  
 APPLICANT: Madkour, Magdy A.  
 APPLICANT: Bulla, Lee A.  
 TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
 TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
 STREET: 3605 Glenwood Ave. Suite 310  
 CITY: Raleigh  
 STATE: NC  
 COUNTRY: US  
 ZIP: 27622  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/003,217  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Spruill, W. Murray  
 REGISTRATION NUMBER: 32,943  
 REFERENCE/DOCKET NUMBER: 5718-3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919 420 2202  
 TELEFAX: 919 881 3175  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 719 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-003-217-2

Query Match 89.8%; Score 3377; DB 2; Length 719;  
 Best Local Similarity 89.8%; Pred. No. 4.6e-294;  
 Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEIFMEHVBEIINQKISTYA 120  
 QY 121 RNKALTDKGLGDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDKGLGDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVQKLPSPFVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSISTFTYNRQVERAGDYSCHVKWYS 240

Db 181 BEVPLPIYAQAANLHLLLRDASIFEKNGG-SASEISTFYNRQVERTRDYSYHCVKWN 240  
 Qy 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFSDYDTOMYPIKTTAQLTREVYTD 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFSDYDTOMYPIKTTAQLTREVYTD 300  
 Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPPLHLLDFLEQVITYSLLSRWSNTQYMNW 360  
 Db 301 GTVDPNQLRSTTWYNNAPSFSAIEAAVVRNPPLHLLDFLEQVITYSLLSRWSNTQYMNW 360  
 Qy 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGNLFILTPQVNGVR 420  
 Db 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLPFTSRDVRYESLAGNLFILTPQVNGVR 420  
 Qy 421 VDFHWKFTPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 Qy 481 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 GSHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDDLYK 600  
 Db 541 SGTFGHIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDDLYK 600  
 Qy 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5

US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; TITLE OF INVENTION: Activity  
 ; FILE REFERENCE: CryII  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; CURRENT FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 89.7%; Score 3372; DB 3; Length 719;  
 Best Local Similarity 89.8%; Pred. No. 1.3e-293;  
 Matches 646; Conservative 33; Mismatches 40; Indels 0; Gaps 0;  
 Qy 1 MGLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINHEPCLKSEYENVEPVSASTI 60  
 Db 1 MGLKNQDKHQSTLSSNAKVDKISTSLKNETDIELQINHEPCLKSEYENVEPVSASTI 60  
 Qy 61 QTGIGIAGKILGTGVPFAGQVASYLSIFILGELWPKGNQWEIFMEHVEIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSIFILGELWPKGNQWEIFMEHVEIINQKISTYA 120  
 Qy 121 RNKALTDLKGLDALAVHDSLSWGNRNTRARSVVKSOYIALELMFVOKLPSFAVSG 180  
 Db 121 RNKALTDLKGLDALAVHDSLSWGNRNTRARSVVKSOYIALELMFVOKLPSFAVSG 180

Qy 181 BEVPLPIYAQAANLHLLLRDASIFEKNGG-SASEISTFYNRQVERAGDYSCHCVKWS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFEKNGG-SASEISTFYNRQVERTRDYSYHCVKWN 240  
 Qy 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFSDYDTOMYPIKTTAQLTREVYTD 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFSDYDTOMYPIKTTAQLTREVYTD 300  
 Qy 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPPLHLLDFLEQVITYSLLSRWSNTQYMNW 360  
 Db 301 GTVDPNQLRSTTWYNNAPSFSAIEAAVVRNPPLHLLDFLEQVITYSLLSRWSNTQYMNW 360  
 Qy 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGNLFILTPQVNGVR 420  
 Db 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLPFTSRDVRYESLAGNLFILTPQVNGVR 420  
 Qy 421 VDFHWKFTPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTPIASDNFYYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 Qy 481 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTK 540  
 Qy 541 TGTFGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDDLYK 600  
 Db 541 SGTFGHIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDDLYK 600  
 Qy 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6

US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENK, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARB & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989

```

; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-870A-6

Query Match 74.6%; Score 2804; DB 3; Length 535;
Best Local Similarity 100.0%; Pred. No. 7.7e-243;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSSNAKVDKISTDSLKNETDIQLQINIHEDCLKXSEYENVEPVSASTI 60
DB 1 MKLNQDKHQSSNAKVDKISTDSLKNETDIQLQINIHEDCLKXSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPPAGOVASLYSIFLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120
DB 61 QTGIGIAGKILGTGVPPAGOVASLYSIFLGELWPKGNQWEIFMEHVEEIIINOKISTYA 120

QY 121 RNKALTDLKGICDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180
DB 121 RNKALTDLKGICDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISIFYNQVERAGDYSCHVKWYS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISIFYNQVERAGDYSCHVKWYS 240

QY 241 TGLNLRGNTAESWRYNQFRDMLTMVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDI 300
DB 241 TGLNLRGNTAESWRYNQFRDMLTMVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDI 300

QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEPRTIGTGLNLTSTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420
DB 361 GGHKLEPRTIGTGLNLTSTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFTHTPIASDNFYYPGAGICTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKFTHTPIASDNFYYPGAGICTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDI 535
DB 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 5322687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

```

```

; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-100-709-4

Query Match 65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.7e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPVSNPSTQMNLSPDARIEDSLCVAEVDNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTIGVPPAGOVASLYSIFLGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
DB 67 LGTIGVPPAGOVASLYSIFLGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVKLPSPAVSGEVPPLPIYA 190
DB 127 LGRGVSRYQALETWLDNRDARSILERYVALELDITTAIPLFRIRNEEVPPLMVYA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISIFYNQVERAGDYSCHVKWYSTGLNLRGNTN 250
DB 187 QAANLHLLLRDASIFGSEWGMASDVYQYQEQIERYTEEYSNHCVQWYNTGLNLRGNTN 246

QY 251 AESWRYNQFRDMLTMVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDIAGTVHHPSPFT 310
DB 247 AESWRYNQFRDMLTMVLDLVALFPSTYDTQMPYIKTTAQLTREVYTDIPIGRTHNAPSFG 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMWGKHLEFRTI 370
DB 307 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYNNMWGKHLEFRTI 366

QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPRVDFHWKFTV 429
DB 367 GGTINISTQGST-NTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPRVDFHWKFTV 422

QY 430 HPIASDNFYYPG-----YAGICTQLQDSNELPPEATGQPNYESYSHRLSHIGLISAS 482
DB 423 --INPQNIYERGATTSYQYQGVGIQQLFDSFETLPPEATGQPNYESYSHRLSHIGLIS 480

QY 483 HVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTNTG 542
DB 481 TLAPVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRTNTG 540

QY 543 TFGDIRVININPPFAQRYVRIRYASTTDLQFHTSINGKALNQGNFSATMNRGDDLDYKTF 602
DB 541 TFGDIRLININPVLPSQRYVRIRYASTTDLQFHTSINGKALNQGNFSATMNRGDDLDYKTF 600

QY 603 RTVGFTTTPSFSLDVQSTETIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTA 662
DB 601 RTAGFSTPFFNLNAQSTFTLGAQSFSN-QEVYIDRVFVPAEVTAEAYDLERAQKAVNA 659

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RESULT 9
US-08-474-038-4
; Sequence 4, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS GYET4 AND GYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      65.1%; Score 2446.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.7e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVNNDPFFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQLASFYFLVGLWPSGRDPWEIFLEHVEQLIRQVVTENTRTAARLEG 126

QY 131 LGDALAVHDSLESVGNRNNTARSVVKSYIALELMFVQKLPFAVSAGEEVLPIIYA 190
DB 127 LGRGYSYQQALETWLDNRDARSRSILERYVALELDITTAIPLFRIRNEEVLPMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEWGWASSDVNQYQOEIRYTEEYSHCHVQWYNTGLNNLRGTN 246

QY 251 AESWVRYNQFRDMDTLMVLDLVALFPSYDTQWPIKTTAQLTREYVTDAGTVPHPSPFT 310
DB 247 AESWLRYNQFRDMDTLMVLDLVALFPSYDTQWPIKTTAQLTREYVTDAGTVPHPSPFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSKSNQYMNWGWGKLEFRTI 370
DB 307 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSKSNQYMNWGWGKLEFRTI 366

QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRATESLAGNLELTQPVNGVPRVDFHWKFTV 429
DB 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRATESLAGNLELTQPVNGVPRVDFHWKFTV 422

QY 430 HPIASDNFYYPG-----YAGIGTQDSENELPPEATQGNPYESYSHLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQGVGIQVDFSETLPETTERPNYESYSHLSHIGLIIGN 480

QY 483 HVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTG 542
DB 481 TLRAPVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTG 540

; QUERY MATCH
; Score 2446.5; DB 2; Length 1229;
; Best Local Similarity 65.6%; Pred. No. 3.7e-210;
; Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVNNDPFFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQLASFYFLVGLWPSGRDPWEIFLEHVEQLIRQVVTENTRTAARLEG 126

QY 131 LGDALAVHDSLESVGNRNNTARSVVKSYIALELMFVQKLPFAVSAGEEVLPIIYA 190
DB 127 LGRGYSYQQALETWLDNRDARSRSILERYVALELDITTAIPLFRIRNEEVLPMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEWGWASSDVNQYQOEIRYTEEYSHCHVQWYNTGLNNLRGTN 246

QY 251 AESWVRYNQFRDMDTLMVLDLVALFPSYDTQWPIKTTAQLTREYVTDAGTVPHPSPFT 310
DB 247 AESWLRYNQFRDMDTLMVLDLVALFPSYDTQWPIKTTAQLTREYVTDAGTVPHPSPFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSKSNQYMNWGWGKLEFRTI 370
DB 307 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSKSNQYMNWGWGKLEFRTI 366

QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRATESLAGNLELTQPVNGVPRVDFHWKFTV 429
DB 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRATESLAGNLELTQPVNGVPRVDFHWKFTV 422

QY 430 HPIASDNFYYPG-----YAGIGTQDSENELPPEATQGNPYESYSHLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQGVGIQVDFSETLPETTERPNYESYSHLSHIGLIIGN 480

QY 483 HVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTG 542
DB 481 TLRAPVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTG 540

; ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match      65.1%; Score 2446.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.7e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIEIQ-NINHEDECLMSEYENVEPVSASTIQTGIGIAGKI 70
DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCAEVNNDPFFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIQKISTYARNKALTDLKG 130
DB 67 LGVLGVPPAGQLASFYFLVGLWPSGRDPWEIFLEHVEQLIRQVVTENTRTAARLEG 126

QY 131 LGDALAVHDSLESVGNRNNTARSVVKSYIALELMFVQKLPFAVSAGEEVLPIIYA 190
DB 127 LGRGYSYQQALETWLDNRDARSRSILERYVALELDITTAIPLFRIRNEEVLPMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNNLRGTN 250
DB 187 QAAHLHLLLRDASLFGSEWGWASSDVNQYQOEIRYTEEYSHCHVQWYNTGLNNLRGTN 246

QY 251 AESWVRYNQFRDMDTLMVLDLVALFPSYDTQWPIKTTAQLTREYVTDAGTVPHPSPFT 310
DB 247 AESWLRYNQFRDMDTLMVLDLVALFPSYDTQWPIKTTAQLTREYVTDAGTVPHPSPFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSKSNQYMNWGWGKLEFRTI 370
DB 307 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSKSNQYMNWGWGKLEFRTI 366

QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRATESLAGNLELTQPVNGVPRVDFHWKFTV 429
DB 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRATESLAGNLELTQPVNGVPRVDFHWKFTV 422

QY 430 HPIASDNFYYPG-----YAGIGTQDSENELPPEATQGNPYESYSHLSHIGLISAS 482
DB 423 --INPQNIYERGATTYSQYQGVGIQVDFSETLPETTERPNYESYSHLSHIGLIIGN 480

QY 483 HVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTG 542
DB 481 TLRAPVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTNTG 540

; TITLE OF INVENTION: BACILLUS THURINGIENSIS c1yET4 AND c1yET5
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

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QY 543 TFGDIRVNINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDTKTF 602
D 541 TFGDIRLNVPLSQRVVRIRYASTTDLQFTRINGTTVNIQGNFSAATMNRGDLDTKTF 600
QY 603 RTVGFTTFFSLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVT 662
D 601 RTAGFSTPNFLNAQSTTLGAQFSN-QEVYIDRVFVPAEVTFAEYDLERAKAVNA 659
QY 663 LFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEFYLDEKRELFEIKYAKOLHIERNM 719
D 660 LFTSTNPRGLKTDVTDYHIDQVSNMVAACLSDEFCLDEKRELFEIKYAKOLHIERNL 716

RESULT 11
US-08-881-340-4
; Sequence 4, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-881-340-4

Query Match 65.1%; Score 2446.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 3.7e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLNQ-ETDIELQ-NINHEDCIKMSEYENVEPFSASTTGTGIGAKI 70
D 7 NENEINALSIPVSNPSTQMNLSPDARIEDSLCVAEVNNDIFFVSASTVQTGNIAGRI 66
QY 71 LGTLGVPPAGQVASYLSFTLGLWPKGNQWEIFMEHVEELINQKISTVARNKALTDLKG 130
D 67 LGVLGVPPAGQVASYLSFTLGLWPKGNQWEIFMEHVEELINQKISTVARNKALTDLKG 126
QY 131 LGDALAVHDSLSWVGNEVGNTRARSVVKSQVIALELMFVQKLPSPAVSGEEVPLPIYA 190
D 131 LGDALAVHDSLSWVGNEVGNTRARSVVKSQVIALELMFVQKLPSPAVSGEEVPLPIYA 190

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D 127 LGRGYSYQOALETWLNDNRDARSRSILRYVALELDITTAIPLFRIRNEEVPLLMVTA 186
QY 191 QANLHLLLRDASIFGKWLGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGTN 250
D 187 QANLHLLLRDASLFGSEWGMASDVQYQYQBYIRYTESYHNCVQVYNTGLNLRGTN 246
QY 251 AESWRYNQFRDMTLMVLDLVALFPYDTPYQYQBYIRYTESYHNCVQVYNTGLNLRGTN 310
D 247 AESWRYNQFRDMTLMVLDLVALFPYDTPYQYQBYIRYTESYHNCVQVYNTGLNLRGTN 306
QY 311 STTWNNNAPSFAIAEAAVVRNPHLLDLEQVTIYSLLSRWSTNTQYNNMGGHKLFRFTI 370
D 307 STTWNNNAPSFAIAEAAVVRNPHLLDLEQVTIYSLLSRWSTNTQYNNMGGHKLFRFTI 366
QY 371 GGTLNISTGSGT-NTSINPVTLPFTSRDVTYTESLGLNLFELTQPVNGVPRVDFHWKFTV 429
D 367 GGTLNISTGSGT-NTSINPVTLPFTSRDVTYTESLGLNLFELTQPVNGVPRVDFHWKFTV 422
QY 430 HPIASDNFYYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRSLSHGLISAS 482
D 423 --INPQNIYERGATTYSQPYQGVGQLFDSFETELPPTETTERPYESYSHRSLSHGLIIGN 480
QY 483 HVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542
D 481 TLRAVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 540
QY 543 TFGDIRVNINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDLDTKTF 602
D 541 TFGDIRLNVPLSQRVVRIRYASTTDLQFTRINGTTVNIQGNFSAATMNRGDLDTKTF 600
QY 603 RTVGFTTFFSLDVQSTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVT 662
D 601 RTAGFSTPNFLNAQSTTLGAQFSN-QEVYIDRVFVPAEVTFAEYDLERAKAVNA 659
QY 663 LFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEFYLDEKRELFEIKYAKOLHIERNM 719
D 660 LFTSTNPRGLKTDVTDYHIDQVSNMVAACLSDEFCLDEKRELFEIKYAKOLHIERNL 716

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RESULT 12
US-08-448-170-10
; Sequence 10, Application US/08448170
; Patent No. 5723758
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Dencted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 424

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/759,247  
FILING DATE: 13-SEPT-1991  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Salivanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/S 102D.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 375-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-448-170-10

Query Match 62.4%; Score 2344.5; DB 1; Length 488;  
Best Local Similarity 89.7%; Pred. No. 1.2e-201;  
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

QY 1 MRLKQKHQSSNAKVDKISTSLKNETDIELQNHEDCLXSEYENVEPVSASTI 60  
DB 1 MRLKQKHQSSNAKVDKISTSLKNETDIELQNHEDCLXSEYENVEPVSASTI 51  
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLFGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
DB 52 QTGIGIVGKILGNLGVFPAGQVASYLFGELWPKGKQWEIFMEHVEEIIINQKISTYA 111  
QY 121 RNKALTDLGLDALAVYHDSLESWGVRNNTTRSVKSOYIALFLMFKVQLPSPAVSG 180  
DB 112 RNKALADLGLDALAVYHDSLESWGVRNNTTRSVKSOYIALFLMFKVQLPSPAVSG 171  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWYN 240  
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWYN 231  
QY 241 TGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVTDI 300  
DB 232 TGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVTDI 291  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360  
DB 292 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 351  
QY 361 GGHKLEPRTIGTGLNITQGSTNTSINPVLPTFTSRDVRTESLAGNLFLTPQVNGVPR 420  
DB 352 GGHKLEPRTIGTGLNITQGSTNTSINPVLPTFTSRDVRTESLAGNLFLTPQVNGVPR 411  
QY 421 VDFHKKFVTHPIASDNFYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLHIGLIS 480  
DB 412 VDFHKKFVTHPIASDNFYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRSLHIGLIS 471  
QY 481 ASHKALVYSWTHRSAD 497  
DB 472 ASHKALVYSWTHRSAD 488

RESULT 13  
US-08-961-803-10  
Sequence 10, Application US/08961803  
Patent No. 6150589  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel  
APPLICANT: Cummings, David A.  
APPLICANT: Cannon, Raymond J.C.  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Stelman, Steve  
TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted  
TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jay M. Sanders  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,803  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/069,902  
FILING DATE: 01-JUNE-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/759,247  
FILING DATE: 13-SEPT-1991  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/448,170  
FILING DATE: 23-MAY-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: M/S 102DCD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-961-803-10

Query Match 62.4%; Score 2344.5; DB 3; Length 488;  
Best Local Similarity 89.7%; Pred. No. 1.2e-201;  
Matches 446; Conservative 13; Mismatches 29; Indels 9; Gaps 1;

QY 1 MRLKQKHQSSNAKVDKISTSLKNETDIELQNHEDCLXSEYENVEPVSASTI 60  
DB 1 MRLKQKHQSSNAKVDKISTSLKNETDIELQNHEDCLXSEYENVEPVSASTI 51  
QY 61 QTGIGIAGKILGTLGVFPAGQVASYLFGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
DB 52 QTGIGIVGKILGNLGVFPAGQVASYLFGELWPKGKQWEIFMEHVEEIIINQKISTYA 111  
QY 121 RNKALTDLGLDALAVYHDSLESWGVRNNTTRSVKSOYIALFLMFKVQLPSPAVSG 180  
DB 112 RNKALADLGLDALAVYHDSLESWGVRNNTTRSVKSOYIALFLMFKVQLPSPAVSG 171  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWYN 240  
DB 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDHCVKWYN 231  
QY 241 TGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVTDI 300  
DB 232 TGLNLRGNTNAESWVRYNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVTDI 291  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360  
DB 292 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 351

QY 361 GGKLEFRIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNGVPR 420  
 Db 352 GGKLEFRIGTGLNISTQSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNGVPR 411  
 QY 421 VDFHWKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 412 VDFHWKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471  
 QY 481 ASHVKALVYSWTHRSAD 497  
 Db 472 ASHVKALVYSWTHRSAD 488

RESULT 14  
 US-07-951-715A-7  
 ; Sequence 7, Application US/07951715A  
 ; Patent No. 5625136  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Naini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.  
 ; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 ; NUMBER OF SEQUENCES: 94  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CIBA-GEIGY Corporation  
 ; STREET: 7, Skyline Drive  
 ; CITY: Hawthorne  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10532  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30B  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/951,715A  
 ; FILING DATE: 25-SEP-1992  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/772,027  
 ; FILING DATE: 04-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spruill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8615  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1207 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-951-715A-7

Query Match 60.3%; Score 2265.5; DB 1; Length 1207;

Best Local Similarity 64.3%; Pred. No. 6.3e-194;  
 Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
 QY 40 EDCLXMEVENVEPVSASTIQTGIGIAGKILGTLGVPPFAGOVASLYSFIIGELWPKGN 99  
 Db 10 EDCLXMEVENVEPVSASTIQTGIGIAGKILGTLGVPPFAGOVASLYSFIIGELWPKGN 69  
 QY 100 QWEIPEHVEEIIINQKISTYARNKALDGLGDLALAVYHDSLESVGNMNRTRSVVK 159  
 Db 70 QWEIPEHVEEIIINQKISTYARNKALDGLGDLALAVYHDSLESVGNMNRTRSVVK 129  
 QY 160 SOYIALELMPVQKLPSFAVSGEVEPLPIYAQAANLHLLLDASIFGKEWGLSSEIST 219  
 Db 130 TOYIALELDFLNAMPFLFAIRNQEVPLLMVYAQAANLHLLLDASIFGSEFGLTSQEIQR 189  
 QY 220 FYNQVERAGDYSCHVKWYSTGLNLRGTNAESVRYNQFRDRMTLMVLDLVALPSPYD 279  
 Db 190 YERQVTRTDYSDYCVWYNTGLNSLGTNAASVRYNQFRDRMTLMVLDLVALPSPYD 249  
 QY 280 TQMYPIKTAQLTREVYTDALGTGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFL 339  
 Db 250 TRTYPINTSAQLTREVYTDALGTGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFL 307  
 QY 340 EQVTIYSLSRWSNTQYMMNMGHKLERTIGTGLNISTQSTNTSINPVTLPFTSRDVI 399  
 Db 308 EQVTIYSLSRWSNTQYMMNMGHKLERTIGTGLNISTQSTNTSINPVTLPFTSRDVI 367  
 QY 400 RTESLAGLNLF--LTQPVNGVPRVDEHMKFVTHP-----IASDNFYPGYAGIGTQLODS 452  
 Db 368 RTESLAGLNLF--LTQPVNGVPRVDEHMKFVTHP-----IASDNFYPGYAGIGTQLODS 423  
 QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADTNTIEPNSITQIPL 512  
 Db 424 ETELPPETTERPNYESYSHRLSHIGLISASHVKALVYSWTHRSADTNTIEPNSITQIPL 483  
 QY 513 VKAFNLSSGAAVRGPGTGGDILRRNTGTGDIRVNINPPFAQYRVIRYASTDLO 572  
 Db 484 VKASELPQGTTVRGPGTGGDILRRNTGTGDIRVNINPPFAQYRVIRYASTDLO 543  
 QY 573 FHTSINGKAINQGNFSATMNRGDLKYKTRTVGFTTFFSFLDVQSTFTIGAMNFSNGNE 632  
 Db 544 FVSRGGTTNNFRLTNWNGDELKYNFVRFAFTTFTTQIQDIIRTSIQIGLNGGE 603  
 QY 633 VYIDRIEFPVVEVTEAEYDFEKAQEKVYALFTSTNPRGLKTDVYHIDQVSNLVESLS 692  
 Db 604 VYIDRIEFPVVEVTEAEYDFEKAQEKVYALFTSTNPRGLKTDVYHIDQVSNLVESLS 663  
 QY 693 DEFYLDKRELFELVKYAKQLHIERNM 719  
 Db 664 DEFYLDKRELFELVKYAKQLHIERNM 690

RESULT 15  
 US-08-459-448A-7  
 ; Sequence 7, Application US/08459448A  
 ; Patent No. 5859336  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Naini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5859336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIVA  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-448A-7

Query Match 60.3%; Score 2265.5; DB 2; Length 1207;  
Best Local Similarity 64.3%; Fred. No. 6.3e-194;  
Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
QY 40 EDCMKSEYNEVPEFVSASTTGTGIGIAGKILGTGVPFAGQVASLYSILGELWPKGN 99  
Db 10 EDSLICIAEGNNIDPFVSASTTGTGINAGRIAGILGVLGVPFAGQVAFYSLVGLWPRGRD 69  
QY 100 QWEIFMHEVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESWVGNRNTRARSVVK 159  
Db 70 QWEIFLEVEQLINQITENARNALARLQGLGDSFRAYQOSLEDWLENRDDRTRSVLY 129  
QY 160 SQYIALELMFVQKLPSEFVSGVEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIST 219  
Db 130 TQYIALELDFINAMPLFAIRNOEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189  
QY 220 FYNQVERAGDYSDHCWKWYSGLNNLRGTNAESVRYNQFRDMTLMVLDLVALFPSYD 279  
Db 190 YYERQVERTRDYSYCVVEWYNTGLNSLRGTNAASWVRYNQFRDRLTLGVLDLVALFPSYD 249  
QY 280 TQMPYIKTAQLTREVTDAIGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFL 339  
Db 250 TRTYPINTSAQLTREVTDAIGAT--GVNMAAMNWNNAAPSFAIEAAAIRSPHLLDFL 307  
QY 340 EQVTIYLLSRWNTQYNNMGHKLFRITGGTJNISTOGSTNTSINPVTLPFTSRDVI 399  
Db 308 EQLTIFSASSRNSNRHTYWGHTIQSRPIGGGLNTSHTGATNTSINPVTLPFASRDVI 367  
QY 400 RTBSLAGLNLF--LTQPVNGVPRVDFHWKFVTHP-----IASDNFYYPGYAGIGTQLODS 452  
Db 368 RTESYAGVLLWGLYLEPIHGVTVRNF---TNPNISDRGTANYSQP-YESFGLQLKDS 423

QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSTIQIPL 512  
Db 424 ETELPPETTERPNYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTICPNRTIQIPM 483  
QY 513 VKAFNLSSGAADVVRGPGGTGGDILRRNTGTGDIRVNINPPEAORYVRIRYASTTDLQ 572  
Db 484 VKASELPQGTTVVRGPGGTGGDILRRNTGGFGPIRVTVNGELTQRYRIGRYASTVDFD 543  
QY 573 FHTSINGKALINQGNFSAWNRGDLDTFTFRVGFITTFPSFLDVQSTFTTICAWNFSSGNE 632  
Db 544 FFVSRGGTTVNNPFRFLRTMNSGDELKYGNFVRAFTTPTFTQIQDIIRTSIQGLSGNGE 603  
QY 633 VYIDRIEFVPEVTEAEYDFEKAQEKVTALTSTNPRGLKTDVYHIDQVSNLVESLS 692  
Db 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVYHIDQVSNLVACLS 663  
QY 693 DEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 664 DEFCLDEKRELLEKVKYAKLSDERNL 690

Search completed: October 28, 2004, 18:34:13  
Job time : 24.3343 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19,191 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MKLKNQDKHQSFSNNAKVDK.....KRELFVVKYAKLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: Pir1:\*  
2: Pir2:\*  
3: Pir3:\*  
4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3760	100.0	719	2 I39815	insecticidal prote
2	3751	99.8	719	2 S25383	parasporal crystal
3	3743	99.5	719	2 I39814	insecticidal prote
4	3520	93.6	719	2 I40590	cryv465 protein -
5	2277.5	60.6	1228	2 S00873	parasporal crystal
6	1900	50.5	380	2 B42459	hypothetical prote
7	1492	39.7	1157	1 S49247	parasporal crystal
8	1492.5	39.4	1166	2 S32645	parasporal crystal
9	1474	39.2	1155	2 A26513	parasporal crystal
10	1471	39.1	1174	2 S32649	parasporal crystal
11	1467	39.0	1155	2 JD0002	parasporal crystal
12	1467	39.0	1156	2 A29125	parasporal crystal
13	1454.5	38.7	934	2 A22798	parasporal crystal
14	1453.5	38.7	1176	2 JT0241	parasporal crystal
15	1450	38.6	1155	2 S02134	parasporal crystal
16	1449.5	38.6	1181	2 A41052	parasporal crystal
17	1447.5	38.5	1176	2 JC2219	parasporal crystal
18	1446	38.5	1155	2 I39838	parasporal crystal
19	1443.5	38.4	1176	2 A22617	parasporal crystal
20	1443.5	38.4	1176	2 S02215	parasporal crystal
21	1360	36.2	1174	2 A42459	parasporal crystal
22	1353	36.0	1138	2 A48944	parasporal crystal
23	1339.5	35.6	1156	2 A29838	parasporal crystal
24	1331.5	35.4	823	2 S04181	parasporal crystal
25	1322.5	35.2	1189	2 S00944	parasporal crystal
26	1310	34.8	1154	2 S39536	parasporal crystal
27	1272	33.8	1171	2 I40572	parasporal crystal
28	1272	33.8	1171	2 A37829	parasporal crystal
29	1263	33.6	1176	2 A48970	parasporal crystal

30 1234 32.8 1160 2 S32647 parasporal crystal  
31 1219.5 32.4 1165 2 S11446 parasporal crystal  
32 1209.5 32.2 655 2 JC7140 protoxin - Bacillu  
33 1196 31.8 1172 2 S32689 parasporal crystal  
34 1186 31.5 1160 2 I40589 parasporal crystal  
35 1163.5 30.9 1178 1 USBSXH parasporal crystal  
36 1163 30.9 1177 2 A49785 parasporal crystal  
37 1156 30.7 652 2 A27323 parasporal crystal  
38 1133 30.1 659 2 S10228 parasporal crystal  
39 1100.5 29.3 652 2 I39811 parasporal crystal  
40 986 26.2 649 1 JH0261 parasporal crystal  
41 935 24.9 618 2 S11445 parasporal crystal  
42 886 23.6 1156 2 S19306 parasporal crystal  
43 828 22.0 1136 1 USBS81 parasporal crystal  
44 594.5 18.5 934 2 B29838 parasporal crystal  
45 667 17.7 1180 2 I39870 parasporal crystal

ALIGNMENTS

RESULT 1

I39815  
insecticidal protein cryV - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I39815  
R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1681-1687, 1993  
A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for t  
iensis subsp. kurstaki.  
A:Reference number: I39815; MUID:93298009; PMID:8517758  
A:Accession: I39815  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768  
C:Genetics:  
A:Gene: cryV  
C:Superfamily: parasporal crystal protein

Query Match		Score 3760; DB 2; Length 719;
Best Local Similarity		100.0%; Pred. No. 2.9e-256;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MKLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQINHEDCLKMSEYENVEPFGASTI 60
Db	1	MKLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQINHEDCLKMSEYENVEPFGASTI 60
Qy	61	QTGIGIAGKILGTIGVPPAGQVASYLSYFILGELWPKGNQWEIFMEHVEEINQKISTYA 120
Db	61	QTGIGIAGKILGTIGVPPAGQVASYLSYFILGELWPKGNQWEIFMEHVEEINQKISTYA 120
Qy	121	RNKALTDLXGLGDALAVVHDSLSWVGNRNNTRARSVVKSOYIALELMFVKLPSPAVSG 180
Db	121	RNKALTDLXGLGDALAVVHDSLSWVGNRNNTRARSVVKSOYIALELMFVKLPSPAVSG 180
Qy	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKWYS 240
Db	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKWYS 240
Qy	241	TGLNNLRGTNAESWVRYNQFRDRTLMLVDLVALFPDYDTQMPYIKTTAQLTREVTDAI 300
Db	241	TGLNNLRGTNAESWVRYNQFRDRTLMLVDLVALFPDYDTQMPYIKTTAQLTREVTDAI 300
Qy	301	GTVHPHPSFTSTTWYNNNAPSFSIAEAAVVRNPHLLDPLEQVTIYLSLSRWSNTQNMNMW 360
Db	301	GTVHPHPSFTSTTWYNNNAPSFSIAEAAVVRNPHLLDPLEQVTIYLSLSRWSNTQNMNMW 360
Qy	361	GGHKLFEFRITGGTILNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFLTQPVNGVPR 420
Db	361	GGHKLFEFRITGGTILNISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFLTQPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHKKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIIPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRNTIIPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 QY 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2  
 S25383  
 parasporal crystal protein cryIIa1 - Bacillus thuringiensis  
 N;Alternate names: delta-endotoxin; parasporal crystal protein cryV  
 C;Species: Bacillus thuringiensis  
 C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C;Accession: S25383  
 R;Author: R. J. Tippet, J. J. Gibb, G. J. Pells, S. J. Pike, D. J. Jordan, L. J. Ely, S. J. Mol. Microbiol. 6, 1211-1217, 1992  
 A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin  
 A;Reference number: S25383; MUID:92269582; PMID:1588820  
 A;Accession: S25383  
 A;Molecule type: DNA  
 A;Residues: 1-719 <TAI>  
 A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PIDN:CAA44633.1; PID:G40290  
 C;Genetics:  
 A;Gene: cryV  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 99.8%; Score 3751; DB 2; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 1.3e-255;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 Db 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLSWVGNNRNTARSVVKVSKQYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGLDALAVYHDSLSWVGNNRNTARSVVKVSKQYIALELMFVQKLPFAVSG 180  
 QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTNQRQVERAGDYSDHCVKWYS 240  
 Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTNQRQVERAGDYSDHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFITQPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFITQPVNGVPR 420

QY 421 VDFHKKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHKKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIIPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRNTIIPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 QY 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TFRVTGFTTTPSFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3  
 I39814  
 insecticidal protein cryVI - Bacillus thuringiensis  
 C;Species: Bacillus thuringiensis  
 C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
 C;Accession: I39814  
 R;Author: R. J. Tippet, S. H. Choi, S. K. Koo, B. T. Lee, S. T. Kim, J. I. Appl. Environ. Microbiol. 61, 2402-2407, 1995  
 A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis tomocidus.  
 A;Reference number: I39814; MUID:95314293; PMID:7793960  
 A;Accession: I39814  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-719 <RES>  
 A;Cross-references: GB:L36338; NID:G540281; PIDN:AAC36999.1; PID:G540282  
 C;Genetics:  
 A;Gene: cryVI  
 C;Superfamily: parasporal crystal protein

Query Match 99.5%; Score 3743; DB 2; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 4.6e-255;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 Db 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLSWVGNNRNTARSVVKVSKQYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGLDALAVYHDSLSWVGNNRNTARSVVKVSKQYIALELMFVQKLPFAVSG 180  
 QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTNQRQVERAGDYSDHCVKWYS 240  
 Db 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFTNQRQVERAGDYSDHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFITQPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFITQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVININPPFAQRYRVRIRYASTTDLOFHSTINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVININPPFAQRYRVRIRYASTTDLOFHSTINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRVTGFTTTPFSDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
DB 601 TFRVTGFTTTPFSDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

## RESULT 4

I40590  
cryV465 protein - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I40590  
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis tonocidus.  
A;Reference number: I39814; MUID:95314293; PMID:7793960  
A;Accession: I40590  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-719 <RES>  
A;Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:9467234; PIDN:AAA82114.1; PID:94672  
C;Genetics:  
A;Gene: cryV465  
C;Superfamily: parasporal crystal protein

Query Match 93.6%; Score 3520; DB 2; Length 719;  
Best Local Similarity 92.9%; Pred. No. 2.2e-239;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQINIHEDCLKXSEVENVEPVASATI 60  
DB 1 MCLKNPDKHQSSNAKVDKIATDSLKNETDIELKNMNEIDYLRVSEHSIDPVASATI 60  
QY 61 QTGIGIAGKILGTLGVPAGQVASYLGFILGELWPKGKNQWEIFMEHVBEIINOKISTYA 120  
DB 61 QTGIGIAGKILGTLGVPAGQIASLYLGFILGELWPKGKSQWEIFMEHVBEIINOKILTYA 120  
QY 121 RNKALTDLGLDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180  
DB 121 RNKALSRLGLDALAVYHDSLESWGNRNTRARSVVKQYIALELMFVQKLPFAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWYS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASISTFYNRQVERTRDYSHCIKWYN 240  
QY 241 TGLNLRGTNAESWVRNQFRDMLMVLDLVALFPSYDTQMYP:KTTAQLTRVYTDAT 300  
DB 241 TGLNLRGTNAESWVRNQFRDMLMVLDLVALFPSYDILVYPIKTTSQLTRVYTDAT 300  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYXNMW 360  
DB 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVVRNPHLLDLEKVTIYSLLSRWNSNTQYXNMW 360  
QY 361 GGHKLEFRTIGGFLNISTQGSTNTSINPVTLPFTSRDVTSTESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHRLSPIGGALNTSQGSTNTSINPVTLPFTSRDVTSTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVININPPFAQRYRVRIRYASTTDLOFHSTINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVININPPFAQRYRVRIRYASTTDLOFHSTINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRVTGFTTTPFSDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
DB 601 TFRVTGFTTTPFSDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

## RESULT 5

S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N;Alternate names: parasporal crystal protein cryA4  
C;Species: Bacillus thuringiensis subsp. thuringiensis  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: S00873  
R;Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A;Reference number: S00873; MUID:88203216; PMID:3362680  
A;Accession: S00873  
A;Molecule type: DNA  
A;Residues: 1-1228 <BRI>  
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:940264; PIDN:CAA29898.1; PID:958094;  
C;Genetics:  
A;Gene: cryA4  
A;Start codon: TTG  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 60.6%; Score 2277.5; DB 2; Length 1228;  
Best Local Similarity 62.7%; Pred. No. 1.2e-151;  
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQINIH-----EDCLKMSEVENVEPVFVSASTIQTGIGIAGKI 70  
DB 2 TSNRKNENIINAVSNHSAQMDLLPDARIEDSLCAEGNNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPFAGQVASYLGFILGELWPKGKNQWEIFMEHVBEIINOKISTYARKALTDLKG 130  
DB 62 LGVLGVPPFAGQVASYLGFILGELWPRGRDQWEIFLEHVEQLNQITENARNTALARLQ 121  
QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSGEVPPLPIYA 190  
DB 122 LGDSFRAYQOSLEDWLENEDDARTESVLYTQYIALELDLFANMPLFAIRNQEVPLAMVYA 181  
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGTN 250  
DB 182 QAANLHLLLRDASLFGSEFGLTSQEIORYERYERQVERTRDYSYCVWEYNTGLNSRGTN 241  
QY 251 AESWVRNQFRDMLMVLDLVALFPSYDTQMYP:IKTTAQLTRVYTDATIGTVHPHPSFT 310  
DB 242 AASWVRNQFRDMLMVLDLVALFPSYDTQYPIKTTAQLTRVYTDATIGAT--GVNMA 299  
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYXNMWGHKLEFRTI 370  
DB 300 SMWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYXNMWGHKLEFRTI 359  
QY 371 GGTNLNISTQGSTNTSINPVTLPFTSRDVTSTESLAGLNLFLTQPVNGVPRDHWKVF 428  
DB 360 GGGLNTSTHGTATNTSINPVTLPFTSRDVTSTESYAGVLLGVIYLEPIHGVPTVRNF--- 416

QY 429 THP-----IASDNFYPGYAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLISASH 483  
DB 417 TNPQNISDRGTANYSQP-YESPGIQLKDSSETLPPETTERPNYESYSHRLSHIGLILQSR 475  
QY 484 VKALVSWTHRSADRTNTEPNSTIQTPLVKAFNLSGAAVVRGPGFTGGDILRRNTGT 543  
DB 476 VWPVYSWTHRSADRTNTEPNSTIQTPLVKAFNLSGAAVVRGPGFTGGDILRRNTGT 535  
QY 544 FGDIRVNIINPPFAQRVRIYASTTDLQFHTSINGKAINQGNFATMNGEDLDYKTR 603  
DB 536 FGPIRVTVNGPLTQRYRIGFRYASTVDFVSRGGTAVNFRFLRTMNSGDELKYGNFV 595  
QY 604 TVGFTTFFSFLDVQSTFTIGAMNFFSGNEVYIDRIEFPVVEVTEYAEYDFEKAQKV 663  
DB 596 RRAFTTFTTQIQDIIRTSIQGLSNGEVIYDKIEIIPVTATFRAEYDLERAQAVNAL 655  
QY 664 FTSINPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDKRELLEKVKYAKRLSDERNL 711

## RESULT 6

B42459  
hypochemical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag  
C;Species: Bacillus thuringiensis  
C;Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 09-Jul-2004  
C;Accession: B42459  
R;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.  
J. Bacteriol. 173, 3966-3976, 1991  
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene fro  
A;Reference number: A42459; MUID:91286178; PMID:2061280  
A;Accession: B42459  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-380 <CHA>  
A;Cross-references: UNIPROT:Q8KY61; UNIPROT:Q45740; GB:M63897  
C;Superfamily: parasporal crystal protein

Query Match 50.5%; Score 1900; DB 2; Length 380;  
Best Local Similarity 95.5%; Pred. No. 6.6e-126;  
Matches 363; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKMSYENVEPFFVSASTI 60  
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLNKNETDIELQNHEDCLKISEYENVEPFFVSASTI 60  
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFIFGLBWPVKGNOWEIFMEHVEIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFIFGLBWPVKGNOWEIFMEHVEIINOKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLSWGNRNTRARSVVKQSYIALELMFYQKLPFSAVSG 180  
DB 121 RNKALTDLKGLDALAVYHDSLSWGNRNTRARSVVKQSYIALELMFYQKLPFSAVSG 180  
QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTNROVERAGDYSDHCVKWS 240  
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTNROVERAGDYSDHCVKWS 240  
QY 241 TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALFPSTYDQMPYPIKTTAQLTREYVTD 300  
DB 241 TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALFPSTYDQMPYPIKTTAQLTREYVTD 300  
QY 301 GTVHPHPSFTSTTWNNAEYAEYDFEKAQKVATLFTSTNPRGLKTDVXDYHIDQVSNLV 360  
DB 301 GTVHPHPSFTSTTWNNAEYAEYDFEKAQKVATLFTSTNPRGLKTDVXDYHIDQVSNLV 360  
QY 361 GGHKLEFRITGGTLNISTQG 380  
DB 361 GGHKLEFRITGGTLNISTQG 380

## RESULT 7

S49247  
parasporal crystal protein cry9Ca1 [validated] - Bacillus thuringiensis  
N;Alternate names: parasporal crystal protein cryIH  
C;Species: Bacillus thuringiensis  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: A59350; S49247  
R;Lambert, B.; Buyse, L.; Decock, C.; Jansens, S.; Pien, C.; Saey, B.; Seurinck, J.; V  
Appl. Environ. Microbiol. 62, 80-86, 1996  
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity again  
A;Reference number: A59350; MUID:96141404; PMID:8572715  
A;Accession: A59350  
A;Molecule type: DNA  
A;Residues: 1-1157 <LAM>  
A;Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:G547554; PIDN:CAA85764.1; PID:G54755  
A;Experimental source: serovar tolworthi  
C;Comment: This parasporal crystal protein, active against corn borer and other insects,  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 39.7%; Score 1492; DB 1; Length 1157;  
Best Local Similarity 43.3%; Pred. No. 1.9e-96;  
Matches 322; Conservative 115; Mismatches 217; Indels 90; Gaps 15;

QY 26 LKNETDIELQNHEDCLKMSYENVEPFFVSAS-----TIQTGIGIAGKILGTGVFP 78  
DB 29 LASDPNALQNMVYKDYLTQMTDEDYDTSYINPSLSISGRDAVQTALTAVVGRILGALGVFP 88  
QY 79 AGQVASYLSFIFGLBWPVKGNOWEIFMEHVEIINOKISTYARNKALTDLKLGLDALAV 137  
DB 89 SGQIVSFYQELNLTPNDTALWEAFNRQVEELVNOQITFARNQALARQLGLGDSFNV 148  
QY 138 YHDSLSWGNRNTRARSVVKQSYIALELMFYQKLPFSAVSGEVEPLLPYIAQAANLHL 197  
DB 149 YORSQNLADLRNLSVVRQAQFIALDLDFVNAIPFLFVANGQQVPLLSVYAQAANLHL 208  
QY 198 LLLRDASIFGKEWGLSSSEISTFTNROVERAGDYSDHCVKYSTGLNLRGNTNAESWRY 257  
DB 209 LLLKDALSGEGWGTQGEISTYDROLELTAKYTNCTYNTYNTYNTYNTYNTYNTYNTY 268  
QY 258 NQFRDMTLMVLDLVALFPSTYDQMPYPIKTTAQLTREYVTDALGTVHPHPSFTSTTWN 317  
DB 269 HQFRDMTLMVLDLVALFPSTYDQMPYPIKTTAQLTREYVTDALGTVHPHPSFTSTTWN 328  
QY 318 NAPSFAIEAAVVRNPHLLDFLEQVITYLSLSRWS-NQYMMWGGHLE----- 366  
DB 329 PYNTSELENAFIRPPHFLDRLNSLTISS--NRFPVSSNFMWDYWSCHTLRRSYLNDASVQ 386  
QY 367 -----FRITGGTLNISTQSTNTSINPVTLPPTSRDYRTESLAGLNLFTQPVNGVPR 420  
DB 387 EDSYGLITTRATINPGVDGTRN--IESTAVDFRS-----ALIG-----IYGNR 429  
QY 421 VDFHVKFVTHPIASDNFYPGYAGIGT-----QLQDSENELPP-EATGQPNYESYS 470  
DB 430 ASF-----VPGGLFNGTSPANGCCRDLYDNDDELPPDESG-----SST 469  
QY 471 HRLSHIGLIS-----ASHVKALVSWTHRSADRTNTEPNSTIQTPLVKAFNLSG 521  
DB 470 HRLSHVTFPSFQTNQAGSIANAGSVPTVWTRDRDVLNNTITPNRITQLPLVKASAPVSG 529  
QY 522 AAVVGPFGFTGGDILRRNTGTGDIRVNIINPPFAQRVRIYASTTDLQFHTSINGKA 581  
DB 530 TTVLXGPGFTGGGILRRITNTGTGLRTVNSPLTQCYRLRVRFASTGNFSIRVLRGVS 589  
QY 582 INQNFSAVNRGSDLDYKTRFTVGTFT-----PFSFLDVQSTFTIGAMNFFSGNEVYI 635  
DB 590 IGDVRLGSTMNRGQELTYESFFTRFTTGPFPNPPFTTQAEILLTVAEGVSTGGEYI 649  
QY 636 DRIEFPVPEVTEYAEYDFEKAQKVATLFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEF 695  
DB 650 DRIEFPVNPAREAEEDLEAAKAVASLFTTRFD-GLQVNVTDYQVDQAANLVSLSDEQ 708  
QY 696 YLDEKRELFEIVKYAKQLHIERNM 719



parasporal crystal protein cry1Fa3 - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649

Accession: 002015  
R: Lambert, B.

submitted to the EMBL Data Library, April 1993

A;Reference number: S32645

A;Accession: S32649

A;Status: preliminary

A;Molecule type: DNA

A:Residues: 1-1174 <LAM>

A:Cross-references: UNIPROT:045749; EMBL:Z22512; NID:Q295865; PIDN:CAA80235.1; PID:Q295865

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match	39.1%	Score 1471;	DB 2;	Length 1174;
Best Local Similarity	44.8%	Pred. No. 5.8e-95;		
Matches 325;	Conservative	103;	Mismatches 202;	Indels 96;
				Gaps 17;

36 NINHE ---DCI.KMSEYENVEPEVSASTTOTGIGTA-GKTI.GTIGVPEAGOVASLYSEFIL 90

QY 38 NINHE--DCRWSIEINVEFVSASITQIGIGIA-ONITGIDOVFFASQVASDIT 30

DB 4 NIQNQCVPINCLSNPEVELTSEERSTGRFLDLSLSLIRFLSEFVFGVGVAFGFLDLW 63

01 CBI WPKYCINOWETEMPHHETI INOKTSTYAPNKAI ENL KCI CDAI AIVWDSI ESMVUCBN 150

[illegible]

DB 64 GETP---SEWSLFLQLIEQRIETLERNRAITTLRGLADSYEVYLEALREWEENPN 120

Qy 151 NTRARSVKSYIALELMFVQKLPSFAVSGEEVPLLPYAAANLHLLLRDASIFGKEW 210

[illegible]

QY 211 GLSSEISTFYNRQVERAGDYS DHCVKWYSTGLNNLRGTNAESWVRYNQFRRDMLMVL D 270

Db 181 GLDIATVNNHYNRLINLIHRYTEHCLDTYNQGLENLRGNTNRQWSRFNQFRRELTTLTVLD 240

[illegible]

Db 241 IVALFPNYDARAYPIOTSSOLTTREIYTSSV--IEDSP-----VSANI PNGFNRAEFG- 290

330 VRNP<sub>HI</sub>.I.D.F.I.E.Q.V.T.T.Y.S.I.L.S.R.W.S.N.T.O.Y.M.N.M.W.G.G.H.K.L.E.F.R.T.I.G.G.T.I.N.I.S.T.O.G.S.T.N.T.S.I.N.P.V. 389

QY 330 V A N F A L L D F D E Q V I I I S L S K W S N I Q I M N M W G G H R L E F K I I G G I T N I S I Q E S I N I S I N E V 368

DB 291 VRPFHMDFMN-----SLFVIAETVRSQIVMGHDLV-----SSRNIAGNET 331

200 TIDE-----TERMINATED AT 12:01:00 PM 4/3/4

[illegible]

D5 332 NFPYIGIFNPGGAIWIADEDPRPFYRT-----LSDPV-----FVRGGFGN 371

Qy 435 DNFYPPGYAGIGTQLQ-----DSENELPPEATGQPNYESYSHRLSHI----- 476

[illegible]

QY 477 --GLISASHV-KALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGG 533

Db 431 WPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIITQIPAVKAHNLHSGSTVVRGPGFTGG 490

RESULT 11

Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLVDVSVEG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKWYSTGLNNLRTGNAESWVRYNQFRDMLTLM 267  
Db 180 QRWGFDAAATINSRYNDLRLIGNYTDHVRWYNTGLERWGPDSRDWRWYRQFRRLTLT 239  
QY 268 VLDLVALPSSYDTQMPYPIKTAQLTREVYTDAGTVHPHPSFTTWTWNNAPSF-----S 323  
Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYNPV-----LENFDSFRGSAQ 285  
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR---WSNTQYMMN---WGGHKLERTIGTGLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITITDAHRGEYVWSGHQIMASPVGSGPEFTPLVGTMGNA 344  
QY 377 STQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPRVDFHMKVTHPIASDN 436  
Db 345 APOQRIVAQLGQGVVRLTSSLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF 453  
QY 490 SWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRV 513  
QY 550 NINPPFAQRYVRIRYASTTDLQFHTSINGKAINQNFSAATMNRGEDLDYKTRTVGFTT 609  
Db 514 NITAPLSQRYVRIRYASTTDLQFHTSINGKAINQNFSAATMNRGEDLDYKTRTVGFTT 573  
QY 610 PFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEKVTLFTSTNP 669  
Db 574 PFNFSNGSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633  
QY 670 RGLKTDVKDHYDQVSNLVESLSDFEYLDKRELFEIVKAKQLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVESLSDFEYLDKRELFEIVKAKQLHIERNM 683

## RESULT 12

A29125  
parasporal crystal protein Bt2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)  
C:Species: *Bacillus thuringiensis* subsp. *kurstaki*  
C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A29125  
R/Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme  
Bio/Technology 5, 807-813, 1987  
A>Title: Insect tolerant transgenic tomato plants.  
A/Reference number: A29125  
A/Accession: A29125  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-1156 <FIS>  
A/Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21  
C:Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 39.0%; Score 1467; DB 2; Length 1156;  
Best Local Similarity 44.5%; Pred. No. 1.1e-94;  
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

QY 36 NINHEDCLKMSYENVE-PFVSASTIQG-----IGIACKILGTGLVFPFAGQVASLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLQFLLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGDLAVYHDSLSWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAISRLGLSNLYQIYAESFREWEA 119  
QY 148 NRNNTARSVVKSQYIAELMFVQKLPFSFVSGEEVPLLPYIAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLVDVSVEG 179

QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKWYSTGLNNLRTGNAESWVRYNQFRDMLTLM 267  
Db 180 QRWGFDAAATINSRYNDLRLIGNYTDHVRWYNTGLERWGPDSRDWRWYRQFRRLTLT 239  
QY 268 VLDLVALPSSYDTQMPYPIKTAQLTREVYTDAGTVHPHPSFTTWTWNNAPSF-----S 323  
Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYNPV-----LENFDSFRGSAQ 285  
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR---WSNTQYMMN---WGGHKLERTIGTGLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITITDAHRGEYVWSGHQIMASPVGSGPEFTPLVGTMGNA 344  
QY 377 STQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVPRVDFHMKVTHPIASDN 436  
Db 345 APOQRIVAQLGQGVVRLTSSLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF 453  
QY 490 SWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRV 513  
QY 550 NINPPFAQRYVRIRYASTTDLQFHTSINGKAINQNFSAATMNRGEDLDYKTRTVGFTT 609  
Db 514 NITAPLSQRYVRIRYASTTDLQFHTSINGKAINQNFSAATMNRGEDLDYKTRTVGFTT 573  
QY 610 PFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEKVTLFTSTNP 669  
Db 574 PFNFSNGSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633  
QY 670 RGLKTDVKDHYDQVSNLVESLSDFEYLDKRELFEIVKAKQLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVESLSDFEYLDKRELFEIVKAKQLHIERNM 683

## RESULT 13

A22798  
parasporal crystal protein - *Bacillus thuringiensis*  
C:Species: *Bacillus thuringiensis*  
C/Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C/Accession: A22798  
R/Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
Gene 34, 243-251, 1985  
A>Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thuring*  
Bio/Technology 5, 807-813, 1987  
A/Reference number: A22798; PMID:85232070; PMID:2989108  
A/Accession: A22798  
A/Molecule type: DNA  
A/Residues: 1-934 <SHI>  
A/Cross-references: UNIPROT:Q9S5V8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713  
C:Comment: The authors translated the codon ACA for residue 264 as Ser.  
C:Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 38.7%; Score 1454.5; DB 2; Length 934;  
Best Local Similarity 43.5%; Pred. No. 5.8e-94;  
Matches 310; Conservative 119; Mismatches 222; Indels 61; Gaps 12;

QY 36 NINHEDCLKMSYENVE-PFVSASTIQG-----IGIACKILGTGLVFPFAGQVASLYS 87  
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLQFLLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGDLAVYHDSLSWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFARNQAISRLGLSNLYQIYAESFREWEA 119  
QY 148 NRNNTARSVVKSQYIAELMFVQKLPFSFVSGEEVPLLPYIAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLVDVSVEG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHCKWYSTGLNNLRTGNAESWVRYNQFRDMLTLM 267

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Db      180 QRWGDAATNSRYNDLRLIGNYTDYAVRWYNTGLERVMGPDSDRWVYNQFRELTLT 239
QY      268 VLDLVALFSDYDTOMYPIKTAQLTREYVYTDAGTVHHPHPSFTSTWYNNAPSAIEA 327
Db      240 VLDLVALFSDYDSTRYPIRTVSQLTREIYTNV-----LENFDGSPRGMAQ 285
QY      328 AV---VRNPHLLDFLEQVITYLLSRNSNTQYMMWGHKLEFRITGGT---LNISTQGS 381
Db      286 RIEQNIQPHLMDILNRIITYTDVHRG-----FNWMSGHQITASPVGSGPEFAFLFGN 340
QY      382 TMTSINPVLPTFTSRDVRVTESEL-----AGLNLFLTQPVNGVPRVDFHWKVFTHPI 432
Db      341 AGNAAPPVLVSLTGLGIFRTLSPLRYRILGSGPN---NQELFVLDTGTFESFASLTTLN 397
QY      433 ASDNFYYPGVAGICTQLODSNELPPEATQPNYESYSHRLSHIGLISAS-----HVKAL 487
Db      398 PSTIYRQRTV-----DSLVIPOQNSVPPRAGFSHRUSHVTLMSQAAGAVYTLRAP 450
QY      488 VYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAUVVRGPGFTGGDILRRNTGTGDI 547
Db      451 TFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRNTGTGDI 510
QY      548 RVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKTFRTVGF 607
Db      511 RVNITAPLSQRYRIRYASTTDLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRVTVGF 570
QY      608 TTPSFELDVQSTFTIGANFSSGNEVYDRIEFVPEVTEYAEYDEKAKQKVTALFTST 667
Db      571 TTPFNFSNGSSVFTLSAHVFNSEVYDRIEFVPAEVTPEAEYDLERAQKAVNELFTSS 630
QY      668 NPGRLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFIEIVKYAKQLHIERNM 719
Db      631 NQIGLKTVDYDHYDQVSNLVESLSDEFYLDKRELFIEIVKYAKQLHIERNM 682

RESULT 14
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N/Alternate names: 135K insecticidal protein
C/Species: Bacillus thuringiensis
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: JT0241
R/Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Okawa, H.
Agric. Biol. Chem. 52, 1565-1573, 1988
A/Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A/Reference number: JT0241
A/Accession: JT0241
A/Molecule type: DNA
A/Residues: 1-1176 <SHI>
A/Cross-references: UNIPROT:P02965
A/Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein
C/Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match      38.7%; Score 1453.5; DB 2; Length 1176;
Best Local Similarity 43.5%; Pred. No. 9.9e-94;
Matches 310; Conservative 118; Mismatches 223; Indels 61; Gaps 12;

QY      36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIACKILGTGLVPPFAGQVASLYS 87
Db      4  NPINNECIPVCLSNPEVEVLGGERIERGTPTDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY      88 FILGELMPKGNQWEIFEHEVBEIINOKISTYARNKALTDLKGLDALAYHDSLESWVG 147
Db      63 IIWGF--GPSQWDAFLVQIEQLINQRIEIEFARNQAISRLGLESLNLYQIYAESFRENEA 119
QY      148 NRNNTARSVVKSYIAELMFVQKLPFSFVSGEEVPLLPYIAQANLHLLLRDASIFG 207
Db      120 DPTPALREMRICQNDWNNSALTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179
QY      208 KEWGLSSSISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRDMLM 257

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Db      180 QRWGDAATNSRYNDLRLIGNYTDYAVRWYNTGLERVMGPDSDRWVYNQFRELTLT 239
QY      268 VLDLVALFSDYDTOMYPIKTAQLTREYVYTDAGTVHHPHPSFTSTWYNNAPSAIEA 327
Db      240 VLDLVALFSDYDSTRYPIRTVSQLTREIYTNV-----LENFDGSPRGMAQ 285
QY      328 AV---VRNPHLLDFLEQVITYLLSRNSNTQYMMWGHKLEFRITGGT---LNISTQGS 381
Db      286 RIEQNIQPHLMDILNRIITYTDVHRG-----FNWMSGHQITASPVGSGPEFAFLFGN 340
QY      382 TMTSINPVLPTFTSRDVRVTESEL-----AGLNLFLTQPVNGVPRVDFHWKVFTHPI 432
Db      341 AGNAAPPVLVSLTGLGIFRTLSPLRYRILGSGPN---NQELFVLDTGTFESFASLTTLN 397
QY      433 ASDNFYYPGVAGICTQLODSNELPPEATQPNYESYSHRLSHIGLISAS-----HVKAL 487
Db      398 PSTIYRQRTV-----DSLVIPOQNSVPPRAGFSHRUSHVTLMSQAAGAVYTLRAP 450
QY      488 VYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAUVVRGPGFTGGDILRRNTGTGDI 547
Db      451 TFSWQHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVGPGFTGGDILRRNTGTGDI 510
QY      548 RVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNGEDLDYKTFRTVGF 607
Db      511 RVNITAPLSQRYRIRYASTTDLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRVTVGF 570
QY      608 TTPSFELDVQSTFTIGANFSSGNEVYDRIEFVPEVTEYAEYDEKAKQKVTALFTST 667
Db      571 TTPFNFSNGSSVFTLSAHVFNSEVYDRIEFVPAEVTPEAEYDLERAQKAVNELFTSS 630
QY      668 NPGRLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFIEIVKYAKQLHIERNM 719
Db      631 NQIGLKTVDYDHYDQVSNLVESLSDEFYLDKRELFIEIVKYAKQLHIERNM 682

RESULT 15
S02134
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai IC1)
N/Alternate names: delta-endotoxin IC1; entomocidal crystal protein
C/Species: Bacillus thuringiensis
A/Variety: strain aizawai IC1
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S02134; S04994
R/Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A/Title: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal
A/Reference number: S02134; MUID:89083518; PMID:3205732
A/Accession: S02134
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-1155 <HAI>
A/Cross-references: UNIPROT:P06578; EMBL:X13233; NID:G40277; PIDN:CAA31620.1; PID:G40278
A/Experimental source: strain aizawai IC1
R/Haider, M.Z.; Ellar, D.J.
J. Mol. Biol. 208, 183-194, 1989
A/Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes
A/Reference number: S04994; MUID:89362455; PMID:2769751
A/Accession: S04994
A/Molecule type: DNA
A/Residues: 429-449, 'A', 451-724 <HAW>
A/Cross-references: EMBL:X16315
A/Experimental source: strain aizawai IC1
C/Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C/Superfamily: parasporal crystal protein
C/Keywords: delta-endotoxin

Query Match      38.6%; Score 1450; DB 2; Length 1155;
Best Local Similarity 44.1%; Pred. No. 1.7e-93;
Matches 313; Conservative 112; Mismatches 229; Indels 56; Gaps 13;

QY      36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIACKILGTGLVPPFAGQVASLYS 87

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Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLGLVD 62  
Qy 88 FILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGLGDALAVYHDSLEWVG 147  
Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEEFARNQAISRLGSLNLYQIYAESPWEA 119  
Qy 148 NNNNTRARSVVKSQVIALELMFVQKLPSPAVSGEEVPLLPYIAQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREENRIQFNDMSALTTAIPFAVQNVQVPLLSVYQAAANLHLSVLRDYSVFG 179  
Qy 208 KEMGLSSSEISTFYNNRQVERAGDYSDHCVKWYSTGLNNLRGTNAESWVRYNQFRRDWTL 267  
Db 180 QRWGDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWGPDSRDWIRYNQFRRELTLT 239  
Qy 268 VLDLVALPPSYDTQMPYPIKTAQLTREVTDAICTVHPHPSFTSTTWYNNNAPSF----S 323  
Db 240 VLDIVSLFPNYDSRTYPIRTVSQLTREIYNPV-----LENFGSFRGSAQ 285  
Qy 324 AIEAAVVRNPHLLDFLEQVYIYSLLSR----WSNTQYNNM--WGCHKLEFETIGGTINI 376  
Db 286 GIEGS-IRSPHLMIDILNSIITYTDAHRGEYWSGHQIMASPVGFSGPPEFTFELYGTMGNA 344  
Qy 377 STQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDN 436  
Db 345 APQORIVAQLCGQVYRTLSSLYRRPFNIGIN---NQQLSVLDGTEPAYG-----TSSN 395  
Qy 437 FYYPGAGIGTQLQDSENEPLPEATGQPNYESYSHRLSHGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNNVPPQGFHSHLSHVMPSRSGFSNSSVSIIRPPMF 453  
Qy 490 SMTNRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRRNTGTGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDIILRRISPCQISTLRV 513  
Qy 550 NINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTRTVGFTT 609  
Db 514 NITAPLSQRYRIRYASTTNLQHTSIDGRINQGNFSATMSSGSLQSGSPRIVGFTT 573  
Qy 610 PFSFLDVQSTFTIGAMNPFSSGNEVYIDRIEFPVPEVYEAEDFEKAQEKVTALFTSTNP 669  
Db 574 PFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFPVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633  
Qy 670 RGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFPEIVKYAKQLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVECLSDFECLDEKKELSEKVKHAKRLSDERNL 683

Search completed: October 28, 2004, 18:31:50  
Job time : 22.191 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-55  
Perfect score: 3760  
Sequence: 1 MRLKNQDKHQSFSSNAKVDK.....KRELFVIVKAYQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	17	US-10-782-020-10
2	3760	100.0	719	17	US-10-782-141-8
3	3760	100.0	719	17	US-10-782-096-10
4	3760	100.0	719	17	US-10-782-570-7
5	3476.5	92.5	710	14	US-10-428-961-42
6	2278.5	60.6	1228	16	US-10-809-953-10
7	2265.5	60.3	1207	10	US-09-988-462-7
8	2186.5	58.2	1227	14	US-10-428-961-63
9	2171.5	57.8	1186	9	US-09-826-660-23
10	2116	56.3	1228	14	US-10-428-961-38
11	2116	56.3	1228	15	US-10-614-524-2
12	1932.5	51.4	643	9	US-09-826-660-25
13	1722.5	45.8	1167	14	US-10-089-678-1
					Sequence 10, Appl
					Sequence 8, Appl
					Sequence 10, Appl
					Sequence 7, Appl
					Sequence 42, Appl
					Sequence 10, Appl
					Sequence 7, Appl
					Sequence 63, Appl
					Sequence 23, Appl
					Sequence 38, Appl
					Sequence 2, Appl
					Sequence 25, Appl
					Sequence 1, Appl

14	1681.5	44.7	653	14	US-10-428-961-6	Sequence 6, Appl
15	1670.5	44.4	1157	17	US-10-782-141-16	Sequence 16, Appl
16	1670.5	44.4	1157	17	US-10-782-096-17	Sequence 17, Appl
17	1670.5	44.4	1157	17	US-10-782-570-13	Sequence 13, Appl
18	1511	40.2	1206	13	US-10-032-717-2	Sequence 2, Appl
19	1511	40.2	1206	14	US-10-414-637-2	Sequence 2, Appl
20	1511	40.2	1206	15	US-10-606-320-2	Sequence 2, Appl
21	1511	40.2	1206	17	US-10-746-914-2	Sequence 2, Appl
22	1495	39.8	1210	13	US-10-032-717-4	Sequence 4, Appl
23	1495	39.8	1210	14	US-10-414-637-4	Sequence 4, Appl
24	1495	39.8	1210	15	US-10-606-320-4	Sequence 4, Appl
25	1495	39.8	1210	17	US-10-746-914-4	Sequence 4, Appl
26	1485.5	39.5	1156	14	US-10-099-285-72	Sequence 72, Appl
27	1485.5	39.5	1156	14	US-10-428-961-28	Sequence 28, Appl
28	1467	39.0	1155	9	US-09-756-643-2	Sequence 2, Appl
29	1467	39.0	1155	10	US-09-988-462-9	Sequence 9, Appl
30	1467	39.0	1155	14	US-10-136-998A-2	Sequence 2, Appl
31	1467	39.0	1177	14	US-10-035-060-6	Sequence 6, Appl
32	1467	39.0	1181	10	US-09-988-462-11	Sequence 11, Appl
33	1467	39.0	1181	10	US-09-988-462-13	Sequence 13, Appl
34	1467	39.0	1181	10	US-09-988-462-15	Sequence 15, Appl
35	1467	39.0	1181	10	US-09-988-462-17	Sequence 17, Appl
36	1467	39.0	1181	10	US-09-988-462-28	Sequence 28, Appl
37	1467	39.0	1181	14	US-10-136-998A-4	Sequence 4, Appl
38	1467	39.0	1181	14	US-10-136-998A-8	Sequence 8, Appl
39	1467	39.0	1181	14	US-10-136-998A-10	Sequence 10, Appl
40	1467	39.0	1181	14	US-10-136-998A-12	Sequence 12, Appl
41	1462	38.9	1177	14	US-10-035-060-2	Sequence 2, Appl
42	1460	38.8	1177	14	US-10-035-060-8	Sequence 8, Appl
43	1459	38.8	1177	14	US-10-102-469-24	Sequence 24, Appl
44	1443.5	38.4	1176	17	US-10-782-141-6	Sequence 6, Appl
45	1443.5	38.4	1176	17	US-10-782-096-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 100.0%; Score 3760; DB 17; Length 719;  
Best Local Similarity 100.0%; Pred. No. 2.7e-309;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRLKNQDKHQSFSSNAKVDKISTDKNKTDTLQININHECLKMKSEYENVEPFFVSASTI	60
Db	1	MRLKNQDKHQSFSSNAKVDKISTDKNKTDTLQININHECLKMKSEYENVEPFFVSASTI	60
Qy	61	QTGIGTAGKILGTIGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120
Db	61	QTGIGTAGKILGTIGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINOKISTYA	120

QY 121 RNKALTDLKGDLAVYHDSLESWGNNRNTARSVVKQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNNRNTARSVVKQYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPYDTQMPYIKTTAQLTREYITDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPYDTQMPYIKTTAQLTREYITDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 DB 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 QY 601 TFRVGTTPFSLDVOSTFTTIGAMFSSGNEVYIDRIEFVPEVTEYAEYDEKAQSKV 660  
 DB 601 TFRVGTTPFSLDVOSTFTTIGAMFSSGNEVYIDRIEFVPEVTEYAEYDEKAQSKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2

US-10-782-141-8  
 ; Sequence 8, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10/782,141  
 ; CURRENT FILING DATE: 2004-02-20  
 ; PRIOR APPLICATION NUMBER: 60/448,632  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-8

Query Match 100.0%; Score 3760; DB 17; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-309;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEFPFVASTI 60  
 QY 61 QTGIGIAGKILGTILGVPFAGQVASYLIFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTILGVPFAGQVASYLIFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGNNRNTARSVVKQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNNRNTARSVVKQYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPYDTQMPYIKTTAQLTREYITDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPYDTQMPYIKTTAQLTREYITDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 QY 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
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 DB 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSAATMNRGDDLYK 600  
 QY 601 TFRVGTTPFSLDVOSTFTTIGAMFSSGNEVYIDRIEFVPEVTEYAEYDEKAQSKV 660  
 DB 601 TFRVGTTPFSLDVOSTFTTIGAMFSSGNEVYIDRIEFVPEVTEYAEYDEKAQSKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3

US-10-782-096-10  
 ; Sequence 10, Application US/10782096  
 ; Publication No. US20040210964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274148  
 ; CURRENT APPLICATION NUMBER: US/10/782,096  
 ; CURRENT FILING DATE: 2004-02-19  
 ; PRIOR APPLICATION NUMBER: 60/448,633  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-096-10

Query Match 100.0%; Score 3760; DB 17; Length 719;

Best Local Similarity 100.0%; Pred. No. 2.7e-309;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKSEYENVEPFVSASTI 60  
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKSEYENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMFVQKLPSPFVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMFVQKLPSPFVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240

QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREVTDAI 300  
Db 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREVTDAI 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420  
Db 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
Db 541 TGTGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

QY 601 TFRVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAQEKV 660  
Db 601 TFRVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELIVKYAKQLHIERNM 719

RESULT 4  
US-10-782-570-7  
; Sequence 7, Application US/10782570  
; Publication No. US20040210965A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMT-007, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274144  
; CURRENT APPLICATION NUMBER: US/10782,570  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,812  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 719

TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-570-7

Query Match 100.0%; Score 3760; DB 17; Length 719;  
Best Local Similarity 100.0%; Pred. No. 2.7e-309;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKSEYENVEPFVSASTI 60  
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLNKNETDIELQININHEDECLKSEYENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMFVQKLPSPFVSG 180  
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSYQYIALELMFVQKLPSPFVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWYS 240

QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREVTDAI 300  
Db 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTOMYPIKTTAQLTREVTDAI 300

QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360  
Db 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420  
Db 361 GGHKLEFRTIGTGLNTSTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
Db 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540

QY 541 TGTGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
Db 541 TGTGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

QY 601 TFRVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAQEKV 660  
Db 601 TFRVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELIVKYAKQLHIERNM 719  
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDSEFYLDKRELFELIVKYAKQLHIERNM 719

RESULT 5  
US-10-428-961-42  
; Sequence 42, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Wei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (200)..(200)  
; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
US-10-428-961-42

Query Match 92.5%; Score 3476.5; DB 14; Length 710;  
Best Local Similarity 92.5%; Pred. No. 2.8e-285;  
Matches 665; Conservative 15; Mismatches 30; Indels 9; Gaps 1;

QY	1	MLKKNQDKHQSFSSNAKVDKIDTSLKNETDIELQNHEDCLKMEYENVEPVSASTI	60
DB	1	MKSXQNNHQSLSNATVDKNFTGSLNNTNTELQNFH-----EGIEPVSASTI	51
QY	61	QTGIGIAGKILGTPAGQVAVSLYFSLGELWPKGKNQWEIEMEHVEEIIINQKISTYA	120
DB	52	QTGIGIAGKILGNLGVPPAGQVAVSLYFSLGELWPKGKSQWEIEMEHVEEIIINQKISYA	111
QY	121	RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVVKSOYIALLELMFVQKLPSFAVSG	180
DB	112	RNKALADLKLGLDALAVYHDSLESWGNRNTRARSVVKSOYITLLELMFVQSLPSFAVSG	171
QY	181	EEVPLPIYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNNROVERAGDYSDHCVKWS	240
DB	172	EEVPLPIYAAQANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSEYSDHCVKWN	231
QY	241	TGLNLRGCTNAESWVYNNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREVTDAI	300
DB	232	TGLNLRGMNAESWVYNNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREVTDAI	291
QY	301	GTVEHPHPSSTTWTYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	360
DB	292	GTVEHPHPSSTTWTYNNNAPSSTIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW	351
QY	361	GGHKLFEFTIGTILNISTQGSNTSINPVTLPFTSRDYRTESLAGNLFQTQPVNGVPR	420
DB	352	GGHKLFEFTIGTILNISTQGSNTSINPVTLPFTSRDYRTESLAGNLFQTQPVNGVPR	411
QY	421	VDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
DB	412	VDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	471
QY	481	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
DB	472	ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	531
QY	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDYK	600
DB	532	TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDYK	591
QY	601	TFRVGFPTFPFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV	660
DB	592	TFRVGFPTFPFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEV	651
QY	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDKFYLDKRELFPIVKYAKQLHIERNM	719
DB	652	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDKFYLDKRELFPIVKYAKQLHIERNM	710

RESULT 6  
US-10-809-953-10  
; Sequence 10, Application US/10809953  
; Publication No. US20040181825A1  
; GENERAL INFORMATION:

; APPLICANT: Van Mellaert, Herman  
; APPLICANT: Botterman, Johan  
; APPLICANT: Van Rie, Jeroen  
; APPLICANT: Joos, Henk  
; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING BT INSECTIC  
; TITLE OF INVENTION: CRYSTAL PROTEINS  
; FILE REFERENCE: 021565-078  
; CURRENT APPLICATION NUMBER: US/10/809,953  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: US/09/661,016  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: PCT/EP90/00905  
; PRIOR FILING DATE: 1990-05-30  
; PRIOR APPLICATION NUMBER: GB 89401499.2  
; PRIOR FILING DATE: 1989-05-31  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1228  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-809-953-10

Query Match 60.6%; Score 2278.5; DB 16; Length 1228;  
Best Local Similarity 62.7%; Pred. No. 2.1e-183;  
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY	23	TDSLKNETDIELQNH-----EDCLKMEYENVEPVSASTIQTGTGIAGKI	70
DB	2	TSNRKNEEIIINAVSNHSAQMDLLDPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI	61
QY	71	LGTGLVPPAGQVAVSLYFSLGELWPKGKNQWEIEMEHVEEIIINQKISTYARNKALTDLKG	130
DB	62	LGVLGVPPAGQVAVSLYFSLGELWPKGKNQWEIEMEHVEEIIINQKISTYARNKALTDLKG	121
QY	131	LGDALAVYHDSLESWGNRNTRARSVVKSOYIALLELMFVQKLPSFAVSGEVEPLPIYA	190
DB	122	LGDSFRAYQOQSLDLEWLNDRDARTSRVLTQYIALELDLFLNAMPLFAIRNOEVEPLPIYA	181
QY	191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNNROVERAGDYSDHCVKYSTGLNLRGTN	250
DB	182	QAANLHLLLRDASIFGSEFGLTSQEIQRYRQVTRDYSDYCVWEYNTGLNLRGTN	241
QY	251	AESWVYNNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREVTDAITGVPHPSFT	310
DB	242	AASWVYNNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREVTDAITGVPHPSFT	299
QY	311	STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMWGGHKLFEFTI	370
DB	300	SMWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMWGGHKLFEFTI	359
QY	371	GGTLNISTQGSNTSINPVTLPFTSRDYRTESLAGNLF--LTQPVNGVPRVDFHWKFV	428
DB	360	GGGLNTSTHGTATNSINPVTLPFASRDYRTESYAGVLLWGLIYLEPIHGVPTVRFNF---	416
QY	429	THP-----IASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASH	483
DB	417	TNPQNISDRGTANYQP--YESPGLQLODSETELPPETERENYESYSHRLSHIGLILQSR	475
QY	484	VKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT	543
DB	476	VNVPYVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT	535
QY	544	FGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMARGEDLDYKTR	603
DB	536	FGPIRVTVNGPLTQRYRIGFRYASTVDFVFSRGGTTVANNFRFLRTMNSGDELKYGNFV	595
QY	604	TVGFTTTPFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV	663
DB	596	RRATFTPTFTQIDIIIRTSIQGLSGNGEVIDKIBIIPVTATFAEYDLERAQEAVAL	655
QY	664	FTSTNPRGLKTDVKDYHIDQVSNLVESLSDKFYLDKRELFPIVKYAKQLHIERNM	719

Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDBFCLDEKRELLEKVKYAKELSDERNL 711

RESULT 7

US-09-988-462-7

; Sequence 7, Application US/09988462

; Publication No. US20030046726A1

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; Desai, Nalini M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warren, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Launis, Karen L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-No. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 60.3%; Score 2265.5; DB 10; Length 1207;

Best Local Similarity 64.3%; Pred. No. 2.6e-182;

Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

Qy 40 EDCIKMSYENVEPVFVASTTQTGTGIGIAGKILGTGVFPAGQVASYLSYFVGLWPKGN 99

Db 10 EDSLCIABGNNDPFGVASTVQTGINAGRIAGLVGVPFAGQVASYLSYFVGLWPKGRD 69

Qy 100 QWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLSWVGNNRNNTRARSVVK 159

Db 70 QWEIFLEHVEQLNQITENANRALTALRQGLGDSFRAVQCSLEDWLENRDDARTSRVLY 129

Qy 160 SOYIALELMFVQKLPSPFAVSGBEVPLLPPIYAAQANLHLLLRDASIFGKEWGLSSSEIST 219

Db 130 TQYIALELDFLNAMPLFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTQEIQR 189

Qy 220 FYNROVERAGDYSCHVKWYSTGLNNLRTGTAESWVRYNQPRRDMTLMVLVLPSPSYD 279

Db 190 YYERQVTRDYSYCVWEYNTGLNLRGTNAASWVRYNQPRRDLTGLVLDLVALPSPSYD 249

Qy 280 TOMYPIKTTAQLTREVYTDAGTVHPHPSFTSTTWNNNAFSFAIEAAVVRNPHLLDFL 339

Db 250 TRTYPINTSAQLTREVYTDAGT--GVNMAWNNWNNNAFSFAIEAAVVRNPHLLDFL 307

Qy 340 EQVTIYSLRSWNTQYMMWGHKLBFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVS 399

Db 308 EQLTIFASRSWNTQYMMWGHKLBFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVS 367

Qy 400 RTESLAGLNLF--LTQPVNGVPRVDFHMKFVTHP-----IASDNFYYPGYAGIGTQLQDS 452

Db 368 RTESYAGVLLWGIYLEPIHGVPTVRFPF--TNPNISDRGTANYSQP-YESPGIQLKDS 423

Qy 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512

Db 424 ETELPPEPPERPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 483

Qy 513 VKAFNLSSGAAVVGPGTGGDILRRNTGTGDIRVNINPFAQRYRIRYASTDLQ 572

Db 484 VKASELPQGTTVVRGPGTGGDILRRNTGTGDIRVNINPFAQRYRIRYASTVDFD 543

Qy 573 FHTSINGKAINQGNFSATWNRGDDLYKTRFTVGFPTFFSLDVSQFTTIGAWNFSSGNE 632

Db 544 FFVSRGGTTVNNPFLRTMNSGDELKYGNFVRAFTTFFTTQIQDIIRTSIQGLSGNGE 603

Qy 633 VYIDRIEFPVPEVTEAYEDFEKAQEKVATLTSTNPRGLTVDKDYHIDQVSNLVESLS 692

Db 604 VYIDKIEIIPVTATFEAYDLEAQAQEAVALFTNPRRLKTDVTDYHIDQVSNLVACL 663

Qy 693 DEFYLDKRELFEIVKYAKQLHIERNM 719

Db 664 DEFCLDEKRELLEKVKYAKELSDERNL 690

RESULT 8

US-10-428-961-63

; Sequence 63, Application US/10428961

; Publication No. US20030237111A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Rupar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; FILE REFERENCE: MECO201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,995

; PRIOR FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 63

; LENGTH: 1227

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 14; Length 1227;

Best Local Similarity 59.2%; Pred. No. 1.3e-175;

Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;

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QY 13 SSNAKVDK1STDSLN-----ETDIELQNIHEDCLKSEYENVEPVSASTIQTGIG 65
Db 7 NENEIINALSIPAVSNHSAQMLSTDARI-----EDSLCIAEGNNDPVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQVASFYSLFGLWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGRILGVLPFAGQIASFYSLFGLWPKGRDPWEIFLEHVEQLIRQVTTENTDTAL 121
QY 126 TDLKGLGDALAVVHDSLSWGNRNTRARSVVKSOYIALELMFVQKLPFAVSGEEVPL 185
Db 122 ARLOGLGNSFRAYQOQSLDWNLRDARTSRVLYTQVIALELDFLNAFLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNN 245
Db 182 LMTYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEKTRREYSDYCARWYNTGLNN 241
QY 246 LRGITNAESVRYNQFRDRMTLWLDLVALFSPSYDTOMYPKTTAQLTREVVYTDAGTVHP 305
Db 242 LRGITNAESVRYNQFRDRMTLWLDLVALFSPSYDTOMYPKTTAQLTREVVYTDAGTVHP 301
QY 306 HPSFTSTTWNNAAPSFSAIEAAVVRPHLLDFLEQVITISLLSWSNTOYMNWVGHL 365
Db 302 PSGFASTNWFNNAPSFSAIEAAVVRPHLLDFLEQVITISLLSWSNTOYMNWVGHL 361
QY 366 EFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHW 425
Db 362 ESRITRGSLSSTWHTGNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHW 421
QY 426 KFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 485
Db 422 RNPLNSLRGSLLYTIGYTGVTGQTFDSETELPPETTERPNYESYSHRLSNIRLISGNTLR 481
QY 546 DIRVNINPFAQRVRYRYASTDLQFHTSINGKAINQGNFSAATNMGEDLDYKTRTV 605
Db 542 SMGLNFNTSLQRYRVRYRYASTDLQFHTSINGKAINQGNFSAATNMGEDLDYKTRTV 601
QY 606 GFTTFFFLDVQSTFTICAWNFSSGNEVYIDRIEFPVVEVYAEYDFEKAQKVTALFT 665
Db 602 EFPVGISASGSQ-TAGISISNAGROTFHDKIEFIPITATFEAEYDLERAQKAVNALFT 660

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RESULT 9
US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826.660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23
Query Match 57.8%; Score 2171.5; DB 9; Length 1186;
Best Local Similarity 59.0%; Pred.No. 2.4e-174;
Matches 421; Conservative 108; Mismatches 172; Indels 13; Gaps 3;
QY 13 SSNAKVDK1STDSLN-----ETDIELQNIHEDCLKSEYENVEPVSASTIQTGIG 65
Db 7 NENEIINALSIPAVSNHSAQMLSTDARI-----EDSLCIAEGNNDPVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQVASFYSLFGLWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGRILGVLPFAGQIASFYSLFGLWPKGRDPWEIFLEHVEQLIRQVTTENTDTAL 121
QY 126 TDLKGLGDALAVVHDSLSWGNRNTRARSVVKSOYIALELMFVQKLPFAVSGEEVPL 185
Db 122 ARLOGLGNSFRAYQOQSLDWNLRDARTSRVLYTQVIALELDFLNAFLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNN 245
Db 182 LMTYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEKTRREYSDYCARWYNTGLNN 241
QY 246 LRGITNAESVRYNQFRDRMTLWLDLVALFSPSYDTOMYPKTTAQLTREVVYTDAGTVHP 305
Db 242 LRGITNAESVRYNQFRDRMTLWLDLVALFSPSYDTOMYPKTTAQLTREVVYTDAGTVHP 301
QY 306 HPSFTSTTWNNAAPSFSAIEAAVVRPHLLDFLEQVITISLLSWSNTOYMNWVGHL 365
Db 302 PSGFASTNWFNNAPSFSAIEAAVVRPHLLDFLEQVITISLLSWSNTOYMNWVGHL 361
QY 366 EFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHW 425
Db 362 ESRITRGSLSSTWHTGNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPRVDFHW 421
QY 426 KFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISASHVK 485
Db 422 RNPLNSLRGSLLYTIGYTGVTGQTFDSETELPPETTERPNYESYSHRLSNIRLISGNTLR 481
QY 486 ALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTG 545
Db 482 APVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTG 541
QY 546 DIRVNINPFAQRVRYRYASTDLQFHTSINGKAINQGNFSAATNMGEDLDYKTRTV 605
Db 542 SMGLNFNTSLQRYRVRYRYASTDLQFHTSINGKAINQGNFSAATNMGEDLDYKTRTV 601
QY 606 GFTTFFFLDVQSTFTICAWNFSSGNEVYIDRIEFPVVEVYAEYDFEKAQKVTALFT 665
Db 602 EFPVGISASGSQ-TAGISISNAGROTFHDKIEFIPITATFEAEYDLERAQKAVNALFT 660

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RESULT 10
US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US2003023711A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

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; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-38

Query Match          56.3%; Score 2116; DB 14; Length 1228;
Best Local Similarity 59.5%; Pred. No. 1.3e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66

QY 71 LGVLGVPPAGQVASYLSEFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQG 126

QY 131 LGDALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVKQLPSFAVSSEVEPLPIYA 190
Db 127 LGDSFRAYQCSLEDWLENRRDARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVVEWYNTGLNSLRGTN 246

QY 251 AESWVRYNQFRDMLTMDLVALPSPYDTQMPYIKTTAQLTREVTDAIGTVHPHSFT 310
Db 247 AASWVRYNQFRDLTLGLVDLVALPSPYDTRTYPINTSAQLTREVTDAIGAT--GVNMA 304

QY 311 STTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKLFRFTI 370
Db 305 SMWYNNAPSAIEATAVIRSPHLLDFLEQVTIYSLSRWSATRHMTYWRGHTIQSRPI 364

QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNL--LTPVNGVPRVDFHWKFV 428
Db 365 GGGTNTSTHGSTNTSINPVLRSFFSRDVTYTESYAGVLLWGIYLEPIHGVTVRFRNP 424

QY 429 --THPIASDNFYYPGYAGIGTOLQDSNELPPEATQPNYESYSHRLSHIGLISASHVKA 486
Db 425 QNTFERGTANYSQP--YESPGQLQKSETLPPETTERPNYESYSHRLSHIGLISQSRVHV 483

QY 487 LVYSWTHRSADRTNTEPNSTIQIPLVKAENLSSGAAVVRGPGFTGGDILRRNTGTFTVG 546
Db 484 PVISWTHRSADRTNTEPNSTIQIPLVKAENLSSGTSVVSVPFTGGDIIRTNVNGSVLS 543

QY 547 IRVYNINPPFAQRYRVRIRYASTDQLQHTSINGKAINQGNFSAATNRGCDLKYTFRTVG 606
Db 544 MGLNFNNTSLQRYRVRIRYAAASQTMVLRVTGGSTTFDQGFPSMTSANESLTSQSRFAE 603

QY 607 FTTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVPEVYEAEDYFKAQEKVTAFTS 666
Db 663 TNPRLKTDVTDYHIDQVSNLVACLSDSEFCCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 11
US-10-614-524-2
; Sequence 2, Application US/10614524
; Publication No. US20040016020A1
; GENERAL INFORMATION:
; APPLICANT: Arnaut, Greta
; APPLICANT: Boets, Annemie
; APPLICANT: Damme, Nicole
; APPLICANT: Mathieu, Eva

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; APPLICANT: Vanneste, Stijn
; APPLICANT: Van Rie, Jeroen
; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.
; FILE REFERENCE: NEWBTSUS2
; CURRENT APPLICATION NUMBER: US/10/614,524
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/739,243
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/173387
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-614-524-2

Query Match          56.3%; Score 2116; DB 15; Length 1228;
Best Local Similarity 59.5%; Pred. No. 1.3e-169;
Matches 424; Conservative 98; Mismatches 181; Indels 10; Gaps 7;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLMSEYENVEPFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSEFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 67 LGVLGVPPAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQG 126

QY 131 LGDALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVKQLPSFAVSSEVEPLPIYA 190
Db 127 LGDSFRAYQCSLEDWLENRRDARTSRVLYTQYIALELDFLNAMPLFAIRNQEVPLLMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVVEWYNTGLNSLRGTN 246

QY 251 AESWVRYNQFRDMLTMDLVALPSPYDTQMPYIKTTAQLTREVTDAIGTVHPHSFT 310
Db 247 AASWVRYNQFRDLTLGLVDLVALPSPYDTRTYPINTSAQLTREVTDAIGAT--GVNMA 304

QY 311 STTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMWGGHKLFRFTI 370
Db 305 SMWYNNAPSAIEATAVIRSPHLLDFLEQVTIYSLSRWSATRHMTYWRGHTIQSRPI 364

QY 371 GGTINISTQGSTNTSINPVTLPFTSRDVTYTESLAGLNL--LTPVNGVPRVDFHWKFV 428
Db 365 GGGTNTSTHGSTNTSINPVLRSFFSRDVTYTESYAGVLLWGIYLEPIHGVTVRFRNP 424

QY 429 --THPIASDNFYYPGYAGIGTOLQDSNELPPEATQPNYESYSHRLSHIGLISASHVKA 486
Db 425 QNTFERGTANYSQP--YESPGQLQKSETLPPETTERPNYESYSHRLSHIGLISQSRVHV 483

QY 487 LVYSWTHRSADRTNTEPNSTIQIPLVKAENLSSGAAVVRGPGFTGGDILRRNTGTFTVG 546
Db 484 PVISWTHRSADRTNTEPNSTIQIPLVKAENLSSGTSVVSVPFTGGDIIRTNVNGSVLS 543

QY 547 IRVYNINPPFAQRYRVRIRYASTDQLQHTSINGKAINQGNFSAATNRGCDLKYTFRTVG 606
Db 544 MGLNFNNTSLQRYRVRIRYAAASQTMVLRVTGGSTTFDQGFPSMTSANESLTSQSRFAE 603

QY 607 FTTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFPVPEVYEAEDYFKAQEKVTAFTS 666
Db 604 FPVGISASGSQ--TAGISISNAGROTFHFKIEFIPITATFEAEYDLERAEAVNALFTN 662

QY 667 TNPRLKTDVTDYHIDQVSNLVACLSDSEFCCLDEKRELLEKVKYAKRLSDERNL 719
Db 663 TNPRLKTDVTDYHIDQVSNLVACLSDSEFCCLDEKRELLEKVKYAKRLSDERNL 715

RESULT 12
US-09-826-660-25

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; Sequence 25, Application US/09826660
; Patent No. US2001002640A1
; GENERAL INFORMATION:
; APPLICANT: Carineau, Guy A.
; APPLICANT: Steilman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
; US-09-826-660-25

Query Match          51.4%; Score 1932.5; DB 9; Length 643;
Best Local Similarity 57.7%; Pred. No. 1.6e-154;
Matches 371; Conservative 100; Mismatches 159; Indels 13; Gaps 3;

QY 13 SSNAKVDKSTDSLN-----ETDELQNHEDCLMKSEYENVEPVSASTIQTGIG 65
DB 7 NENEIINALSIPAVNSHSAQNLSTDAI-----EDSLCIAEGNIDPFVSASTVQTGIN 61

QY 66 IAGKILGTGVPFAGQVASYLSFILGELMPKQKQWEIFMEHVEEIIINQKISTVARNKAL 125
DB 62 IAGRLGVJGVFPAGQIASFYSFLVGLMPGRDPWEIFLEHVEQIRQOVTEHTRDTAL 121

QY 126 TDLKGLGDALAVHDSLESVWGNRNTRARSVVKSOVIALLELMFVQKLPFSFVSGEEVPL 185
DB 122 ARLOGLGNFRAVQCSLEDWLENRDDARTSRVLYTOYIALELDFLNAMPLFAIRNQEVPL 181

QY 186 LPIVAAQANLHLLLRDASIFGKXEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLNN 245
DB 182 LMVYAAQANLHLLLRDASLFGSEFGLTSQEIORYYERQVEKTRYSIDYCARWNTGLNN 241

QY 246 LRGITNAESWVRYNQFRDMLTAVLDVALFPSYDTQMPYPIKTTAQLTREYVTDAGTVP 305
DB 242 LRGITNAESWVRYNQFRDMLTAVLDVALFPSYDTQMPYPIKTTAQLTREYVTDAGTVP 301

QY 306 HPSFTSTTWNNAAPSFSIAEAAVVRNPHLLDFLEQVTIYLSLRSWNTQYMMNMGHKL 365
DB 302 PSFGFASTNWNNAAPSFSIAEAAVVRNPHLLDFLEQVTIYLSLRSWNTQYMMNMGHKL 361

QY 366 EFRITGGTINISTOGSTNTSINPVLFTSRDVRYESLAGNLFILTOPVNGVRVDVFW 425
DB 362 ESRTIRGSLSTSTHGNTNTSINPVLFTSRDVRYESLAGNLFILTOPVNGVRVDVFW 421

QY 426 KFTVTHPIASDNFYYPGYAGIGTQLODSNELPPEATQOPNYESYSHRLSHIGLSASHVK 485
DB 422 RNPLNSLRGSLLYTIGYGVGTQLFDSSTELPPEATQOPNYESYSHRLSHIRLSGNTLR 481

QY 486 ALVYSWTHRSADRNTNTPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTG 545
DB 482 APVYSWTHRSADRNTNTPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTG 541

QY 546 DIRVNNPFAQVRVRIYASITDLOPHTSINGKAINQGNFSAIWNRGEDLDVKTFRV 605
DB 542 SMGLNFNTSLQRYRVRVYAAQTMVLRTVVGSTTFDQGPPTNSANESLTSQSFRFA 601

QY 606 GFTTFFSFLDVQSFTIGAWNFSSGNEVYIDRIEFVPEVIYE 648
DB 602 EFPVGISASGSQ-TAGISISNNAQRQTFFHDKIEFIPITATLE 643

; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; OTHER INFORMATION:
; US-10-089-678-1

Query Match          45.8%; Score 1722.5; DB 14; Length 1167;
Best Local Similarity 47.9%; Pred. No. 2.6e-136;
Matches 361; Conservative 126; Mismatches 218; Indels 49; Gaps 12;

QY 1 MKLKNQDKHQ---SFSSNAKVDKISTDSLNKTDIELQNHEDCLMKSEYE-----NV 51
DB 1 MSPNNQNEVELDASSSTVSNSVRYPANDQTTLQNNVYKDYLRMSEGENPELFGNP 60

QY 52 EPPFVASTIQTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKQK-NOWEIFMEHVEE 110
DB 61 ETFISSSTVQTGIGIVGVLGALGVFPAGQIASFYSFIVGQLWPSSTVSVWEMIKQVED 120

QY 111 IINOKISTVARNKALTDLKGLGDALAVHDSLESVWGNRNTRARSVVKSOVIALELMFV 170
DB 121 LIDQKITDSVRKTAAGLQGLGDLGVYQKSLKNWLENRNDTRARSVVVQYIALELDFV 180

QY 171 QKLPFSFVSGEEVPLPIVAAQANLHLLLRDASIFGKXEWGLSSSEISTFYNRQVERAGD 230
DB 181 AKIPSFASISQCEVELLSVYAAQANLHLLLRDASIFGAEWGTGPGISTFYDQVTRTAQ 240

QY 231 YSDHCVKWYSTGLNNLRGTNAESWVRYNQFRDMLTAVLDVALFPSYDTQMPYPIKTTA 290
DB 241 YSDYCVKWTNTGLDKLKGTAASWLVKQHFREMTLLVLDLVALFPNYDRTYPIETTAQ 300

QY 291 LTREYVTDAGTVPHPSTSTTWNNAAPSFSIAEAAVVRNPHLLDFLEQVTIYLSL 349
DB 301 LTREYVTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHPLFDILSEIEFYTRAG 360

QY 350 -RWSNTQYMMNMGHKLFPRTIGTGLNSTQGSTNTSINPVLFTSRDVRYESI-AGL 407
DB 361 LPLNTEYLEYVWGHISIKYKNTNASSALERNYGTITSNKIYVDLANKDIFQVRSIGADL 420

QY 408 NLFLTQPVNGVRVDVFWKVFVTHPIASDNFYYPGYAGIG-----TQLODSE 453
DB 421 ANYVQA-VYGVPIYASF-----TLDDKQ---TGSGVGGFTYKPHKTTMQVCTQNTI 469

QY 454 NELPPEATQOPNYESYSHRLSHIGLS-----ASHVKALVYSWTHRSADRNTNTPNS 505
DB 470 DEIPPE--NEPLSRGYSHLSHITSYSPSKNASSPARVGNLDFVFAWTHRSADVTNTVYS 527

QY 506 SITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRNTGTGDIRVNNPFAQVRVRIY 565
DB 528 KITQIPVWKAHTLVSGTTVIKGPGFTGGNLTSGPLAYTSVSKSPLSQRYRARIY 587

QY 566 ASTTDLOQHTSINGKAINQGNFSAIWNRGEDLDYKTRFTVGTGTTTSPFLDVQSTFTIGAW 625
DB 588 ASTTNLRLFTVITSGTRIYSINVNKTMKGGDLTENTDLATIGTATFTSNYSDSLTVGAD 647
```

**QY**      626 NFSSGNEVYIDRIEFPVPVEVTYELEYDEFAKQSKVTALTFTSTNPRGLTKTDVKDYHIDQVS     68S  
             :  
             :  
**Dd**      648 SFASGEVVVDKFELIPVNATFEAEEDLDVAKKAVNGLFTSKKD-ALQTSVTDIYNQA     70E  
             :  
             :  
**QY**      686 NLVESLSDFYLDBKEFLFPIVIKYAKQLHIERNM     719  
             :  
             :  
**Dd**      707 NIVECLSDLYPNFKMLWDVAEKRLVQARNL     740  
             :  
             :

**RESULT 14**

**US-10-428-961-6**

; Sequence 6, Application US/10428961  
; Publication NO. US2003023711A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-ENDOTOXIN  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 6 :  
; LENGTH: 653  
; TYPE: PRP  
; ORGANISM: Bacillus thuringiensis

**US-10-428-961-6**

Query Match          44.7%; Score 1681.5; DB 14; Length 653;  
Best Local Similarity 51.5%; Pred. No. 3.le-133;  
Matches 346; Conservative 106; Mismatches 173; Indels 47; Gaps 14;

**QY**      13 SSNAKVDPKISTDNLKN---ETDIELONINHEDCLKMSEVENPEPVSAITQTGTIGIGIAKG     69  
             :  
             :  
**Dd**      2 NENEIIINALSIAPSVNHSAQMDSL-DARIEDSLCIAEGNNINPLVASLTQGNIAGR     60  
             :  
             :  
**QY**      70 ILGTGVPPFAGOVASYFSILGELWPKGNOWEIFWEHVBEIINKISIVARKALKTLDK     129  
             :  
             :  
**Dd**      61 ILCVLGVPPFAGOLASFYSFLVGELWPGRPFWEIFLEYEQLRQQVTRNTAIRLE     120  
             :  
             :  
**QY**      130 GLGDALAAYHDLESYGVRNRRNRTRSVMKSXYIALALEMFVKLPSPFAVSGEEVPLLPIY     189  
             :  
             :  
**Dd**      121 GLRGYRSYYQAALETWLDRNDARSIIERYVALEDITTAIPLFRIRNEEVPLLMMVY     180  
             :  
             :  
**QY**      190 AQAAHLHLLLRDASTFGKEWGSLSSSEISTFYNQVERAGDYSCHCVKWYSTGLNNLRGT     249  
             :  
             :  
**Dd**      181 AQAAHLHLLLRDASLFGESEGMASSDVNOYQEIQRYTEESNHCQWYNTGLNNLRGT     240  
             :  
             :  
**QY**      250 NAESWRVYNQRFRDMTLMVLDLVALFPSYTOMPTIKTTAQLTREITYDTAIGTVHPHSF     309  
             :  
             :  
**Dd**      241 NAESWLAHYNQERRDLTLGVLDLVALFPSYDRTYPINTSAQLTREITYDDPGRTNAPSGF     300  
             :  
             :  
**QY**      310 TSTTWNNNASPSATAEAUVNPBPHLLDFLEQVTIYSLSRWSNTQYNNMWGGHKLBFR     369  
             :  
             :  
**Dd**      301 ASTNWFNNAIFSASAIEAAIPRPPLDLLFPLOLIYASASSRWSTQHMYNVGWGHRLNERP     360  
             :  
             :  
**QY**      370 IG GTLNISTQSST-NITSINPYTLFF-TSRDVYRTESLAGNLFLTQP VNGVPRVDFHWKF     427  
             :  
             :  
**Dd**      361 IGGTLATSTOGLTNNTSINPYTLHYVSSRDVYRTESNAGTNILEFTP VNGVWARFN-F     418  
             :  
             :  
**QY**      428 WTHPIADSNFYYP-----GYAGTGTOQDSNELPEPATGPQNYESYSHLSHG--     477  
             :  
             :  
**Dd**      419 ITLRFWKEARPLPTVNRIRELGFNVLIOKLNYHOK-----QQNDQIMNHIVIDISYR     470  
             :  
             :  
**QY**      478 LISASHVKALVISWTHTSRADRNTITEPNSITOIPLVKAENISSCAAUVRGPCGTGCCTIB     537  
             :  
             :

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Db      471 LIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIPAVKGRFLFNG-SVISGPGFTGQDVR 529
QY      538 -RTWTGTF---GDIRVNIN-PPFAQRYVRIRYASTDLOQHTSINKAINQGNFSATMN 592
Db      530 LARNNGNIQNRGYIEVPIQFTSTSTRYVRVRYASVTSELENVLGNSSIFNTNLPATAA 589
QY      593 RGEDLDYKTFRTVGTTPFPFGLDVOSTFT-----IGAWNPFSSGNEVYIDRIEFVPEVT 646
Db      590 SLDNLQ-----SGDFGVEINNAFTSATGNIVGARNFSAEVIIDREFEPIPTAT 640
QY      647 YEAEYDFEKAQE 658
Db      641 FEVEYDLERAQK 652

RESULT 15
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No: US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match      44.4%; Score 1670.5; DB 17; Length 1157;
Best Local Similarity 49.1%; Pred. No. 6.4e-132;
Matches 371; Conservative 98; Mismatches 230; Indels 57; Gaps 18

QY      1  MCLKNQDHQHSFNNAKVDKISTDS----LKNETDIELOINIHEDCLMXSEYE-----N 50
Db      1  MSPNNQNEYIIDATPST-SVSSDSNRYPFANEPTDALQNMNYKDYLRKMSGGENPELFGN 59
QY      51  VEPFVSASTIQTGIGIAGKILGTGLVPAGOVASLYSILGELWP-KGKNQWEI FMEHVE 109
Db      60  PETFISSITQIGIGIVGRILGALGVPPASQIASFYSPITVGQLWPSKSDIWGEIMERVE 119
QY      110 EIINQKISTYARNKALTDLKLGDALAVYHDSLESVGNRNNTPARSVVKSQYIALELMF 169
Db      120 ELVDQKIEKYVKDKALAEKLGALNDVYQQSLEDWLENRNDARTSRVSVNQFALDLNF 179
QY      170 VQKLPSFAVSGEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAG 229
Db      180 VSSIPSAVSGHEVLLLAAYAQAANLHLLLRDASIFGEEWGTTPGEISRFYNRQVQLTA 239
QY      230 DYSDHCVKWTSTGLNNLRGTNAESWRYNQFRDMLTMLVLDLVALFPSYDTQVYPIKTTA 289
Db      240 EYSDYCVKWKYKGLDKLGTTSKSWLNYHQFRREMTLLVLDLVALFPNYDTHMYPITTA 299
QY      290 QLTREVYTDAGTVHPHPSFTST---TWNNNAPSFAIEAAVVRNPHLLDFLEQVYTIY 345
Db      300 QLTRDVYTDPIA---FNIVTSTGFCNPWSTHSGILEYEVENNVRPPHLPDLILSSVEIN 355
QY      346 SLLSR-----WSNTQYMNWGGHKLFR-----TIGGTILNISTQGSTWTSINPVTLPPTS 396
Db      356 T---SRGGITLNDAYINWSGHTLKYRRRTADSTVITYANYGRITSEKNS-----FALEDR 408

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.2996 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-54  
Perfect score: 3749  
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 718

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1825181 seqs, 575374646 residues  
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3722.5	99.3	719	1 C1IA_BACTK	Q45752 bacillus th
2	3722.5	99.3	719	2 Q6X181	Q6X181 bacillus th
3	3722.5	99.3	719	2 AAP86782	AAP86782 bacillus
4	3717.5	99.2	719	2 Q93NJ5	Q93NJ5 bacillus th
5	3716.5	99.1	719	2 O85796	O85796 bacillus th
6	3714.5	99.1	719	2 CAC85964	CAC85964 bacillus
7	3587.5	95.7	719	2 Q8KY61	Q8KY61 bacillus th
8	3513.5	93.7	719	2 Q9F0P8	Q9F0P8 bacillus th
9	3482.5	92.9	719	1 C1IB_BACTE	Q45709 bacillus th
10	3359.5	89.6	719	1 C1ID_BACTU	Q9XG11 bacillus th
11	3358.5	89.6	719	1 C1IC_BACTU	O87404 bacillus th
12	2415	64.4	1229	1 C1BB_BACTU	Q45739 bacillus th
13	2415	64.4	1233	1 C1BC_BACTM	Q45774 bacillus th
14	2249	60.0	1228	2 Q9T75	Q9T75 bacillus th
15	2248	60.0	1228	1 C1BA_BACTK	P05517 bacillus th
16	2240	59.7	1228	2 Q93NM5	Q93NM5 bacillus th
17	2165	57.7	849	2 O6PYW8	O6PYW8 bacillus th
18	2165	57.7	849	2 AAS93797	AAS93797 bacillus
19	2165	57.7	1227	1 C1BE_BACTU	O85805 bacillus th
20	2089	55.7	1231	2 Q8KNY2	Q8KNY2 bacillus th
21	2084	55.6	1231	1 C1BD_BACTZ	Q9ZAZ5 bacillus th
22	1974	52.7	1215	1 C1KA_BACTM	Q45715 bacillus th
23	1895	50.5	381	2 Q45740	Q45740 bacillus th
24	1652	44.1	1157	1 C8AA_BACUK	Q45704 bacillus th
25	1643.5	43.8	1144	2 Q8KZL7	Q8KZL7 bacillus th
26	1480.5	39.5	1157	1 C8CA_BACTO	Q45733 bacillus th
27	1473	39.3	1169	1 C8BA_BACUK	Q45705 bacillus th
28	1462	39.0	1166	1 C1GA_BACTU	Q45746 bacillus th
29	1461.5	39.0	1169	1 C1FB_BACTM	O66377 bacillus th
30	1456.5	38.9	1167	1 C1JA_BACTU	Q45738 bacillus th
31	1455.5	38.8	1174	2 Q45749	Q45749 bacillus th

RESULT 1				
C1IA_BACTK	STANDARD;	PRT;	719 AA.	
ID	C1IA_BACTK	Q45750; Q45751; Q45756;		
AC	Q45752; P71092; Q45750; Q45751; Q45756;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Pesticidal crystal protein cryIIa (Insecticidal delta-endotoxin)			
DE	CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein)			
GN	Name=cryIIa; Synonyms=cryII(a), cryV, cryVI, CGCryV;			
OS	Bacillus thuringiensis (subsp. kurstaki).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OC	NCBI_TaxID=29339;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSIR732;			
RX	MEDLINE=93298009; PubMed=8517758;			
RA	Gleave A.P., Williams R., Hedges R.J.;			
RT	"Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for the presence of cryV-like insecticidal protein genes and characterization of a cryV gene cloned from B. thuringiensis subsp. kurstaki."			
RL	Appl. Environ. Microbiol. 59:1683-1687(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=JHCC4835;			
RX	MEDLINE=92269582; PubMed=1588820;			
RA	Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;			
RT	"Identification and characterization of a novel Bacillus thuringiensis delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."			
RL	Mol. Microbiol. 6:1211-1217(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HD-1;			
RX	MEDLINE=95314293; PubMed=7793960;			
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;			
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis and cloning of cryV-type genes from Bacillus thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp. entomocidus."			
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AS88;			
RX	MEDLINE=96178985; PubMed=8606196;			
RA	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.;			
RT	"Cloning of a cryV-type insecticidal protein gene from Bacillus thuringiensis: the cryV-encoded protein is expressed early in stationary phase."			
RL	J. Bacteriol. 178:2141-2144(1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=61;			

32	1445.5	38.6	1118	2 Q9AM83	Q9am83 bacillus th
33	1441.5	38.5	1155	1 C1AB_BACTK	P06578 bacillus th
34	1441.5	38.5	1155	2 Q7BE98	Q7be98 bacillus th
35	1441.5	38.5	1155	2 Q9F296	Q9f296 bacillus th
36	1441.5	38.5	1155	2 AAN76494	Aan76494 bacillus
37	1441.5	38.5	1155	2 AAO13302	Aao13302 bacillus
38	1436.5	38.3	1156	2 Q6GUA7	Q6gua7 bacillus th
39	1433	38.2	1180	2 Q9SSV8	Q9ssv8 bacillus th
40	1432	38.2	1176	2 Q7WZT9	Q7wzt9 bacillus th
41	1431.5	38.2	1177	2 Q6EIX3	Q6eix3 bacillus th
42	1430	38.1	793	2 Q6PYW7	Q6pyw7 bacillus th
43	1430	38.1	793	2 AAS93798	Aas93798 bacillus
44	1429.5	38.1	1155	2 Q93T21	Q93t21 bacillus th
45	1426	38.0	1176	2 Q45736	Q45736 bacillus th

ALIGNMENTS

RA Selvapandian A., Bhatnagar R.K.;  
 RT "Isolation, cloning and expression of cryV gene";  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella and Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M98544; AAA22354.1; -;  
 CC EMBL; X62821; CAA44633.1; -;  
 CC EMBL; L36338; AAC36999.1; -;  
 CC EMBL; L49391; AAB00958.1; -;  
 CC EMBL; Y08920; CAA70124.1; -;  
 CC PIR; I39815; I39815.  
 CC PIR; S25383; S25383.  
 CC HSP; P02965; ICIV.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin\_C.  
 CC InterPro; IPR005639; endotoxin\_N.  
 CC InterPro; IPR008979; Gal\_bind\_Like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin.  
 KW VARIANT 159 159 K -> R (in strain 61).  
 FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 FT 1).  
 FT VARIANT 443 443 A -> V (in strain AB88).  
 FT VARIANT 711 712 KO -> NE (in strain HD-1 and strain 61).  
 FT SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
 SQ  
 Query Match 99.3%; Score 3722.5; DB 1; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-251;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPXGKNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPXGKNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLSWVGNNRNTARSVVKVSYQVIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGDLALAVYHDSLSWVGNNRNTARSVVKVSYQVIALELMFVQKLPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSYHCVKWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSYHCVKWYS 240  
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 DB 241 TGLNLRGNTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 419

DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
 DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 480 ASHVXALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 539  
 DB 481 ASHVXALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 540 TGTGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGSDLDYK 599  
 DB 541 TGTGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGSDLDYK 600  
 QY 600 TFXTVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVFPVEVTEAYDFEKAQEKV 659  
 DB 601 TFRIVGFTTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVFPVEVTEAYDFEKAQEKV 660  
 QY 660 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 718  
 DB 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 RESULT 2  
 Q6X181 PRELIMINARY; PRT; 719 AA.  
 ID Q6X181  
 AC Q6X181;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CryII.  
 GN Name=cryII;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY262167; AAP86782.1; -;  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
 Query Match 99.3%; Score 3722.5; DB 2; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-251;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPXGKNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPXGKNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLSWVGNNRNTARSVVKVSYQVIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGDLALAVYHDSLSWVGNNRNTARSVVKVSYQVIALELMFVQKLPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSYHCVKWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGNTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300  
 DB 241 TGLNLRGNTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI 300

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QY 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITIGTINISTCGSTNTSINPVTLPFTSRDVRRTESLAGNLFLLTQPVN-VPR 419
DB 361 GGHKLEFRITIGTINISTCGSTNTSINPVTLPFTSRDVRRTESLAGNLFLLTQPVN-VPR 420
QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSNELPPEATGQPNYESYSHRLSHIGLIS 479
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
DB 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 540 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 599
DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 600 TEXTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659
DB 601 TFRVTGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
DE CryII.
GN Bacillus thuringiensis.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC SFRAIN-T01 328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RT "Complete sequence of cryII gene of isolate T01 328 from Bacillus
RT thuringiensis from Cubatao (SP - Brazil) soil.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY262167; AAP86782.1; -
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 99.3%; Score 3722.5; DB 2; Length 719;
Best Local Similarity 99.4%; Pred. No. 1.2e-251;
Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKSEYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFIILGELWPKGNQWEIFMHEVBEIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFIILGELWPKGNQWEIFMHEVBEIINQKISTYA 120
QY 121 RNKALTDLKGLDALAVYHDSLESWVGNRNNTARSVVKSQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGLDALAVYHDSLESWVGNRNNTARSVVKSQYIALELMFVQKLPFAVSG 180
QY 181 BEVPLPIYAQAANLHLLLEDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCWKWYS 240
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QY 241 TGLNNLRGTNAESWRYNQRRDMTLMVLDLVALFPSSYDVTOMYPIKTTAQLTREVYTDAI 300
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QY 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360
DB 301 GTVHPHPSFTSTTWNNAAPSAIEAAVVRNPHLLDPLEQVITYSLLSRWSNTQYNNMW 360
QY 361 GGHKLEFRITIGTINISTCGSTNTSINPVTLPFTSRDVRRTESLAGNLFLLTQPVN-VPR 419
DB 361 GGHKLEFRITIGTINISTCGSTNTSINPVTLPFTSRDVRRTESLAGNLFLLTQPVN-VPR 420
QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSNELPPEATGQPNYESYSHRLSHIGLIS 479
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSNELPPEATGQPNYESYSHRLSHIGLIS 480
QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539
DB 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 540 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 599
DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 600 TEXTVGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 659
DB 601 TFRVTGFTTFFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE CryIIa.
GN Name=cryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF373207; AAK66742.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.2%; Score 3717.5; DB 2; Length 719;
Best Local Similarity 99.3%; Pred. No. 2.6e-251;
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKSEYENVEPVSASTI 60
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFIILGELWPKGNQWEIFMHEVBEIINQKISTYA 120

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Db 61 QTGIGIACKILGTGVPFAGQVNASLYSIFLGLWPKGKNQWEIFMEHVVEIINQKISTYA 120
QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVQKLPFSFVSG 180
Db 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVQKLPFSFVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGNTNAESWVRNQFRDMLMVLVDFVPSYDTQMPYIKTTAQLTREYVTDAL 300
Db 241 TGLNLRGNTNAESWVRNQFRDMLMVLVDFVPSYDTQMPYIKTTAQLTREYVTDAL 300
QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTLPVNGVPR 420
Db 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTLPVNGVPR 420
QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 540 TGTFGDIRVNINPPFAQRYVRIRYASITDLOFHTSINGKAINQGNFSATMNRGEDLDYK 599
Db 541 TGTFGDIRVNINPPFAQRYVRIRYASITDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 600 TFXTVGTFPFLDLVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659
Db 601 TFRTVGTFPFLDLVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
O85796 PRELIMINARY; PRT; 719 AA.
AC O85796; 1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=crv101;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S101;
RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; F:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
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KW Plasmid.
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match 99.1%; Score 3716.5; DB 2; Length 719;
Best Local Similarity 99.3%; Pred. No. 3.1e-251;
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKLNQDKHQSFSSNAKYDKISTDSLKNETDIELQNIHEDCLKSEYENVEPFSASTI 60
Db 1 MKLNQDKHQSFSSNAKYDKISTDSLKNETDIELQNIHEDCLKSEYENVEPFSASTI 60
QY 61 QTGIGIACKILGTGVPFAGQVNASLYSIFLGLWPKGKNQWEIFMEHVVEIINQKISTYA 120
Db 61 QTGIGIACKILGTGVPFAGQVNASLYSIFLGLWPKGKNQWEIFMEHVVEIINQKISTYA 120
QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVQKLPFSFVSG 180
Db 121 RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKSQYIALELMFVQKLPFSFVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGNTNAESWVRNQFRDMLMVLVDFVPSYDTQMPYIKTTAQLTREYVTDAL 300
Db 241 TGLNLRGNTNAESWVRNQFRDMLMVLVDFVPSYDTQMPYIKTTAQLTREYVTDAL 300
QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTLPVNGVPR 420
Db 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTLPVNGVPR 420
QY 420 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479
Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 480 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 539
Db 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 540 TGTFGDIRVNINPPFAQRYVRIRYASITDLOFHTSINGKAINQGNFSATMNRGEDLDYK 599
Db 541 TGTFGDIRVNINPPFAQRYVRIRYASITDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 600 TFXTVGTFPFLDLVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659
Db 601 TFRTVGTFPFLDLVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 660 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 718
Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6
CAC85964 PRELIMINARY; PRT; 719 AA.
ID CAC85964
AC CAC85964;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Delta-endotoxin.
GN CRV11A.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group; Bacillus thuringiensis.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ENS3;
RA Tounsi S., Zouari N., Jaoua S.;
```

RT "Cloning and study of the expression of a novel cryIIa-type gene from  
RT Bacillus thuringiensis subsp. kurstaki.";  
RL J. Appl. Microbiol. 95:23-28(2003).  
DR EMBL; AJ315121; CAC85964.1; -.  
SQ SEQUENCE 719 AA; 81203 MW; 86765A6C25DAFE8 CRC64;

Query Match 99.1%; Score 3714.5; DB 2; Length 719;  
Best Local Similarity 99.2%; Pred. No. 4.2e-251;  
Matches 713; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVKSQYIALELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVKSQYIALELMFVKLPSPAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQYPIKTTAQLTREVTDAI 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQYPIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
QY 420 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
DB 420 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
QY 480 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
DB 480 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
DB 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
QY 600 TFXTVGFTTFFSLLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 659  
DB 600 TFXTVGFTTFFSLLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 659  
QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 718  
DB 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 718

RESULT 7  
Q8KY61 PRELIMINARY; PRT; 719 AA.  
ID Q8KY61  
AC Q8KY61  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Cry.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Porcar M., Martinez C., Caballero P.;

Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
EMBL; AF278797; AM73516.1; -.  
PIR; B42459; B42459.  
DR HSSP; P02965; 1CIY.  
DR CO; CO:0005102; F:receptor binding; IEA.  
DR CO; CO:0006952; P:defense response; IEA.  
DR CO; CO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR011178; Endotoxin.  
DR InterPro; IPR005639; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 95.7%; Score 3587.5; DB 2; Length 719;  
Best Local Similarity 95.7%; Pred. No. 3.3e-242;  
Matches 688; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVKSQYIALELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVKSQYIALELMFVKLPSPAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQYPIKTTAQLTREVTDAI 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQYPIKTTAQLTREVTDAI 300  
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVN-VPR 419  
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVN-VPR 420  
QY 420 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
DB 420 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 479  
QY 480 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
DB 480 ASHKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 539  
QY 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
DB 540 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
QY 600 TFXTVGFTTFFSLLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 659  
DB 600 TFXTVGFTTFFSLLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 659  
QY 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 718  
DB 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM 718

RESULT 8  
Q9F0P8 PRELIMINARY; PRT; 719 AA.  
ID Q9F0P8  
AC Q9F0P8;

QY	Db	QY	Db	QY	Db
540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSA	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSA	540	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSA
541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSA	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSA	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSA
500	TFXTVGFTTFPSLLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTYEA	500	TFXTVGFTTFPSLLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTYEA	500	TFXTVGFTTFPSLLDVQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTYEA
501	TFRTVGFTTFPSFSVDQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTYEA	501	TFRTVGFTTFPSFSVDQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTYEA	501	TFRTVGFTTFPSFSVDQSTFTIGAMNFSNGNEVYIDRIEFPVPEVTYEA
660	TALFTSTNPRLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVKYAKQI	660	TALFTSTNPRLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVKYAKQI	660	TALFTSTNPRLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVKYAKQI
661	TALFTSTNPRLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVKYAKQI	661	TALFTSTNPRLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVKYAKQI	661	TALFTSTNPRLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFELVKYAKQI

RESULT 9

CLIB BACTE

ID

CLIB BACTE

STANDARD;

PRT;

719 AA.

AC

Q45709;

DT

30-MAY-2000 (Rel. 39, Created)

DT

30-MAY-2000 (Rel. 39, Last sequence update)

DT

05-JUL-2004 (Rel. 44, Last annotation update)

DE

Pesticidal crystal protein cryIIb (Insecticidal delta-endotoxin

DE

CryII(b)) (Crystalline entomocidal protoxin) (81 kba crystal protein).

GN

Names=cryIIb; Synonyms=cryII(b), cryV, cryV465;

DE

Bacillus thuringiensis (subsp. entomocidus).

OS

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OC

NCBI\_TaxID=1436;

RN

{1}

RP

SEQUENCE FROM N.A.

RC

STRAIN=BP465;

RX

MEDLINE=95314293; PubMed=7793960;

RA

Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;

RT

"Distribution of cryv-type insecticidal protein genes in Bacillus

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thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.
entomocidus.";
RT Appl. Environ. Microbiol. 61:2402-2407(1995).
RL
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of certain coleopteran and lepidopteran species.
CC Active on Plutella xylostella but not on Bombyx mori.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U07642; AAA82114.1; -.
CC PIR; I40590; I40590.
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal_bind_Like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Sporulation; Toxin.
CC SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;
CC
CC Query Match 92.9%; Score 3482.5; DB 1; Length 719;
CC Best Local Similarity 92.4%; Pred. No. 7.3e-235;
CC Matches 664; Conservative 31; Mismatches 23; Indels 1; Gaps 1;
CC
CC 1 MKLQNDQKHQSFSSNAKVDKJSTDSLKQVETDIELQNIHEDCLKXSEYENVEPFSASTI 60
CC

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Db 1 MCLKNPKDQKHSNAKVDKIATDSLKNETDIELKNNMNDYLRSEHSIDPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLGLGDALAVYHDSLESWGNNRNRTRARSVKQYIALELMFVQKLPSPFAVSG 180  
 Db 121 RNKALSDURGLGDALAVYHDSLESWGNNRNRTRARSVKQYIALELMFVQKLPSPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRNQFRDMLMVLVALPSPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNNLRGTNAESWVRNQFRDMLMVLVALPSPSYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSTQYMMW 360  
 Db 301 GTVHPNQAFASITTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSTQYMMW 360  
 QY 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTQPVN-VPR 419  
 Db 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTQPVN-VPR 420  
 QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 479  
 Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTGFDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 599  
 Db 541 TGTGFDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 600 TFXTVGFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFEKAQKV 659  
 Db 601 TFXTVGFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFEKAQKV 660  
 QY 660 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDSEYDLDEKRELFEIVKAKQIHIERNM 718  
 Db 661 TALFTSTNPRGLKTDVKDHYHIDQVSNLVESLSDSEYDLDEKRELFEIVKAKQIHIERNM 719

RESULT 10

CILD\_BACTU STANDARD; PRT; 719 AA.  
 ID CILD\_BACTU STANDARD; PRT; 719 AA.  
 AC Q9YDL1.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (Insecticidal delta-endotoxin  
 DE CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIId; Synonyms=cryII(d), NRcryV;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RX MEDLINE=20374042; PubMed=10919402;  
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 RT gene."  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of

CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF047579; AAD44366.1; -.  
 DR HSSP; P02965; 1CIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 DR Sporulation; Toxin.  
 KW SEQUENCE 719 AA; F335F5689D3B0C45 CRC64;  
 SQ  
 Query Match 89.6%; Score 3359.5; DB 1; Length 719;  
 Best Local Similarity 89.3%; Pred. No. 3e-226;  
 Matches 642; Conservative 35; Mismatches 41; Indels 1; Gaps 1;  
 QY 1 MCLKNPKDQKHSNAKVDKIATDSLKNETDIELKNNMNDYLRSEHSIDPVSASTI 60  
 Db 1 MCLKNPKDQKHSNAKVDKIATDSLKNETDIELKNNMNDYLRSEHSIDPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLGLGDALAVYHDSLESWGNNRNRTRARSVKQYIALELMFVQKLPSPFAVSG 180  
 Db 121 RNKALADLGLGDALAVYHDSLESWGNNRNRTRARSVKQYIALELMFVQKLPSPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNNLRGTNAESWVRNQFRDMLMVLVALPSPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNNLRGTNAESWVRNQFRDMLMVLVALPSPSYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSTQYMMW 360  
 Db 301 GTVHPNAPFSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVITYLSLSRWSTQYMMW 360  
 QY 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTQPVN-VPR 419  
 Db 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRVRESLAGLNFLTQPVN-VPR 420  
 QY 420 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 479  
 Db 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 QY 480 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 539  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 540 TGTGFDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 599  
 Db 541 TGTGFDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 600 TFXTVGFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFEKAQKV 659  
 Db 601 AFRTVGFTTFFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDEFEKAQKV 660

QY 660 TALTSTNPRGLKTDVKYHIDQVSNLVSDEFLDKRELPEIVKYAKQLHIERNM 718  
 DB 661 TALTSTNPRGLKTDVKYHIDQVSNLVSDEFLDKRELPEIVKYAKQLHIERNM 719

RESULT 11  
 C1CB\_BACTU STANDARD; PRT; 719 AA.  
 AC 087404;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pestidial crystal protein cryIIc (insecticidal delta-endotoxin  
 DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIc; Synonyms=cryII(c);  
 OS Bacillus thuringiensis.  
 OG Plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RC STRAIN=C18 / Egypt;  
 RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut  
 CC epithelial cells of insects.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC  
 CC EMBL; AF056933; AAC62933.1; -.  
 DR HSSP; P02965; 1CIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 DR Plasmid; Sporulation; Toxin.  
 KW SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;  
 SQ

Query Match 89.6%; Score 3358.5; DB 1; Length 719;  
 Best Local Similarity 89.6%; Pred. No. 3.5e-226;  
 Matches 644; Conservative 33; Mismatches 41; Indels 1; Gaps 1;  
 QY 1 MKLKNQDKHCSFSSNAKYDKISDLSKNETDIELQNHEDCLKMSEYENVEPVVSASTI 60  
 DB 1 MKLKNPDKHQTLSSNAKYDKIATDLSKNETDIELKMNEDYLRMSEHSIDPFVSASTI 60  
 QY 61 QTGIGIAGKILGTVPPAGQVASYLSFILGELWPKGKQWEIFMEHVHEIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTVPPGQIASYLSFILGELWPKGKQWEIFMEHVHEIINRKISTYA 120  
 QY 121 RNKALTDKGLDALAVTHDSLESWGNRNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDKGLDALAVVHESLESWGNRNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 EEVPLLPYQAANLHLLLRDASIFPKWGLSSSEISTFTYNRQVERAGDYSYHCVKWYS 240  
 DB 181 EEVPLLPYQAANLHLLLRDASIFPKWGLSSSEISTFTYNRQVERAGDYSYHCVKWNN 240

QY 241 TGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFSPSYDTQWYPIKTTAQLTREYVYDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDWTLMVLDLVALFSPSYDTQWYPIKTTAQLTREYVYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMNW 360  
 DB 301 GTVDPNQALRSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMMNW 360  
 QY 361 GGHKLEFRIGTGLNISTOGSTNTSINPVTLPFTSRDVRVYTESLACLNLFLOPYN-VPR 419  
 DB 361 GGHLESRPIGGALNTSTOGSTNTSINPVTLPFTSRDVRVYTESLACLNLFLOPYN-VPR 420  
 QY 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNVYESYSHRLSHIGLIS 479  
 DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNVYESYSHRLSHIGLIS 480  
 QY 480 ASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVGPFGTGGDILRRTN 539  
 DB 481 GSHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVGPFGTGGHLLRRTK 540  
 QY 540 TGTGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 599  
 DB 541 SGTGHIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 QY 600 TFXTVGTFPFSLLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659  
 DB 601 TFRTVGTFPFSDVQSTFTIGAWNFSSGNEVYIGRIEFVPEVTEAEYDFEKAQEKV 660  
 QY 660 TALTSTNPRGLKTDVKYHIDQVSNLVSDEFLDKRELPEIVKYAKQLHIERNM 718  
 DB 661 TALTSTNPRGLKTDVKYHIDQVSNLVSDEFLDKRELPEIVKYAKQLHIERNM 719

RESULT 12  
 C1CB\_BACTU STANDARD; PRT; 1229 AA.  
 AC Q45739;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pestidial crystal protein cryIIB (insecticidal delta-endotoxin  
 DE CryIIB(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN Name=cryIIB; Synonyms=cryIIB(b), cryET5;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RC STRAIN=NRRL B-21110 / EG5847;  
 RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;  
 RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins  
 RT toxic to lepidopteran insects."  
 RL Patent number US5322687, 21-JUN-1994.  
 CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
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 CC  
 CC EMBL; L32020; AAA22344.1; -.  
 DR HSSP; P02965; 1CIY.  
 DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;  
 Query Match 64.4%; Score 2415; DB 1; Length 1229;  
 Best Local Similarity 65.1%; Pred. No. 8.2e-160;  
 Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
 QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCVAEVNNDPFFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVFPAGQVASYLSTILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
 DB 67 LGVLGVFPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQVQVTEVTRNTAARLEG 126  
 QY 131 LGDALAVYHDSLESWVGNRNTARSVVKSVYIALELMFVKLPFAVSGEEVPLLPPIYA 190  
 DB 127 LGRGYSYQQALLETWLDNRNDARSITILERYVALELDITTAIPFRIRNEEVPLLMVYA 186  
 QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNNLRGN 250  
 DB 187 QAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEYSNHCQVWNTGLNNLRGN 246  
 QY 251 AESWRYNQFRDMTLMVLVDLVALFSPYDTQMPYIKTAQITREYVTDALGTVHPHPSFT 310  
 DB 247 AESWRYNQFRDMTLMVLVDLVALFSPYDTQMPYIKTAQITREYVTDALGTVHPHPSFT 306  
 QY 311 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWKNTQYMNWGGHKLFRFTI 370  
 DB 307 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWKNTQYMNWGGHKLFRFTI 366  
 QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFQTQPVN-VPRVDFHMKFVT 428  
 DB 367 GGTLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFQTQPVN-VPRVDFHMKFVT 422  
 QY 429 HPIASDNFYYPG-----YAGIGTQLODSENELPPATGQPNYESYSHRLSHIGLISAS 481  
 DB 423 --INPQNIYERGATTYSQPYQGVQIQLFDSSETLPETTERPNYESYSHRLSHIGLIGN 480  
 QY 482 HVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDILRRNTG 541  
 DB 481 HVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDILRRNTG 540  
 QY 542 TFGDIRVNINPFAQRYRIRYASITDQLQHTSINGKAINQGNFSAVNRGDLDTYKTF 601  
 DB 541 TFGDIRVNINPFAQRYRIRYASITDQLQHTSINGKAINQGNFSAVNRGDLDTYKTF 600  
 QY 602 XTGVFTTFFSLDVQSTTIGAWNFSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 661  
 DB 601 RTAGFSTPFNFNAQSTFTLGAQSFN-QEYVIDRVEFVPAEVTFAEYDLERAQKAYNA 659  
 QY 662 LFTSTNPRGLKTDVKYHIDQVSNLVESLSDFFYLDEKRELFEIKYAKQLHIERNM 718  
 DB 660 LFTSTNPRGLKTDVKYHIDQVSNLVESLSDFFYLDEKRELFEIKYAKQLHIERNM 716

RESULT 13  
 CIBC\_BACTM STANDARD; PRT; 1233 AA.  
 ID CIBC\_BACTM  
 AC Q45774;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin  
 DE CryIb(c)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN Name=cryIbC; Synonyms=cryIb(c), cryIbC;  
 OS Bacillus thuringiensis (subsp. morrisoni).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1441;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bishop A.H., Bone E.J., Ellar D.J.;  
 RT "Cloning of novel Bacillus thuringiensis delta-endotoxin."  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 epithelial cells of insects.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 sporulation and is accumulated both as an inclusion and as part of  
 the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; Z46442; CAA86568.1; -.  
 DR HSSP; P02965; 1CIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_N.  
 DR InterPro; IPR005639; endotoxin\_C.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;

Query Match 64.4%; Score 2415; DB 1; Length 1233;  
 Best Local Similarity 65.1%; Pred. No. 8.2e-160;  
 Matches 467; Conservative 91; Mismatches 141; Indels 18; Gaps 7;  
 QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQMLSPDARIEDSLCVAEVNNDPFFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVFPAGQVASYLSTILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130  
 DB 67 LGVLGVFPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQVQVTEVTRNTAARLEG 126  
 QY 131 LGDALAVYHDSLESWVGNRNTARSVVKSVYIALELMFVKLPFAVSGEEVPLLPPIYA 190  
 DB 127 LGRGYSYQQALLETWLDNRNDARSITILERYVALELDITTAIPFRIRNEEVPLLMVYA 186  
 QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNNLRGN 250  
 DB 187 QAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEYSNHCQVWNTGLNNLRGN 246  
 QY 251 AESWRYNQFRDMTLMVLVDLVALFSPYDTQMPYIKTAQITREYVTDALGTVHPHPSFT 310  
 DB 247 AESWRYNQFRDMTLMVLVDLVALFSPYDTQMPYIKTAQITREYVTDALGTVHPHPSFT 306  
 QY 311 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWKNTQYMNWGGHKLFRFTI 370  
 DB 307 STWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWKNTQYMNWGGHKLFRFTI 366  
 QY 371 GGTLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFQTQPVN-VPRVDFHMKFVT 428  
 DB 367 GGTLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFQTQPVN-VPRVDFHMKFVT 422  
 QY 429 HPIASDNFYYPG-----YAGIGTQLODSENELPPATGQPNYESYSHRLSHIGLISAS 481  
 DB 423 --INPQNIYERGATTYSQPYQGVQIQLFDSSETLPETTERPNYESYSHRLSHIGLIGN 480  
 QY 482 HVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDILRRNTG 541

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Db 481 TLAPVYVTHRSADRTNIGNRITQIPLVKALNLSHGVTVVGGPGFTGGDILRRNTG 540
Qy 542 TFGDIRVNPVPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATNMGEDLDYKTF 601
Db 541 TFGDIRVNPVPPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATNMGEDLDYKTF 600
Qy 602 XTVCFTTSPSLDVSQFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTA 661
Db 601 RTAGFSTPNFLNAQSTTFLQAQFSN-QEVYIDRVFVPAEYVTEAEYDFEKAQKVTA 659
Qy 662 LFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
Db 660 LFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 14
Q93T75 PRELIMINARY; PRT; 1228 AA.
ID Q93T75;
AC Q93T75;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin Cry1Ba2.
GN Name=Cry1Ba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSP; P07130; IDLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.0%; Score 2249; DB 2; Length 1228;
Best Local Similarity 62.3%; Pred. No. 3.4e-148;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7;

Qy 23 TDSLKNETDIELQNH-----EDCLKMEYENVEPVSASTIQTGTGIAGKI 70
Db 2 TSNRKNENIINAVSNHSAQMDLLPDARIEDSLCIAEGNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPAQVAVSLYFTLGLWPKGNQKQWEIFMEHVEEINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAQVAVSLYFTLGLWPKGNQKQWEIFMEHVEEINQKISTYARNKALTDLKG 121
Qy 131 LGDALAVYHDSLSWVGVRNNTNARSVVKVQYIALELMFVOKLPSPAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQCSLEWLENRDADRTRSVLHTQYIALELDLFNAMPFAIRNQEVPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKEWLSSETSTFYNRQVERAGDYSHCVKQWYSTGLANLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIQRQYERQVERTRDYSQVCVEWYNTGLSLRGYN 241
Qy 251 AESWRYNQPRRDMTLMVLDLVALFPSYDTQVPIKTAQLTREVVYTDALGTVHPHPSPT 310
Db 242 AASWRYNQPRRDLTLGLVLDLVALFPSYDTQVPIKTAQLTREVVYTDALGT--GVNNA 299
Qy 311 STTWANNAPSFSAIEAAVVRNPHLLDLEQYTIYLSLRSNTQVMWVGKHKLEFRI 370

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Db 300 SMWYNNAPSFSAIEAAVVRNPHLLDLEQYTIYLSLRSNTQVMWVGKHKLEFRI 359
Qy 371 GGTLNISTQGSTNTSINPVTLPFTSRDVRYSRESLAGNLP--LTQPVN-VPRVDHMKFV 427
Db 360 GGGLNTSTHGATNTSINPVTLPFTSRDVRYSRESLAGNLP--LTQPVN-VPRVDHMKFV 416
Qy 428 THP-----TASDNFYYPGAGICTQLOSENELPPEATGQNYESYSHRSLSHIGLISASH 482
Db 417 TNPQNISDRGTANYSQP-YESPGLOKQDSETELPPETERNYESYSHRSLSHIGLISASH 475
Qy 483 VKALVYVSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGT 542
Db 476 VNPVYVSWTHRSADRTNTEPNISITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTGT 535
Qy 543 FGDIVNINPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATNMGEDLDYKTF 602
Db 536 FGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVNNFRFLTMNSGDELKIGNFV 595
Qy 603 TVGFTTTPFSLDVSQFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKVTA 662
Db 596 RRAFTTPTFTQIDIIIRTSIQGLSGNGEYIDKIEIPVTATFEAEYDLERAQAVNAL 655
Qy 663 FTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 718
Db 656 FTSTNPRGLKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYAKQLHIERNM 711

RESULT 15
C1BA_BACTK STANDARD; PRT; 1228 AA.
ID C1BA_BACTK
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cry1Ba (Insecticidal delta-endotoxin
DE Cry1B(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=Cry1Ba; Synonyms=cry1B(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RC MEDLINE=88203216; PubMed=3362680;
RX Brizzard B.L., Whiteley H.R.;
RA "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis.",
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RC Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X06711; CAA29898.1; -
DR EMBL; X95704; CAA65003.1; -

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DR PIR; S00873; S00873.
DR HSSP; P07130; 1DLG.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_Like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match      60.0%; Score 2248; DB 1; Length 1228;
Best Local Similarity 62.3%; Pred. No. 4e-148;
Matches 446; Conservative 80; Mismatches 164; Indels 26; Gaps 7.

Qy    23 TDSLKNETDIELQNINH-----EDCLKMSEVENVEPFVSASTQTGTIGIAGKI 70
Db    2 TSNRKNENELINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASVTQTGINIAGEI 61
Qy    71 LGTLGVPPAGQVASLYSFILGELWPKGNQWEIFMEHVHEEI INOKISTYARNKALTDLKG 130
Db    62 LGLVLGVPPAGQLASFYSFLVGGELWPRGRDQCWEIFLHVLEQLINOQITENARTALARQG 121
Qy    131 LGDALAVYHDSLSGSWGVRNNTARSVVKSQXIALELMFVKLPSPFAVGSEEVPLLPYA 190
Db    122 LGSFRAYQQSLEDWLENRDDARTRSVLTYQYIALELDLFNAMELFAIRNQVEVPLLWVYA 181
Qy    191 QAANLHLLLRDASI PGKEWGLSSSEISTFYNRQVERAGDYSHCVKVYSTGLNNLRGTN 250
Db    182 QAANLHLLLRDASLFGSEFGLTSQEIQRYRQVERTRDYSDCYVEWYNTGLNSLRGTN 241
Qy    251 AEGWVRYNQRRDMTLMVDLVLPSPSYDTOMYPDKTTAQLTREVTYTDAGTVHPHPSPT 310
Db    242 AAEWVRYNQRRDLTLGLVDLVLPSPSYDTRTYPIINTSAQLTREVTYDAIGAT--GVNMA 299
Qy    311 STTWYNNAPSFSAIEAAVVRNPHELLDFLEQVTIYSLSRWSNTQYMMNWGGHKLEFRTI 370
Db    300 SMWYNNAPSFSAIEAAAIRSPHELLDFLEQLTIFFASSRWSTRHMTYWRGHTIQSRPI 359
Qy    371 GGTLNIISOGSTNTSINPVTLPTTSRDVVYRTESLAGLNLF--LTQPVN-VPRYDFHWKFV 427
Db    360 GGLNTSTHGATNTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIHGVPTRYFN--- 416
Qy    428 THP----IASDNFYPGYAGIGTGLODSENELPPEATQPNVESYSHLSHLGISASH 482
Db    417 TNFQNISDRGTANYSQP-YESPGIQLKDSETELPETTERPNVESYSHLSHLGIIQSRI 475
Qy    483 VKALVSWTHRSADRTNTILEPNSITQIPLVKAFNLSSGAADVVRGPFGTGGDILERTNTGT 542
Db    476 VNVPYVSWTHRSADRTNIGPNRITQIPWKASELPQGGTTVVRGPFGTGGDILERTNTGG 535
Qy    543 FGDIVRNINPPFAQRYRVRIYASTTDLQFHTSINGKAINQGFNSATMNRGEDLDYKTFX 602
Db    536 FGDIRVTWNGPLTQRIRYGFRYASTVDPDFVSRGGTTVNNFRFLRTMMSGDELKYGNFV 595
Qy    603 TVGFTTPFSLLDVQOSTFTIGAMWPSGNEBVIYDRIEFVPEVETVEAADFEKAQEKVAL 662
Db    596 RRAFTTPFTTQIDIIRTSIQGLSGNGEVIYDKIEIIPVTATFEAYDLERAQEAVAL 655
Qy    663 FTSTNPRGLKTDVKYDHIDOVSNLIVESLSDEFYLDEKRELFEIVKYAKOLHIERNM 718
Db    656 FTNTNPRLKTDVTYHHIDOVSNLVACLSDEFCLDEKRELLEKKYAKELSDERNL 711

```

Search completed: October 28, 2004, 18:29:48  
Job time : 102.442 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.191 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-56  
Perfect score: 3762  
Sequence: 1 MKLNQDKHQSFSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3762	100.0	719	2 I39814	insecticidal prote
2	3753	99.8	719	2 S25383	parasporal crystal
3	3743	99.5	719	2 I39815	insecticidal prote
4	3503	93.1	719	2 I40590	cryv465 protein -
5	2262	60.1	1228	2 S00873	parasporal crystal
6	1891	50.3	380	2 B42459	hypothetical prote
7	1483	39.4	1157	1 S42447	parasporal crystal
8	1467	39.0	1166	2 S32645	parasporal crystal
9	1461	38.8	1174	2 S32649	parasporal crystal
10	1459	38.8	1155	2 A28513	parasporal crystal
11	1452	38.6	1155	2 JD0002	parasporal crystal
12	1452	38.6	1156	2 A29125	parasporal crystal
13	1443	38.4	1155	2 I39838	parasporal crystal
14	1439	38.3	934	2 A22798	parasporal crystal
15	1438	38.2	1176	2 JT0241	parasporal crystal
16	1435	38.1	1155	2 S02134	parasporal crystal
17	1434	38.1	1181	2 A41052	parasporal crystal
18	1432	38.1	1176	2 JC2219	parasporal crystal
19	1428	38.0	1176	2 A22617	parasporal crystal
20	1428	38.0	1176	2 S02215	parasporal crystal
21	1353	36.0	1174	2 A42459	parasporal crystal
22	1338	35.6	1138	2 A48944	parasporal crystal
23	1324	35.2	1156	2 A29838	parasporal crystal
24	1316	35.0	823	2 S04181	parasporal crystal
25	1307	34.8	1189	2 S00944	parasporal crystal
26	1301	34.6	1154	2 S39536	parasporal crystal
27	1257	33.4	1171	2 I40572	parasporal crystal
28	1257	33.4	1171	2 A37829	parasporal crystal
29	1254	33.3	1176	2 A48970	parasporal crystal

30 1219 32.4 1160 2 S32647 parasporal crystal  
31 1210.5 32.2 1165 2 S11446 parasporal crystal  
32 1200.5 31.9 655 2 JC7140 protoxin - Bacillu  
33 1181 31.4 1172 2 S32689 parasporal crystal  
34 1171 31.1 1160 2 I40589 parasporal crystal  
35 1148.5 30.5 1178 1 USBSXH parasporal crystal  
36 1148 30.5 1177 2 A49785 parasporal crystal  
37 1147 30.5 652 2 A27323 parasporal crystal  
38 1124 29.9 659 2 S10228 parasporal crystal  
39 1091.5 29.0 652 2 I39811 parasporal crystal  
40 983 26.1 649 1 JH0261 parasporal crystal  
41 926 24.6 618 2 S11445 parasporal crystal  
42 871 23.2 1156 2 S19306 parasporal crystal  
43 820 21.8 1136 1 USBS8I parasporal crystal  
44 679.5 18.1 934 2 B29838 parasporal crystal  
45 656 17.4 1180 2 I39870 parasporal crystal

ALIGNMENTS

RESULT 1

I39814  
insecticidal protein cryv1 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis

C:Date: 19-Jul-1996 #sequence revision 19-Jul-1996 #text change 26-Aug-1999

C:Accession: I39814

R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.

A:Title: Distribution of cryv-type insecticidal protein genes in Bacillus thuringiensis &

tomocidus.

A:Reference number: I39814; MUID:95314293; PMID:7793960

A:Accession: I39814

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A:Cross-references: GB:I36338; NID:G540281; PIDN:AAC36999.1; PID:G540282

C:Genetics:

A:Gene: cryv1

C:Superfamily: parasporal crystal protein

Query Match 100.0%; Score 3762; DB 2; Length 719;  
Best Local Similarity 100.0%; Pred. No. 1.3e-251;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDCDKMSYENVEPFPVSASTI 60  
Db 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDCDKMSYENVEPFPVSASTI 60  
Qy 61 QTGIGTAGKILGTIGVPPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEINQKISTYA 120  
Db 61 QTGIGTAGKILGTIGVPPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEINQKISTYA 120  
Qy 121 RNKALTDLKGDLAVYHDSLSWVGNNRNTARSVVKSQVIALELMFVKLPSPAVSG 180  
Db 121 RNKALTDLKGDLAVYHDSLSWVGNNRNTARSVVKSQVIALELMFVKLPSPAVSG 180  
Qy 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKYS 240  
Db 181 EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCWKYS 240  
Qy 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAI 300  
Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAI 300  
Qy 301 GTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYLSLSRSWNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYLSLSRSWNTQYNNMW 360  
Qy 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVYRTESLAGLNFLTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVYRTESLAGLNFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFFYPGYAGIGTQDSENELPPEATQPNVYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTVTHPIASDNFFYPGYAGIGTQDSENELPPEATQPNVYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNINPPFAQRYRIRYASVTDLOPHTSINGKAINQGNFSAATNVRGDDLDYK 600  
DB 541 TGTFGDIRVNINPPFAQRYRIRYASVTDLOPHTSINGKAINQGNFSAATNVRGDDLDYK 600  
QY 601 TFRVTGFTTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
DB 601 TFRVTGFTTTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM 719

RESULT 2  
S25383  
parasporal crystal protein cryIIal - Bacillus thuringiensis  
N;Alternate names: delta-endotoxin; parasporal crystal protein cryV  
C;Species: Bacillus thuringiensis  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C;Accession: S25383  
R;Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
Mol. Microbiol. 6, 1211-1217, 1992  
A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
toxin subunit.  
A;Reference number: S25383; MUID:92269582; PMID:1588820  
A;Accession: S25383  
A;Molecule type: DNA  
A;Residues: 1-719 <TAI>  
A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PIDN:CAA44633.1; PID:G40290  
C;Genetics:  
A;Gene: cryV  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 99.8%; Score 3753; DB 2; Length 719;  
Best Local Similarity 99.7%; Pred. No. 5.2e-251;  
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKGDLALAVYHDSLSWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKGDLALAVYHDSLSWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG 180  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNQRQVERAGDYSYHCVKWS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNQRQVERAGDYSYHCVKWS 240  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
QY 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
DB 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNFLTPQVNGVPR 420  
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNFLTPQVNGVPR 420

## RESULT 3

I39815  
insecticidal protein cryV - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I39815  
R;Gleave, A.P.; Williams, R.; Hedges, R.J.  
Appl. Environ. Microbiol. 59, 1683-1687, 1993  
A;Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
a delta-endotoxin subunit.  
A;Reference number: I39815; MUID:93298009; PMID:8517758  
A;Accession: I39815  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-719 <RES>  
A;Cross-references: UNIPROT:Q45752; GB:M98544; NID:9142767; PIDN:AAA23354.1; PID:G142768  
C;Genetics:  
A;Gene: cryV  
C;Superfamily: parasporal crystal protein

Query Match 99.5%; Score 3743; DB 2; Length 719;  
Best Local Similarity 99.6%; Pred. No. 2.6e-250;  
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
QY 121 RNKALTDLKGDLALAVYHDSLSWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKGDLALAVYHDSLSWVGNNRNTARSVVKSQYIALELMFVKQLPSFAVSG 180  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNQRQVERAGDYSYHCVKWS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFNQRQVERAGDYSYHCVKWS 240  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
QY 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
DB 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNFLTPQVNGVPR 420  
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNFLTPQVNGVPR 420

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Qy 421 VDFHWKFVTHPIASDNFYYPGYAGICTQLQDSNELPPEATQGPVYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGICTQLQDSNELPPEATQGPVYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPFSFLDVOSTFTIGAMNPFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660
Db 601 TFRVTGFTTTPFSFLDVOSTFTIGAMNPFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719
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## RESULT 4

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I40590
cryV465 protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40590
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tonocoidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I40590
A>Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672
C:Genetics:
A:Gene: cryV465
C:Superfamily: parasporal crystal protein
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Query Match 93.1%; Score 3503; DB 2; Length 719;
Best Local Similarity 92.5%; Pred. No. 9.5e-234;
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;
```

```
Qy 1 MKLKNQDKHQSFSSNAKVYDKISTDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60
Db 1 MKLKNPDKHQSJSSNAKVYDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFVSASTI 60
Qy 61 QTGIGIACKILGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIQKISTYA 120
Db 61 QTGIGIACKILGTLGVPPAGQIASLYSFILGELWPKGKSQWEIFMEHVEEIIQKILTYA 120
Qy 121 RNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSPFVSG 180
Db 121 RNKALSDLRGLDALAVYHESLESWVENRNNTARSVVKQYIALELMFVQKLPSPFVSG 180
Qy 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTPNRQVERAGDYSYHCVKWSY 240
Db 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTPNRQVERTDYSDHCIKWYN 240
Qy 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTRREYTDAI 300
Db 241 TGLNNLRGTNAKSWVRNQFRKDMTLMVLDLVALFPSYDILVPIKTTISQLTRREYTDAI 300
Qy 301 GTVHPHPGFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMNW 360
Db 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDLEKVTIYSLSRWSNTQYMNW 360
Qy 361 GGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHRLSPRIGGALNTSQGSTNTSINPVTLPFTSRDVYTESLAGLNLFLTQPVNGVPR 420
```

```
Qy 421 VDFHWKFVTHPIASDNFYYPGYAGICTQLQDSNELPPEATQGPVYESYSHRLSHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGICTQLQDSNELPPEATQGPVYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Qy 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Qy 601 TFRVTGFTTTPFSFLDVOSTFTIGAMNPFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660
Db 601 TFRVTGFTTTPFSFLDVOSTFTIGAMNPFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719
```

## RESULT 5

```
S00873
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N:Alternate names: parasporal crystal protein cryA4
C:Species: Bacillus thuringiensis subsp. thuringiensis
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S00873
R:Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t
A:Reference number: S00873; MUID:88203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094;
C:Genetics:
A:Gene: cryA4
A:Start codon: TTG
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
```

```
Query Match 60.1%; Score 2262.5; DB 2; Length 1228;
Best Local Similarity 62.4%; Pred. No. 9.6e-148;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;
```

```
Qy 23 TDSLKNETDIELQINH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENELIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61
Qy 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFYSFLVGLWPRGRDQWEIFLEHVEQLINQOITENARTALARLQ 121
Qy 131 LGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSPFVSGEVPPLPIYA 190
Db 122 LGDSFRAYQOSLEDNLENRDDAATRSVLVYQVIALELDLFLNAMPFAIRNQEVPLLMVYA 181
Qy 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWSYTGNNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYVERQVERTRDSDYCVWEYNTGLNSURGTN 241
Qy 251 AESWVRNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTRREYTDAIQVHPHPSFT 310
Db 242 AASWVRNQFRDMLTGLVLDLVALFPSYDTRTPINTSAQLTRREYTDATGAT--GVNMA 299
Qy 311 STTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMNWCGHKLFEFTI 370
Db 300 SMWYNNNAPSFAIEAAAIRSPHLLDLEQLTIFSSSRWSNTRMTYWRGHTIQSRPI 359
Qy 371 GGTNLNISTQGSTNTSINPVTLPFTSRDVYTESLAGLNLFLTQPVNGVPRDHWKVF 428
Db 360 GGLNTSTHGTATNTSINPVTLPFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRENF--- 416
```

429 THP-----TASDNFYPGVAGICTQLODSENELPPEATQBNYSEYSHRLSHIGLISASH 483  
 417 TNPQNISDRGTANYSQP-YESPLQLKDSSETLPPETTERENYSEYSHRLSHIGILOSR 475  
 484 VKALVSWTHRSADRNTNIEPNSITQPLVKAFNLSSGAUVVRGPGFTGGDILRRNTTGT 543  
 476 VNPVYSWTHRSADRNTNIEPNSITQPLVKAFNLSSGAUVVRGPGFTGGDILRRNTTGT 535  
 544 FDIRVNIINPPFAQRVIRYASTDLOPHTSINGKAINQCNFATMNRGEGDLDYKTFR 603  
 536 FGPIRVTVNGPLTQRYICFRYASTVDFFVSRGGTIVNNFRFLRTMNSGDELKYGNFV 595  
 604 TVGFTTFFSFLDVQSTFTIGAMNFFSGNEVYIDRIEFPVPEVYEAEDFEKAQKVTA 663  
 596 RRAFTTFTTQIQDIIRTSIQGLSNGEVIYDKIEIIPVTATFEAEYDLERAQEAVAL 655  
 664 FTSTNPRGLKTDVYHIDQVSNLVSSEDFYLDKRELPEIVKYANELHIERNM 719  
 656 FTNTNPRRLKTDVYHIDQVSNLVSSEDFYLDKRELPEIVKYANELHIERNM 711

RESULT 6

B42459  
 hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag  
 C;Species: Bacillus thuringiensis  
 C;Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 09-Jul-2004  
 C;Accession: B42459  
 R;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.  
 J. Bacteriol. 173, 3966-3976, 1991  
 A;Title: Isolation and characterization of a novel insecticidal crystal protein gene fro  
 A;Reference number: A42459; MUID:91286178; PMID:2061280  
 A;Accession: B42459  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-380 <CHA>  
 A;Cross-references: UNIPROT:Q8KY61; UNIPROT:Q45740; GB:M63897  
 C;Superfamily: parasporal crystal protein

Query Match 50.3%; Score 1891; DB 2; Length 380;  
 Best Local Similarity 95.3%; Pred. No. 6.7e-123;  
 Matches 362; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MRLKNDKQHSFSSNAKVDKISTDSLNKNETDIELQINHEDECKMSEYENVEPFFVSASTI 60  
 DB 1 MRLKNDKQHSFSSNAKVDKISTDSLNKNETDIELQINHEDECKMSEYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAVVHDSLSWGNRNNTRARSVVKSVQVIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKLGDALAVVHDSLSWGNRNNTRARSVVKSVQVIALELMFVQKLPFAVSG 180  
 QY 181 BEVPILLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSYHCVKWTYS 240  
 DB 181 BEVPILLPIYQAANLHLLLRDASIFGKEWGLSSSEISTFFNROVERAGDYSDHCVKWTYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDNTLMVLDLVALFPDYDTQMPYPIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDNTLMVLDLVALFPDYDTQMPYPIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTTWTNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLSLLSWSNTQYMMNW 360  
 DB 301 GTVHPHPSFTTWTNNNAPSFTIESAVVRNPHLLDFLEQVTIYLSLLSWSNTQYMMNW 360  
 QY 361 GGHKLEFRITGGTLNISTOG 380  
 DB 361 GGHKLEFRITGGTLNISTOG 380

RESULT 7

S49247  
 parasporal crystal protein cry9Ca1 [validated] - Bacillus thuringiensis  
 N;Alternate names: parasporal crystal protein cryIH  
 C;Species: Bacillus thuringiensis  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C;Accession: A59350; S49247  
 R;Lambert, B.; Buyse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V  
 Appl. Environ. Microbiol. 62, 80-86, 1996  
 A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity again  
 A;Reference number: A59350; MUID:96141404; PMID:8572715  
 A;Accession: A59350  
 A;Molecule type: DNA  
 A;Residues: 1-1157 <LAM>  
 A;Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:G547554; PIDN:CAA85764.1; PID:G54755  
 A;Experimental source: serovar tolworthi  
 C;Comment: This parasporal crystal protein, active against corn borer and other insects,  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 39.4%; Score 1483; DB 1; Length 1157;  
 Best Local Similarity 43.1%; Pred. No. 5.7e-94;  
 Matches 321; Conservative 113; Mismatches 220; Indels 90; Gaps 15;

QY 26 LKNETDIELQINHEDECKMSEYENVEPFFVSAS-----TIQTGIGIAGKILGTGVPP 78  
 DB 29 LASDPNALQNMVYKDYLTQWTDYDTSYINPSLSISGRDAVQVLTALTWVGRILGALGVPP 88  
 QY 79 AGQVASYFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDKLGGLDALAV 137  
 DB 89 SGQIVSYFQFLTLNTPVNDTATWAEFQVQVLELVNQITFEARNQALARIQGLGSENFV 148  
 QY 138 YHDSLSWGNRNNTRARSVVKSVQVIALELMFVQKLPFAVSGEVEPLPIYQAANLHL 197  
 DB 149 YORSQNLWADRNTNLSVVRQAQFIALDLDFVNAIFLVANGQQVPLLSVYQAANLHL 208  
 QY 198 LLRLDASIFGKEWGLSSSEISTFFNROVERAGDYSHCVKWTYSTGLNLRGTNABSWRY 257  
 DB 209 LLLKDASLFGEGWGFQGEISTYDRLQELTAKYNTYCETWYNTGLDRLGRTNTESWLRY 268  
 QY 258 NQFRDNTLMVLDLVALFPDYDTQMPYPIKTTAQLTREYVTDALGTVHPHPSFTTWTNN 317  
 DB 269 HQFRREMTLVLDVVALFPDYDRLVLTGSGNPQLTREYVTDALGTVHPHPSFTTWTNN 328  
 QY 318 NAPSFAIEAAVVRNPHLLDFLEQVTIYLSLLSWS--NQYNNMWGGHLE----- 366  
 DB 329 PYNTFSELENAFIRPPHFLDRLNSLTISS--NRFPVSSNFMDYWSGHTLRRSYLNSAVQ 386  
 QY 367 -----FRITGGTLNISTOGSTNTSINPVTLPSTSRDYRTESLAGNLFLOPQVNGVPR 420  
 DB 387 EDSYGLITTTTATINPGVDGTR--IESTAVDFRS-----ALIG-----IYGNR 429  
 QY 421 VDFHMKFVTHPIASDNFYPGYAGIGT-----QLQDSENELPP-EATGQPNYESYS 470  
 DB 430 ASF-----VPGGLENGTTPSPANGCCRDLYDNTDELPPDESTG-----SST 469  
 QY 471 HRLSHIGLIS-----ASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSG 521  
 DB 470 HRLSHVTFQFQTNQAGSIANAGSVPTVWTRRDVLDLNTITPNTITQPLVKASAPVSG 529  
 QY 522 AAVVRGPGFTGGDILRRNTGTGDIRVNIINPPFAQRVIRYASTDLOPHTSINGKA 581  
 DB 530 TTVLKGPGFTGGDILRRNTGTGDIRVNIINPPFAQRVIRYASTDLOPHTSINGKA 589  
 QY 582 INQNFESATMNRGEGDLDYKTFRTVGTFTT-----PFSEFLDVQSTFTIGAMNFFSGNEVYI 635  
 DB 590 IGDVRLGSTVMNRGQELTYSEFTTREFTTGPFNPPFTTQAQOEILLTVNAEGVSTGGEYI 649  
 QY 636 DRIEFVPEVYTYEAFDFEKAQKVTAQLTSTNPRGLKTDVYHIDQVSNLVSSEDF 695  
 DB 650 DRIEIVPNPAREAEEDLEAKKAVASLFTTRTD-GLQVNTDYQVDQAANLVSCLSEQ 708  
 QY 696 YLDEKRELFELVYKYNELHIERNM 719

Db 709 YGDKMKMLLEAVRAAKRLSRNL 732

## RESULT 8

S32645  
parasporeal crystal protein crylGal - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32645  
R:Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645

A:Accession: S32645

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1166 <LAM>

A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958

C:Superfamily: parasporeal crystal protein

C:Keywords: delta-endotoxin

Query Match 39.0%; Score 1467.5; DB 2; Length 1166;  
Best Local Similarity 45.8%; Pred. No. 6.8e-93;  
Matches 323; Conservative 100; Mismatches 207; Indels 75; Gaps 17;

QY 41 DCLKQSEY---NVEPVASITQIGIAGKILGLTGLVPPFAGQVASYLSFILGELWPK 96

Db 13 NCLNPESEIFNARNNSFGLVQVSGSL---TRFLLEAAVPEAGFALGLFDIIWGAL--- 66

QY 97 GKQWEIWEHVEEIIINQKISTYARNKALTDLKLGLDALAVYHDSLESWGNRNTRARS 156

Db 67 GVDQWLFRLQIEQLRQIELEARNRATALLTGLSSSYNLYVEALRENDPNPNAQOE 126

QY 157 VVKSQYIALELMFVQKLPSPFVSGEVEPLPIYAQAANLHLLRLDASIFGKWLSSSE 216

Db 127 RVTRFRLTDDAIVTGLPTLAIRNLEVNLVSYTQAANLHLLRLDASVFGGERGLTQAN 186

QY 217 ISTFYNRQVERAGDYSYHCVKYSTGLNNLRGTNAESWRYNQFRDMTLMVLVALFP 276

Db 187 IEDLYTRLTSNQEYSDHCARNYQNGLEIGGISR---RYLDFQRLDLSVLIDVALFP 242

QY 277 SYDTQMPYIKTTAQLTRVYTDAL--GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPH 334

Db 243 NYDIRTYPIPTOSQLTRIEYTPVAVGNI-----NFGLSIANVLVRAPH 285

QY 335 LLDLFLEQYIYLSLRWSNTQYMMNGGHKLEFRITIG-GTLN-----ISTQGSTNTS 385

Db 286 LMDFDIRIVYITNSVR--STPY--WAGHEVISRRTGQGGQNEIRFPLYGVAANAEPVPT 340

QY 386 INPVTLPFTSRDVRFTS-----LAGLNLELTQPVNGVPRVDFHWKFTVHTPIASDNFY 439

Db 341 IRPTGFTDEQROWYRARSRVVSRSSGQDFSLVDVAVG-----FLT-IFSASVIYR 389

QY 440 PGVAGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLISAS-----HVKALVYSWTHR 494

Db 390 NGF-GENT--DTIDEPIEGTDP--FTGYSHRLCHVGFCLASSPFISQYARAFISWTHR 443

QY 495 SADRTNTEPNSITQIPLKAFNLSSGAAVVRGPGFTGGDILRRTNTGTGFDIRVNINPP 554

Db 444 SATLTNTIAPDVITQPLVKAFNLHSGATIVKPGPGFTGGDILRRTNVGSGDMRVNITAP 503

QY 555 FAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTTPPSFL 614

Db 504 LSQRYRVRIRYASTTDLQFYTNINGTTINGNFSSTMDSGDDLDYGRFRVAGFTTPTFS 563

QY 615 DVQSTFTIGANFSSGNEVYTDRIEVPVVTYEAEDFEKAQEKVTALFTSTNPRGLKT 674

Db 564 DANSTFTIGAFGSPNNEVYTDRIEVPVPAEVTFEAEYDLEKAQKAVNALFTSSNQIGLKT 623

QY 675 DVKDYHIDQVSNLVSLSDEFYLDKRELFELIVKYANELHIERNM 719

Db 624 DVTDYHIDKVSNLVECLDSDEFCLDKRELSKVKHAKRLSDERNL 668

## RESULT 9

S32649

parasporeal crystal protein crylFa3 - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S32649

R:Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645

A:Accession: S32649

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1174 <LAM>

A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA80235.1; PID:g2958

C:Superfamily: parasporeal crystal protein

C:Keywords: delta-endotoxin

Query Match 38.8%; Score 1461; DB 2; Length 1174;  
Best Local Similarity 44.6%; Pred. No. 1.9e-92;  
Matches 324; Conservative 101; Mismatches 205; Indels 96; Gaps 17;

QY 36 NINHE---DCLKQSEYENVEPVFVSASTIQTGIGIA-KILGLTGLVPPFAGQVASYLSFIL 90

Db 4 NIQNCQVPYNCLSNPEVEILSEERSTGRLPLDLSLSLTRLFLSEFVGVGVAFLDLIW 63

QY 91 GELWPKGNQWEIWEHVEEIIINQKISTYARNKALTDLKLGLDALAVYHDSLESWGNRN 150

Db 64 GFITP---SEWSFLQLQIEQLRQIELEARNRATITLRLGLADSYEVLALREWEENPN 120

QY 151 NTRARVSKSQYIALELMFVQKLPSPFVSGEVEPLPIYAQAANLHLLRLDASIFGKEW 210

Db 121 NAQLREDVRIRFANTDDALITANNFTTSFEIPLLSVYVQAANLHLLRLDASVFGQGW 180

QY 211 GLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNNLRGTNAESWRYNQFRDMTLMVL 270

Db 181 GLDIATVNNHNNRLINLIRHYTEHCLDTYNOGLENLRTGTNRQWSRFNQLRELTLT 240

QY 271 LVALPSSYDTQMPYIKTTAQLTRVYTDALGTVHPHPSFTSTTWNNAAPS-FSAIEAAV 329

Db 241 IVALFPNYDARAYPIQTSQLTREIYTSV--IEDSP-----VSANIPNGFNRAEFG- 290

QY 330 VRNPHLLDFLEQVITYLSLRWSNTQYMMNGGHKLEFRITIGTLNISTQGSTNTSINPV 389

Db 291 VRPHLMDFMN-----SLFVTAETVRSQTVWGHV-----SSRNTAGNPI 331

QY 390 TLPF-----TSRDVYRTESLAGLNLELTQPVNGVPRVDFHWKFTVHTPIAS 434

Db 332 NFPIYGVIFNPGGAIWADEDPPEFYRT-----LSDPV-----FVRGGFGN 371

QY 435 DNFYYPGYAGIGTQLQ-----DSENELPPEATGQPNYESYSHRLSHI--- 476

Db 372 PH-YVGLRGVAFQGTGNHTRTRFRNSGTDLSLDEIPPPQDNKSGAPMNDYSHVLNHTFVR 430

QY 477 --GLISASHV-KALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGG 533

Db 431 WPGEIAGSDSWRAPMFSWTHRSADRTNINPNIIITQIPAKAHNLHSGSTVVRGPGFTGG 490

QY 534 DILRRTNTGTGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAITMR 593

Db 491 DLLRRTNTGTGFADIRVNITGPLSQRYRVRIRYASTTDLQFTRINGTSVQNGNFORTMNR 550

QY 594 GEDLDYKTFRTVGTTPPSFLDVQSTFTIGANFSSGNEVYTDRIEVPVVTYEAEDF 653

Db 551 GGNLESNFRTAGFTSTPFSFNAQSTTLGTQAFSN-QEVYIDRIEVPVPAEVTFAESDL 609

QY 654 EKAQEKVTALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFELIVKYANEL 713

Db 610 ERAQKAVNALFTSTSQLGLKTNVTGTHIDQVSNLVACLSDDEFCLDKRELSKVKHAKRL 669

QY 714 HIERNM 719

Db 670 SDRKRL 675

JD0002  
paraspore crystal protein cry1Ab3 - Bacillus thuringiensis  
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prote  
C:Species: Bacillus thuringiensis  
C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C:Accession: A90025; A91560; A90955; S14555; A24172; A29043; JD0002  
R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
Agric. Biol. Chem. 51, 455-463, 1987  
A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
A:Reference number: A90025  
A:Accession: A90025  
A:Molecule type: mRNA  
A:Residues: 1-1155 <KON>  
A:Cross-references: UNIPROT:P06578  
A:Experimental source: subsp. kurstaki  
R:Geiser, M.; Schweitzer, S.; Grimm, C.  
Gene 48, 109-118, 1986  
A:Title: The hypervariable region in the genes coding for entomopathogenic crystal protei  
A:Reference number: A91560; MUID:87163505; PMID:3557124  
A:Accession: A91560  
A:Molecule type: DNA  
A:Residues: 1-1155 <GEI>  
A:Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124  
A:Experimental source: subsp. kurstaki  
R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
DNA 5, 305-314, 1986  
A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal  
A:Reference number: A90955; MUID:86300092; PMID:3743328  
A:Accession: A90955  
A:Molecule type: DNA  
A:Residues: 1-1155 <WAB>  
A:Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720  
A:Experimental source: subsp. berliner  
R:Chak, K.P.; Jen, J.C.  
submitted to the EMBL Data Library, October 1990  
A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
A:Reference number: S14555  
A:Accession: S14555  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <CHA>  
A:Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:G40273  
R:Hofte, H.; de Greve, H.; Seuring, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerck  
Eur. J. Biochem. 161, 273-280, 1986  
A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri  
A:Reference number: A26461; MUID:87054026; PMID:3023091  
A:Accession: A26461  
A:Molecule type: DNA  
A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>  
A:Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255  
A:Experimental source: strain berliner 1715  
C:Comment: This toxin is lethal to the larvae of lepidoptera and dipterans.  
C:Genetics:  
A:Gene: cry-1-2; bt2  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin  
F:82-586/Product: toxic peptide #status predicted <XP>  
F:82-300/Region: toxic #status predicted  
F:300-586/Region: insecticidal #status predicted  
Query Match 38.6%; Score 1452; DB 2; Length 1155;  
Best Local Similarity 44.2%; Pred. No. 7.8e-92;  
Matches 314; Conservative 111; Mismatches 229; Indels 56; Gaps 13;  
QY 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVPFAGQVASLYS 87  
DB 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQKQWEIFMEHVEEIIINQKISTYARNKALTDLKGLDALAVYHDSLSWG 147  
DB 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFPARNQAIISRLGSLNLYQIYAESFREWEA 119  
QY 148 NNNTRARSVVKSQYIALELMFVQKLPSPFVSGSEVPLPIYAQAANLHLLLRDASIFG 207

RESULT 10  
A26513  
paraspore crystal protein - Bacillus thuringiensis (strain aizawai)  
C:Species: Bacillus thuringiensis  
C>Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A26513  
R:Oeda, K.; Ohie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.  
Gene 53, 113-119, 1987  
A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
A:Reference number: A26513; MUID:87248103; PMID:3297927  
A:Accession: A26513  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1155 <OED>  
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:G143098; PIDN:AAA22551.1; PID:G143098  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin  
Query Match 38.8%; Score 1459; DB 2; Length 1155;  
Best Local Similarity 44.1%; Pred. No. 2.6e-92;  
Matches 313; Conservative 112; Mismatches 230; Indels 54; Gaps 12;  
QY 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVPFAGQVASLYS 87  
DB 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQKQWEIFMEHVEEIIINQKISTYARNKALTDLKGLDALAVYHDSLSWG 147  
DB 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFPARNQAIISRLGSLNLYQIYAESFREWEA 119  
QY 148 NNNTRARSVVKSQYIALELMFVQKLPSPFVSGSEVPLPIYAQAANLHLLLRDASIFG 207  
DB 120 DPTNPAALREEMRIQFNDMNSALTAIPFAVQYQVPLSVVQAANLHLSVLDRVSVFG 179  
QY 208 KEWGLSSSEISTFYNRQVRAGYSYCHVKYSTGLNLRGNAESVVRVQNRDMTLM 267  
DB 180 QRWGDAAATNSRYNDLTBLIGNYTHAVRWYNTGLERWGPDSRDWRVYQFRELTLT 239  
QY 268 VLDLVALFPDYDTOMYPIKTAQLTREYVYDAIGTVHFHPSFTSTTYNNNAPSFAIEA 327  
DB 240 VLDIVLSLFPNDYSTRYPIRTVSQTLREYTNPV-----LENFDGSPRALAQ 285  
QY 328 AV---VRNPHLLDFLEQVITYSLSR-----WSNTQYNNM---WGGHKLFRPTIGTLNIS 377  
DB 286 GIEGSIKSPHMLDILNSITITDAHRGEYVWSGHQINASPVGFSGPEFTPLYGTMGNAA 345  
QY 378 TQGSTNTSINPVLFTSRDVRVTESLAGNLFLTQPNVGVPRVDFHWKFTVTHPIASDNF 437  
DB 346 PQQRIVAQLGGQVYRTLSSTLYRRPFNIGIN---NQQLSLVDGTEFAYG-----TSSNL 396  
QY 438 YYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLI-----SASHVXALVYS 490  
DB 397 PSAVYKSGT---VDSLDEIPQNNVPPRQGFHRLSHVSMFSGFSNVSIIIRAPMFS 454  
QY 491 WTHRSADRTNTEPNSITQPLVKAFNLSGAAVVRGFGTGGDILRRTNTGTFGDIRVN 550  
DB 455 WTHRSDEFNNIIPSSQITQIPLTSTNLGSGTGVKGFSGTGGDILRRTSPQISLVRN 514  
QY 551 INPPFAQRYRVRIRYASTTDLQFHTSINGKALNQGNSATMNRGEDLDYKTFRTVGFTTP 610  
DB 515 ITAPLSQRYRVRIRYASTTNLQFHTSIDRPNQGNFSATMSGSLNLSQSGFRFTVGFTTP 574  
QY 611 FSELDVQSTFTIGANFFSGNEVYIDRIEFVPEVTEAEYDPEKAQEKVTLFTSTNPR 670  
DB 575 FNFSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFAEYDLEAKAVNELFTSSNQI 634  
QY 671 GLKTDVYHIDQVSNLVSLSDEYLDKRELFEIVKYNELHIERNM 719  
DB 635 GLKTDVTDYHIDQVSNLVSLSDEYLDKRELFEIVKYNELHIERNM 683

RESULT 11

```
Db 120 DPTNPALREEMRQFNQDMSALTTAIFLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKYSTGLNNLRGTNAESWVRYNQFRDMDTLM 267
Db 180 QRWGFDAAATINSRYNDLTRLIGNYTDHVRWYNTGLERWGPDSRDWIRYNQFRRELTLT 239
QY 268 VLDLVALPSSYDTQWYPIKTTAQLTREVTDAICTVHPHPSFTSTTWYNNAPSF-----S 323
Db 240 VLDIVSLFPNDSTYPIRTVSQLTREIYTNPV-----LENFDGSGFRGSAQ 285
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGHKLEFRITGGTLNI 376
Db 286 GIEGS-IRSPHLMIDLNSITITDAHRGEYYSWGHQIMASPVGFGPEFTFPLYGTMGNA 344
QY 377 STQGSTNTSINPVLTPFTSRDVTYTESLAGNLFLTQPVNGVPRVDFHKKFVTHPIASDN 436
Db 345 APQQRIVAGLGGVYRTLSSTLYRRPNIGIN---NQQLSVLDGTEPAYG-----TSSN 395
QY 437 FYYPGAGIGTQDSENELPPEATGQPNYBSYSHRLSHIGLI-----SASHVKALVY 489
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNVSIIRAPMF 453
QY 490 SWTHRSADRNTTIEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRV 549
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTPSGQISTLRV 513
QY 550 NINPPFAQRVRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTRFTVGFTT 609
Db 514 NITAPLSQRVRYRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGNLQSGSFRFTVGFTT 573
QY 610 PFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQKVLTALFTSTNP 669
Db 574 PFNFSNGSSVFTLSAHVFNFSNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633
QY 670 RGLKTDVKDHYHDQVSNLVESLSDDEFVLDKRELFELVYKYNELHIERNM 719
Db 634 IGLKTDVTDHYHDQVSNLVESLSDDEFVLDKRELFELVYKYNELHIERNM 683
```

## RESULT 12

```
A29125
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29125
R;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/Technology 5, 807-813, 1987
A;Title: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1156 <FIS>
A;Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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Query Match 38.6%; Score 1452; DB 2; Length 1156;
Best Local Similarity 44.2%; Pred. No. 7.8e-92;
Matches 314; Conservative 111; Mismatches 229; Indels 56; Gaps 13;
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```
QY 36 NINHEDCLKMSYENVE-PFVSASTIQTG-----IGIAGKILGTLGVFPAGQVASLYS 87
Db 4 NPINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDKLGDLALAVYHDSLESWVG 147
Db 63 IIWGIFF--GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLESLNLYQIYAESFREWEA 119
QY 148 NNNTRARSVVKSQYIALELMFVQKLPSPAVSGEVEVLLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMSALTTAIFLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179
```

```
QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKYSTGLNNLRGTNAESWVRYNQFRDMDTLM 267
Db 180 QRWGFDAAATINSRYNDLTRLIGNYTDHVRWYNTGLERWGPDSRDWIRYNQFRRELTLT 239
QY 268 VLDLVALPSSYDTQWYPIKTTAQLTREVTDAICTVHPHPSFTSTTWYNNAPSF-----S 323
Db 240 VLDIVSLFPNDSTYPIRTVSQLTREIYTNPV-----LENFDGSGFRGSAQ 285
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGHKLEFRITGGTLNI 376
Db 286 GIEGS-IRSPHLMIDLNSITITDAHRGEYYSWGHQIMASPVGFGPEFTFPLYGTMGNA 344
QY 377 STQGSTNTSINPVLTPFTSRDVTYTESLAGNLFLTQPVNGVPRVDFHKKFVTHPIASDN 436
Db 345 APQQRIVAGLGGVYRTLSSTLYRRPNIGIN---NQQLSVLDGTEPAYG-----TSSN 395
QY 437 FYYPGAGIGTQDSENELPPEATGQPNYBSYSHRLSHIGLI-----SASHVKALVY 489
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNVSIIRAPMF 453
QY 490 SWTHRSADRNTTIEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRV 549
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTPSGQISTLRV 513
QY 550 NINPPFAQRVRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTRFTVGFTT 609
Db 514 NITAPLSQRVRYRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGNLQSGSFRFTVGFTT 573
QY 610 PFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQKVLTALFTSTNP 669
Db 574 PFNFSNGSSVFTLSAHVFNFSNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633
QY 670 RGLKTDVKDHYHDQVSNLVESLSDDEFVLDKRELFELVYKYNELHIERNM 719
Db 634 IGLKTDVTDHYHDQVSNLVESLSDDEFVLDKRELFELVYKYNELHIERNM 683
```

## RESULT 13

```
I39838
parasporal crystal protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39838
R;Helford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
J. Biotechnol. 6, 307-322, 1987
A;Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki
A;Reference number: I39838
A;Accession: I39838
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1155 <RES>
A;Cross-references: UNIPROT:P06578; GB:M37263; NID:G142885; PIDN:AAA22420.1; PID:G142886
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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Query Match 38.4%; Score 1443; DB 2; Length 1155;
Best Local Similarity 44.1%; Pred. No. 3.3e-91;
Matches 313; Conservative 111; Mismatches 230; Indels 56; Gaps 13;
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```
QY 36 NINHEDCLKMSYENVE-PFVSASTIQTG-----IGIAGKILGTLGVFPAGQVASLYS 87
Db 4 NPINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
QY 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDKLGDLALAVYHDSLESWVG 147
Db 63 IIWGIFF--GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLESLNLYQIYAESFREWEA 119
QY 148 NNNTRARSVVKSQYIALELMFVQKLPSPAVSGEVEVLLPIYQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMSALTTAIFLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFG 179
QY 208 KEWGLSSSEISTFYNRQVERAGDYSYHCWKYSTGLNNLRGTNAESWVRYNQFRDMDTLM 267
```

DQ007698.1

268 VLDLVALPESYDTQMYPKTTAQLTREVVYTDALGTGVHPHPSFTSTTWNNNAPSFAIEA 327  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
240 VLDLVALPESYDSRRYPRTVSQLTREIYNPV-----LENFDGSPRGMAQ 285  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
328 AV----VRNPHLDFLEQVTIYLLSRKSNTQYMNMGGHKLEFRITGGT---LNISTQGS 381  
: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
286 RIEQNIRQPHLMDILNRITIYDVRHG-----FNWMSGHQITASPVGSGSEPAFFPLFGN 340  
: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
382 TMTSINPVLPTFSRDVYRTESL-----AGNLFLTQPVNGVPFVDHFHWKEVTHPI 432  
: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
341 AGNAAPPVLAVSLGLGIFRTLSSPLYRRIILGSGPN--NQELFVLDDGTBFASFALTNNL 397  
: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
433 ASDNFYYPGYAGTGLODSENELPPRATGPQNYEYSYHRLSHIGLISAS-----HVKAL 487  
: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
398 PSTIYRQRGTV-----DSLWDVIPQDNSVFPRAGFSHRLSHVTMLSQAAGVVTLRAP 450  
: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
488 VYSWTHRSDARTNTIEPNSITQPLVKAFNLSSGAADVVRGPGFTGGDILLRRTNTGTFGDI 547  
: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
451 TFSQWRSAEFNIIIPSSQITQIPTLKSTNLGSGTSVKGPGFTGGDILLRRTSPGI STL 510  
: |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
548 RVNINPPFAQRVRYRIRYASTTDLQFHTSINGKAINGNFSATMNRGEDLDYKTFTVTGVF 607  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
511 RVNITAPUSQRYRVIRYASTTNLQFHTSIDGRPINGNFSATMSSGSNLCGSGSFVTGVF 570  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
608 TTPSFELDVCSTFTTIGAMWFSSGNEVVIDRIEFVPVEVTVYEAEDPEKAKVIALFTST 667  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
571 TTPFNFGSSVFVTLASHVFNFGNEVVIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSS 630  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
668 NPRGLKTDVKYDHIDQVNLSVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
631 NOIGLKTDVTDHYHDQVSNLVECLSDDEFCLDEKQELSEKVXHAKRUSDERNL 682  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

RESULT 15  
JT0241  
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
N;Alternate names: 135K insecticidal protein  
C;Species: Bacillus thuringiensis  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C;Accession: JT0241  
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
Agric. Biol. Chem. 52, 1565-1573, 1988  
A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein  
A;Reference number: JT0241  
A;Accession: JT0241  
A;Molecule type: DNA  
A;Residues: 1-1176 <SHI>  
A;Cross-references: UNIPROT:P02965  
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins  
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

[illegible]

```

QY 268 VLDLVALFSDYDQMPYPIKTTAQLTREYVYDAIGTVHPHPSTSTWYNNNAPSFAIEA 327
Db 240 VLDIVALFSDYDQMPYPIKTTAQLTREYVYDAIGTVHPHPSTSTWYNNNAPSFAIEA 327
QY 328 AV---VRNPHLLDFLEQVYIYLLSRWSNTQYMNMGHKLFEFRITGGT---LNISTQGS 381
Db 286 RIEQNIRQPHLMILNSITIIDVHRG-----FNYWSGHQITASVGFSGPEFAFPLFCN 340
QY 382 TNGTINPVLPTFSRSDVYRTESL-----AGLNLFLTQPVNGVPRVDFHMKFVTHPI 432
Db 341 AGNAAPPVLVSLGLGIFRTLSPLRYRIILGSGPN---NOELFVLDGTGTFSPASLTNNL 397
QY 433 ASDNFYYPGYAGIGTQLODSENELEPPEATQPNYESYSHRLSHIGLISAS-----HVXAL 487
Db 398 PSTIYRQGTV-----DSLVIPOQDQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRNTIENPNSITQIPLVKAFLSSGAAVVRGPGFTGGDILRRNTGTGDI 547
Db 451 TFSWQHRSAEFNIIIPSSQITQIPLTKSTNLGSGTGVVKGPGFTGGDILRRNTGTGDI 510
QY 548 RVNINPPAORYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGF 607
Db 511 RVNITAPLSQRYVRIRYASTDLOFHTSIDGRPINQGNFSATMSSGSLQSGSFRVTVGF 570
QY 608 TTPFSLDVQSTTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAEKVYALFTST 667
Db 571 TTPFNFSNGSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTEAEYDLERAKAVNELFTSS 630
QY 668 NPGRLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 631 NQIGLKTVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

```

Search completed: October 28, 2004, 18:31:52  
Job time : 21.191 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-56

Perfect score: 3762

Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep: \*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep: \*  
5: /cgn2\_6/ptodata/1/iaa/PCITUS COMB.pep: \*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3739	99.4	719	3	US-08-286-870A-8
2	3459.5	92.0	710	4	US-09-661-322A-42
3	3389	90.1	648	3	US-08-286-870A-4
4	3379	89.8	719	2	US-09-003-217-2
5	3374	89.7	719	3	US-09-218-942-2
6	2795	74.3	535	3	US-08-286-870A-6
7	2437.5	64.8	1229	1	US-08-100-709-4
8	2437.5	64.8	1229	1	US-08-176-865-4
9	2437.5	64.8	1229	1	US-08-474-038-4
10	2437.5	64.8	1229	2	US-08-779-046-4
11	2437.5	64.8	1229	2	US-08-881-340-4
12	2335.5	62.1	488	1	US-08-448-170-10
13	2335.5	62.1	488	3	US-08-961-803-10
14	2250.5	59.8	1207	1	US-07-951-715A-7
15	2250.5	59.8	1207	2	US-08-459-448A-7
16	2250.5	59.8	1207	3	US-08-459-595A-7
17	2250.5	59.8	1207	3	US-08-459-504B-7
18	2250.5	59.8	1207	3	US-08-459-444-7
19	2250.5	59.8	1207	3	US-09-053-549-8
20	2250.5	59.8	1207	3	US-09-547-422-7
21	2250.5	59.8	1207	4	US-09-988-462-7
22	2249.5	59.8	1227	3	US-09-053-549-2
23	2180.5	58.0	1227	1	US-08-448-170-8
24	2180.5	58.0	1227	3	US-08-961-803-9
25	2171.5	57.7	1227	4	US-09-661-322A-63
26	2156.5	57.3	1186	3	US-09-178-252-23
27	2156.5	57.3	1186	4	US-09-826-660-23

28	2101	55.8	1228	4	US-09-661-322A-38	Sequence 38, Appl
29	1923.5	51.1	643	3	US-09-178-252-25	Sequence 25, Appl
30	1923.5	51.1	643	4	US-09-826-660-25	Sequence 25, Appl
31	1891	50.3	380	5	PCT-US91-02560-4	Sequence 4, Appl
32	1678.5	44.6	653	4	US-09-661-322A-6	Sequence 6, Appl
33	1655.5	44.0	1157	1	US-07-876-280-30	Sequence 30, Appl
34	1655.5	44.0	1157	1	US-08-315-468-2	Sequence 2, Appl
35	1655.5	44.0	1157	1	US-07-812-180A-2	Sequence 2, Appl
36	1655.5	44.0	1157	3	US-07-941-650A-2	Sequence 2, Appl
37	1492.5	39.7	1176	1	US-08-257-999-2	Sequence 2, Appl
38	1483	39.4	1157	2	US-08-532-547-5	Sequence 5, Appl
39	1483	39.4	1157	2	US-08-379-656B-5	Sequence 5, Appl
40	1483	39.4	1157	3	US-08-455-838-5	Sequence 5, Appl
41	1483	39.4	1157	3	US-09-019-809-5	Sequence 5, Appl
42	1483	39.4	1157	4	US-09-471-177-5	Sequence 5, Appl
43	1483	39.4	1157	4	US-09-220-806-5	Sequence 5, Appl
44	1476.5	39.2	1156	3	US-09-002-285-72	Sequence 72, Appl
45	1476.5	39.2	1156	4	US-09-589-477-72	Sequence 72, Appl

#### ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

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Query Match      99.4%; Score 3739; DB 3; Length 719;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
D B 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120
D B 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120

QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G V G N R N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
D B 121 R N K A L T D L K G L G D A L A V H D S L E S W G V G N R N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S Y H C V K W Y S 240
D B 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S Y H C V K W Y S 240

QY 241 T G L N L R G T N A E S W V R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300
D B 241 T G L N L R G T N A E S W V R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300

QY 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
D B 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

QY 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420
D B 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420

QY 421 V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
D B 421 V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 540
D B 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 540

QY 541 T G T F G D I R V N I N P P A Q R Y R I R Y A S T D L O P H T S I N G K A I N Q G N F S A T N R G E D L D Y K 600
D B 541 T G T F G D I R V N I N P P A Q R Y R I R Y A S T D L O P H T S I N G K A I N Q G N F S A T N R G E D L D Y K 600

QY 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
D B 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
D B 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

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ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (200)..(200)
OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match      92.0%; Score 3459.5; DB 4; Length 710;
Best Local Similarity 92.1%; Pred. No. 2.2e-301;
Matches 662; Conservative 16; Mismatches 32; Indels 9; Gaps 1;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60
D B 1 M K S K Q N M H Q S L S N N A T V D K N F T G S L E N N T N T L E Q N F H ----- E G I E P F V S V S T I 51

QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120
D B 52 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E I I N Q K I S T Y A 111

QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G V G N R N T R A S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
D B 112 R N K A L A D L K G L G D A L A V H E S L E S W I E N R N T R S V V K S Q Y I T L E L M F V Q S L P S F A V S G 171

QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S Y H C V K W Y S 240
D B 172 E V P L L P I Y A Q A A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S G K S K E Y S D H C V K W Y N 231

QY 241 T G L N L R G T N A E S W V R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300
D B 232 T G L N L R G M N A E S W V R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 291

QY 301 G T V H P H P S F T S T T W Y N N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360
D B 292 G T V H P H P S F T S T T W Y N N N A P S F S T I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 351

QY 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420
D B 352 G G H K L E F R T I G G T L N T S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 411

QY 421 V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
D B 412 V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 471

QY 481 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R T N 540
D B 472 A S H V K A L V S W T H R S A D R N T I E P N S I T Q I P L V K A F N L S S G A A V R G P G T G G D I L R R K N 531

QY 541 T G T F G D I R V N I N P P A Q R Y R I R Y A S T D L O P H T S I N G K A I N Q G N F S A T N R G E D L D Y K 600
D B 532 T G T F G D I R V N I N P P A Q R Y R I R Y A S T D L O P H T S I N G K A I N Q G N F S A T N R G E D L D Y K 591

QY 601 T F R T V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660
D B 592 T F R T V G T T P F S F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E E V 651

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719
D B 652 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D K F Y L D E K R E L F E I V K Y A Q L H I E R N M 710

RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN

```

ADDRESSEE: Intellectual Property Group of  
 ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/286,870A  
 FILING DATE: 05-AUG-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/520228  
 FILING DATE: 09-MAY-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 8910624.9  
 FILING DATE: 09-MAY-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PAUL N. KOKULIS  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 70608/220720  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 648 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-286-870A-4

Query Match 90.1%; Score 3389; DB 3; Length 648;  
 Best Local Similarity 99.8%; Pred. No. 4.1e-295;  
 Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSPFVSG 180  
 QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTEYNNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTEYNNQVERAGDYSYHCVKWS 240  
 QY 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALPSPYDQYPIKTTAQLTREYITDAI 300  
 DB 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALPSPYDQYPIKTTAQLTREYITDAI 300  
 QY 301 GTVHPHPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFEQVTIYSLLSRWSTQYMNW 360  
 DB 301 GTVHPHPFTSTTWYNNNAPSFAIEAAVVRNPHLLDFEQVTIYSLLSRWSTQYMNW 360  
 QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVLPTFRDVRVRESLAGNLFLOTQVNGVPR 420  
 DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVLPTFRDVRVRESLAGNLFLOTQVNGVPR 420  
 QY 421 VDFHWKFTHTPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 DB 421 VDFHWKFTHTPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRSLHIGLIS 480

QY 481 ASHVXALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
 DB 481 ASHVXALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDIILRTN 540  
 QY 541 TGTFGDIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDIYK 600  
 DB 541 TGTFGDIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDIYK 600  
 QY 601 TFRVTGFTTTPFSLDVQSTFTTIGAWNFGSGNEVYIDRIEFVPEVYVE 648  
 DB 601 TFRVTGFTTTPFSLDVQSTFTTIGAWNFGSGNEVYIDRIEFVPEVYVE 648  
 RESULT 4  
 US-09-003-217-2  
 ; Sequence 2, Application US/09003217  
 ; Patent No. 5986177  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia A.  
 ; APPLICANT: Madkour, Magdy A.  
 ; APPLICANT: Bulla, Lee A.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
 ; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
 ; STREET: 3605 Glenwood Ave. Suite 310  
 ; CITY: Raleigh  
 ; STATE: NC  
 ; COUNTRY: US  
 ; ZIP: 27622  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/003,217  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spruill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: 5718-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919 420 2202  
 ; TELEFAX: 919 881 3175  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 719 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-003-217-2

Query Match 89.8%; Score 3379; DB 2; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 3.8e-294;  
 Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSPFVSG 180  
 DB 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSPFVSG 180  
 QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTEYNNQVERAGDYSYHCVKWS 240

Db 181 EEVPLPIYAQAANLHLLLRDASIFKNGGLSASISTFYNQVQVTRDYSYHCVKWN 240

Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPYDQMPYIKTTAQLTREVYTD 300

Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPYDQMPYIKTTAQLTREVYTD 300

Qy 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTVIYSLLSRWSTQYMNW 360

Db 301 GTVDPNQALRSTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTVIYSLLSRWSTQYMNW 360

Qy 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVNGVPR 420

Db 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVNGVPR 420

Qy 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540

Db 481 GSHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540

Qy 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600

Db 541 SGTFGHIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600

Qy 601 TFRVTGFTTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

Db 601 TFRVTGFTTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 5

US-09-218-942-2

Sequence 2, Application US/09218942

Patent No. 6232439

GENERAL INFORMATION:

APPLICANT: Osman, Yehia

TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum

TITLE OF INVENTION: Activity

FILE REFERENCE: Cyt11

CURRENT APPLICATION NUMBER: US/09/218,942

CURRENT FILING DATE: 1998-12-22

EARLIER APPLICATION NUMBER: 60/035,361

EARLIER FILING DATE: 1997-01-10

EARLIER APPLICATION NUMBER: 09/003,217

EARLIER FILING DATE: 1998-01-06

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 719

TYPE: PR1

ORGANISM: Bacillus thuringiensis

US-09-218-942-2

Query Match 89.7%; Score 3374; DB 3; Length 719;

Best Local Similarity 89.7%; Pred. No. 1.1e-293;

Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMSYEYENVEPVSASTI 60

Db 1 MKLKNPDKHQTLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPVSASTI 60

Qy 61 QTGIGIAGKILGTGLVPPFAGQVSLYSFILGELWPKGKNQKQNEIFMEHVEEIIINQKISTVA 120

Db 61 QTGIGIAGKILGTGLVPPFQGIASLYSIFILGELWPKGKSQNEIFMEHVEEIIINQKISTVA 120

Qy 121 RNKALTDLKLIGDALAVYHDSLESWVGNNRNTARSVYVKSQYIALFMFVKLPSPFVSG 180

Db 121 RNKALTDLKLIGDALAVYHDSLESWVGNNRNTARSVYVKSQYIALFMFVKLPSPFVSG 180

Qy 181 EEVPLPIYAQAANLHLLLRDASIFKNGGLSSEISTFYNQVQVTRDYSYHCVKWN 240

Db 181 EEVPLPIYAQAANLHLLLRDASIFKNGGLSSEISTFYNQVQVTRDYSYHCVKWN 240

Qy 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPYDQMPYIKTTAQLTREVYTD 300

Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPYDQMPYIKTTAQLTREVYTD 300

Qy 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTVIYSLLSRWSTQYMNW 360

Db 301 GTVDPNQALRSTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTVIYSLLSRWSTQYMNW 360

Qy 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVNGVPR 420

Db 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLPFTSRDVRYSAGLNLFLTQPVNGVPR 420

Qy 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

Db 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540

Db 481 ASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRTN 540

Qy 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600

Db 541 SGTFGHIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600

Qy 601 TFRVTGFTTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

Db 601 TFRVTGFTTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

Db 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 6

US-08-286-870A-6

Sequence 6, Application US/08286870A

Patent No. 6063605

GENERAL INFORMATION:

APPLICANT: ELY, S

APPLICANT: TAILOR, RH

APPLICANT: TIPPETT, JM

APPLICANT: BLENK, RG

TITLE OF INVENTION: BACTERIAL GENES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of

ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,870A

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/520228

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8910624.9

FILING DATE: 09-MAY-1989

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STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egoľf, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;
Best Local Similarity 65.4%; Pred. No. 2.8e-209;
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVPEFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSPSTQMWLSPARIEDSLCVAEWNIDPFVSASTVQTGINIAGRI 66
QY 71 LGTLGVPPFAGQVASYLFGELWPKGNQWEIFMEHVEEINQKISTYARKALDTLKG 130
Db 67 LGVLGVPPFAGQLASFYFLVGBELWPSGRDPWEIFLEHVEQLIRQVVTENTRTAIARLE 126
QY 131 LGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVOKLPSFAVSGSEVPLPIYA 190
Db 127 LGRGYSYQQALETWLDNRNDARSIIERYVALELDITTAIPLFRNEEVPLLMVYA 186
QY 191 QAANLHLLLRDASIFGKEWGLSSISISTFYNRQVERAGDYSYHCVKWYSTGLNLRGTN 250
Db 187 QAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCVCQWYNTGLNLRGTN 246
QY 251 AESWRYNQFRDMTLMVLVALPFSYDTQMPYIKTTAQLTREYVYTDIAIGTVHPHSFT 310
Db 247 AESWLRYNQFRDITLGVLDLVALPFSYDTETYPINTSAQLTREIYTDPIGRTNAPSGFA 306
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLRWSNNTQYMMWGGHKLBPRTI 370
Db 307 STNWFFNNAPFSALZAAI FAPPPLLDFFPEQLTIYSASSRWSSTQHNNYVWGHRLNFRPI 366
QY 371 GGTLANSTQGST-NTSINPVTLPFTSRDVRVTESLAGNLNLFLLTPQVNGVPRVDFHMKFVT 429
Db 367 GGTLANSTQGLTNNNTSINPVTLPFTSRDVRVTESNAGTNILFTTPVNGVPRVDFHMKFVT 422
QY 430 HPIASDNFYVPG-----YAGIGTQLQDSNELPPEATGQPNYESYSHRUSHIGLISAS 482
Db 423 --INPONIYERGATTYSQPYQGVGQLFDSSETLPETTERPNYESYSHRUSHIGLIIGN 480
QY 483 HVKALVYSWTHRSADRTNTIEPNISITQIPLVKAFNLSSGAAVRGPFGTGGDILRRTNTG 542
Db 481 TLRAPYISWTHRSADRTNTIGPNRITQIPLVKALNLHSGVTVVGGFPGTGGDILRRTNTG 540
QY 543 TFGDIRVNIWNPPEAQRVRYRIRYASTDLQFHTSINGKAINQGNFSAATMREGDLDYKTF 602
Db 541 TFGDIRLNIWNPFSQRVRYRIRYASTDLQFTRINGTTVNIIGNFSRTNRGDNLEYSRF 600
QY 603 RTVGFTPTFPFLDVQSTFTTIGAWNPFSSGNEVVIDRIEFVPVEVTVYEAAYDFEKAQKVTA 662
Db 601 RTAGSTPFPFLNAOSTFTTLGAQSFEN-OEYIYIDRVFVPAEVTPEAEYDLERAOKAVNA 659

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QY 663 LFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELVYKYNELHIERNM 719  
 DB 660 LFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELVYKYNELHIERNL 716

RESULT 8  
 US-08-176-865-4  
 ; Sequence 4, Application US/08176865  
 ; Patent No. 5616319  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-176-865-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;  
 Best Local Similarity 65.4%; Pred. No. 2.8e-209;  
 Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCIKMSYENVEPFSASTTGTGCIAGKI 70  
 DB 7 NENEINALSIPVSNPQMSLSPDARIEDSLCVAEVNNDIPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 130  
 DB 67 LGVLGVPPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLESWGNRNNTARSVVKVQYIALELMFVOKLPSFAVSGEVPPLPIYA 190  
 DB 127 LGRGVSRYQQALETWLDNRNDRARSIIILERYVALELDITTAIPLFRINEEVPPLMVA 186

QY 191 QAAHLHLLLRDASIFGKWLSSSEISTFYXNQVRAGDYSYHCVKWSYGLNNLRGTN 250  
 DB 187 QAAHLHLLLRDASIFGKWLSSSEISTFYXNQVRAGDYSYHCVKWSYGLNNLRGTN 246

QY 251 AESWRYNQFPRDMLVLDLVALFPSTQMPYIKTAQLTREVTDAIGTVHPHPSFT 310

DB 247 AESWRYNQFPRDMLVLDLVALFPSTQMPYIKTAQLTREVTDAIGTVHPHPSFT 306  
 QY 311 STTWNNAPSPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQVMNMGHKLFRIT 370  
 DB 307 STWNNAPSPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQVMNMGHKLFRIT 366

QY 371 GGTNLNISTQGST-NTSINPVTLPFTSRDVTYRTESLACNLNLTQPVNGVPRVDFHFKVFT 429  
 DB 367 GGTNLNISTQGST-NTSINPVTLPFTSRDVTYRTESLACNLNLTQPVNGVPRVDFHFKVFT 422

QY 430 HPIASDNFYYPG-----YAGIGTQLODSENELPPATGQPNYESYSHRLSHIGLISAS 482  
 DB 423 --INPQNIYERGATYTSQPYQGVGIQFDSETELPPTTERPNYESYSHRLSHIGLIGN 480

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 DB 481 TLRAVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRNTG 540

QY 543 TFGDIRVNIWPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSATMARGEDIDYKTF 602  
 DB 541 TFGDIRVNIWPPFAQRYVRIRYASTTDLQPHTSINGKAINQGNFSATMARGEDIDYKTF 600

QY 603 RTVGTTTPSFLDVQSTFTIGAMNFSNVEYIDRIEFVPEVVEYEAEDYFEKAEKVTA 662  
 DB 601 RTAGFSTPFNFLNAQSTFTLGAQSFN-QEVYIDRVFVPAEVTFAEYDLERAQAVNA 659

QY 663 LFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELVYKYNELHIERNM 719  
 DB 660 LFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELVYKYNELHIERNL 716

RESULT 9  
 US-08-474-038-4  
 ; Sequence 4, Application US/08474038  
 ; Patent No. 5679343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,038  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-474-038-4

Query Match 64.8%; Score 2437.5; DB 1; Length 1229;  
 Best Local Similarity 65.4%; Pred. No. 2.8e-209;  
 Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQMLNSPDARIEDSLCVAEWNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALDLDKG 130  
 DB 67 LGVLGVPPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSYQVIALELMFVQKLPSPFAVSGEEVPLPIYA 190  
 DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWTSTGLNLRGTN 250  
 DB 187 QAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTBESYHCVQWYNTGLNLRGTN 246

QY 251 AESWRYNQFRDRLTGLVLDLVALFSPYDTQMPYIKTQAULTREYVTDAGTVPHPSPFT 310  
 DB 247 AESWLRYNQFRDRLTGLVLDLVALFSPYDTQMPYIKTQAULTREYVTDPIGRNAPSFA 306

QY 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNMGHKLFRPTI 370  
 DB 307 STWNNNAPSFAIEAAVVRNPHLLDFPEQVTIYSSASRWSTQHMNYWGHRLNFRPI 366

QY 371 GGTNLINISQTGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHKKFVT 429  
 DB 367 GGTNLINISQTGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHKKFVT 422

QY 430 HPIASDNFYYPG-----YAGIGTQDSENELPEATGQPNYESYSHRLSHIGLISAS 482  
 DB 423 --INPQNIYERGATTSYQPYQGVIGLFDSETELPEPTTERPNYESYSHRLSHIGLIGN 480

QY 483 HVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRNTG 542  
 DB 481 TLRAPIVSWTHRSADRTNTEPNISITQIPLVKALNLSHSGVTVVGGPGFTGGDILRRNTG 540

QY 543 TFGDIRVNINPPAQVRIRYASTDLDQFHTSINGKAINQGNFSAVMNRGEBLDYKTF 602  
 DB 541 TFGDIRLNINVLSQLRVRIRYASTDLDQFTRINGTTVNIQNFRTWNRGNLEYSKF 600

QY 603 RTVGFTTTPFSLDVQSTFTIGAMNPSGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTA 662  
 DB 601 RTAGFSTPFNLNAQSTFTLGAQSFN-QEYVIDRVEFVPAEYFEEAYDLERAQKAVNA 659

QY 663 LFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 LFTSTNPRRLKTDVYHIDQVSNMVACLSDEFCLDEKRELFEIVKYAKRLSDERNL 716

RESULT 10  
 US-08-779-046-4  
 Sequence 4, Application US/08779046  
 Patent No. 5854053  
 GENERAL INFORMATION:  
 APPLICANT: Donovan, William P.  
 APPLICANT: Tan, Yiping  
 APPLICANT: Jan, Christine S.  
 APPLICANT: Gonzalez Jr., Jose M.  
 TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ADDRESSEE: Nadel  
 STREET: 1601 Market Street, 36th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/779,046  
 FILING DATE: 06-JAN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/100,709  
 FILING DATE: 29-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Egolf, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-757-1590  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1229 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-779-046-4

Query Match 64.8%; Score 2437.5; DB 2; Length 1229;  
 Best Local Similarity 65.4%; Pred. No. 2.8e-209;  
 Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQMLNSPDARIEDSLCVAEWNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYARNKALDLDKG 130  
 DB 67 LGVLGVPPAGQLASFYSLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAARLEG 126

QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSYQVIALELMFVQKLPSPFAVSGEEVPLPIYA 190  
 DB 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSYHCVKWTSTGLNLRGTN 250  
 DB 187 QAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTBESYHCVQWYNTGLNLRGTN 246

QY 251 AESWRYNQFRDRLTGLVLDLVALFSPYDTQMPYIKTQAULTREYVTDAGTVPHPSPFT 310  
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QY 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNMGHKLFRPTI 370  
 DB 307 STWNNNAPSFAIEAAVVRNPHLLDFPEQVTIYSSASRWSTQHMNYWGHRLNFRPI 366

QY 371 GGTNLINISQTGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHKKFVT 429  
 DB 367 GGTNLINISQTGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHKKFVT 422

QY 430 HPIASDNFYYPG-----YAGIGTQDSENELPEATGQPNYESYSHRLSHIGLISAS 482  
 DB 423 --INPQNIYERGATTSYQPYQGVIGLFDSETELPEPTTERPNYESYSHRLSHIGLIGN 480

QY 483 HVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSGGAAVVRGPGFTGGDILRRNTG 542  
 DB 481 TLRAPIVSWTHRSADRTNTEPNISITQIPLVKALNLSHSGVTVVGGPGFTGGDILRRNTG 540

QY 543 TFGDIRVNINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATNRGEGDLDYKTF 602  
 Db 541 TFGDIRLNINPLSQRYVRIRYASTTDLQFHTSINGKAINQGNFSATNRGEGDLDYKTF 600  
 QY 603 RTVGFTTSPFLDVQSTTTGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTA 662  
 Db 601 RTAGFSTPNFLNAQSTTFLGAQFSN-QEVYIDRVFVPAEVTFAEYDLERAKAVNA 659  
 QY 663 LFTSTNPRGLKTDVHYDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719  
 Db 660 LFTSTNPRGLKTDVHYDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNL 716

RESULT 11  
 US-08-881-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yaping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CIYET4 AND CIYETS  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-881-340-4

Query Match 64.8%; Score 2437.5; DB 2; Length 1229;  
 Best Local Similarity 65.4%; Pred. No. 2.8e-209;  
 Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;  
 QY 13 SSNAKVDKSTSLKN-ETDIELQ-NINHEDECLKMSYENVEPFPVASTTGTGIGAKI 70  
 Db 7 NENEINALSIPVSNPSTQMLSPDARIEDSLCAEVNNDPFPVASTVQTGINIAGRI 66  
 QY 71 LGTLGVPPAGQVASYLSFTLGLWPKGNQWEIFMEHVEEILNOKISTYARNKALTDLKG 130  
 Db 67 LGVLGVPPAGQVASYLSFTLGLWPKGNQWEIFMEHVEEILNOKISTYARNKALTDLKG 126  
 QY 131 LGDALAVYHDSLSWVGNNRNRNTRARSVYKSOYIALELHMFVKLPFAVSGEEVPLPIYA 190

Db 127 LGRGYSYQQALETWLDNRNDARSRIILERYVALELDITTAIPLFRIIRNEEVPLLMVYA 186  
 QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRAGDYSYHCWKWYSTGLNLRGIN 250  
 Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSNHCQVWYNTGLNLRGIN 246  
 QY 251 AESWRYNQFRDMTLMVLDLVALFPSTQMYPIKTAQLTREVYTDALGTVHPHPSFT 310  
 Db 247 AESWRYNQFRDLTLGLVLDLVALFPSTQMYPIKTAQLTREVYTDALGTVHPHPSFT 306  
 QY 311 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMMGGHKLFRFI 370  
 Db 307 STTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYNNMMGGHKLFRFI 366  
 QY 371 GGTINISTOGST-NTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPRVDHFKFVT 429  
 Db 367 GGTINISTOGST-NTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPRVDHFKFVT 422  
 QY 430 HPIASDNFYPG-----YAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482  
 Db 423 --INPQNIYERGATTYSQPYQGVGQIQLFDSETELPPETTERPNYESYSHRLSHIGLIGN 480  
 QY 483 HVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542  
 Db 481 TLRAVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 540  
 QY 543 TFGDIRVNINPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSATNRGEGDLDYKTF 602  
 Db 541 TFGDIRLNINPLSQRYVRIRYASTTDLQFHTSINGKAINQGNFSATNRGEGDLDYKTF 600  
 QY 603 RTVGFTTSPFLDVQSTTTGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTA 662  
 Db 601 RTAGFSTPNFLNAQSTTFLGAQFSN-QEVYIDRVFVPAEVTFAEYDLERAKAVNA 659  
 QY 663 LFTSTNPRGLKTDVHYDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNM 719  
 Db 660 LFTSTNPRGLKTDVHYDQVSNLVSLSDEFYLDKRELFEIVKYANLHIERNL 716

RESULT 12  
 US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Stelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match      62.1%; Score 2335.5; DB 1; Length 488;
Best Local Similarity 89.5%; Pred. No. 8.9e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
Db 1 M KSKNQNMHQSLSNATVDKNFTGSLNNTNTELQNFH-----EGIEPVSASTI 51

Qy 61 QTGIGIAGKILGTGVFPAGQVASYLFI LGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLFI LGELWPKGKSQWEIFMEHVEELINQKISTYA 111

Qy 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVQKLPSPFVSG 180
Db 112 RNKALADLKLGLDALAVYHDSLESWIENRNTRTSVVKSOYITLELMFVQSLPSPFVSG 171

Qy 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWSY 240
Db 172 EEVPLLPYIAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSKESYSDHCVKWN 231

Qy 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREYVTDAL 300
Db 232 TGLNRLMGNAESWVRNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREYVTDAL 291

Qy 301 GTVHPHPSTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
Db 292 GTVHPHPSTSTWYNNAPSPSTIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 351

Qy 361 GGHKLEFTTIGTGLNTSGSTNTSINPVLPTSRDVRATESLAGLNLFTOPVNGVPR 420
Db 352 GGHKLEFTTIGTGLNTSGSTNTSINPVLPTSRDVRATESLAGLNLFTOPVNGVPR 411

Qy 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRSLSHIGLIS 480
Db 412 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRSLSHIGLIS 471

Qy 481 ASHVKALVYSWTHRSAD 497
Db 472 ASHVKALVYSWTHRSAD 488

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RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes

```

```

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961.803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

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Query Match      62.1%; Score 2335.5; DB 3; Length 488;
Best Local Similarity 89.5%; Pred. No. 8.9e-201;
Matches 445; Conservative 13; Mismatches 30; Indels 9; Gaps 1;

Qy 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
Db 1 M KSKNQNMHQSLSNATVDKNFTGSLNNTNTELQNFH-----EGIEPVSASTI 51

Qy 61 QTGIGIAGKILGTGVFPAGQVASYLFI LGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120
Db 52 QTGIGIVGKILGNLGVFPAGQVASYLFI LGELWPKGKSQWEIFMEHVEELINQKISTYA 111

Qy 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSOYIALELMFVQKLPSPFVSG 180
Db 112 RNKALADLKLGLDALAVYHDSLESWIENRNTRTSVVKSOYITLELMFVQSLPSPFVSG 171

Qy 181 EEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSYHCVKWSY 240
Db 172 EEVPLLPYIAQAANLHLLLRDASIFGKXWGLSDSEISTFYNNRQSGKSKESYSDHCVKWN 231

Qy 241 TGLNNLRGTNAESWVRNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREYVTDAL 300
Db 232 TGLNRLMGNAESWVRNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREYVTDAL 291

Qy 301 GTVHPHPSTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 360
Db 292 GTVHPHPSTSTWYNNAPSPSTIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNW 351

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QY 361 GGKLEFRITGTLNISTOGSNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 420  
DB 352 GGKLEFRITGTLNISTOGSNTSINPVTLPFTSRDVRTESLAGLNLFLTPQVNGVPR 411  
QY 421 VDFHWKFTVTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 412 VDFHWKFTVTHPIASDNFYPYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 471  
QY 481 ASHVKALVYSWTHRSAD 497  
DB 472 ASHVKALVYSWTHRSAD 488

RESULT 14  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/951,715A  
; FILING DATE: 25-SEP-1992  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8615  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-951-715A-7

Query Match 59.8%; Score 2250.5; DB 1; Length 1207;

Best Local Similarity 64.0%; Pred. No. 1.7e-192;  
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;  
QY 40 EDCLKMSEVENVEPVFSASTIQTGIGTAGKILGTGVPEAGQVASILYFSLGELMPPKGN 99  
DB 10 EDLSLCAEGNNIDPFVSASTVQTGINIAGRIILVGLVFPFAGQLASFYSLVGLMPPGRD 69  
QY 100 QWEIPMEHVEEINQKISTYARNKALDGLGDALAVYHDSLESWVGNNTARSVVK 159  
DB 70 QWEIFLEHVEQLNQITENARNALTALQGLGDSFRAYQQSLEDWLENRDADTRSVLY 129  
QY 160 SQYIALELMFVKLPSPFAVSGEVPPLPIYAAQANLHLLLRDASIFGKEWGLSSEIST 219  
DB 130 TOYIALELDFLNAFLFAIRNQEVPLLMVYAAQANLHLLLRDASIFGSEFGLTSQEIOR 189  
QY 220 FYNROVERAGDYSYHCVKWTSTGLNNLRGTNAESWRYNQRRDMLVLDLVALPPSYD 279  
DB 190 YEROVERTRDYSYCVWYNTGLNSLRGTNAASWRYNQRRDLTLGLVLDLVALPPSYD 249  
QY 280 TOMYPIKTTAQLTREVTDAIGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFL 339  
DB 250 TRTYPINTSAQLTREVTDAIGAT--GVNMAWNNWYNNNAPSFAIEAAAIRSPHLLDFL 307  
QY 340 EOVTIYSLSRWSNTQYNNMWGCHKLEPRTIGTGLNISTOGSNTSINPVTLPFTSRDVS 399  
DB 308 EQLTIFSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDVS 367  
QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFTVTHP-----IASDNFYPYAGIGTQLODS 452  
DB 368 RTESVAGVLLGVILEPIHGVPTVRNF--TNPQNISDRGTANYSQP-YESPGQLKXDS 423  
QY 453 ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIPL 512  
DB 424 ETELPETTERPNYESYSHRLSHIGLILQSRVNVVYVSWTHRSADRTNTEPNSITQIPM 483  
QY 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNPFPFAQRYRIRYASTTDLQ 572  
DB 484 VKASELPQGTTVVRGPGFTGGDILRRNTGGPGPIRTVNGPLTQRYRIGRYASTVDFD 543  
QY 573 PHTSINGKAINQGNFSAATMNRGEBLDYKTFRTVGTFTPFSLDQVSTFTTIGAMNFSNGE 632  
DB 544 FVVSREGTTVNNFRFLRTNWSGDELKYNFVRRAFTTPTFTQIQDIIRTSIQGSGNCE 603  
QY 633 VYIDRIEFVPEVTEYAEYDFEKAQEKYKTAFTSTNPRGLTKDVKDHYHDOVSNLVESLS 692  
DB 604 VYIDKIEIIPVTATFEASYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663  
QY 693 DEFYIDKRELFEIVKYANELHIERNM 719  
DB 664 DEFCLDEKRELEKVKYAKRLSDERNL 690

RESULT 15  
US-08-459-448A-7  
; Sequence 7, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.





GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-56  
Perfect score: 3762  
Sequence: 1 MKLKNQDQHQSFSSNAKYDK.....KRELFVIVKYANLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3762	100.0	719	4	AAB66909 Insectici
2	3762	100.0	719	6	Aae36273 B. thurin
3	3753	99.8	719	4	Aau02095 Bacillus
4	3749	99.7	719	4	AAB66911 Insectici
5	3749	99.7	719	6	Aae36275 B. thurin
6	3743	99.5	719	4	AAB66908 Insectici
7	3743	99.5	719	6	Aae36272 B. thurin
8	3741	99.4	719	2	AAR08041 81 kD end
9	3739	99.4	719	4	AAB66910 Insectici
10	3739	99.4	719	6	Aae36274 B. thurin
11	3730.5	99.2	718	6	Aae36271 B. thurin
12	3724.5	99.0	718	4	AAB66907 Insectici
13	3534	93.9	719	7	ADM74717 B. thurin
14	3503	93.1	719	4	AAB66912 Insectici
15	3503	93.1	719	6	Aae36276 B. thurin
16	3459.5	92.0	710	4	Aau02041 B. thurin
17	3380	89.8	719	3	AB07073 Bacillus
18	3379	89.8	719	2	Aaw49089 Bacillus
19	3295	87.6	1217	4	Aau02092 Bacillus
20	2719	72.3	1208	4	Aau02093 Bacillus
21	2439	64.8	1230	8	Adk98484 B thuring
22	2439	64.8	1230	8	Adk98489 B thuring
23	2439	64.8	1230	8	Adk98481 B thuring
24	2439	64.8	1230	8	Adk98491 B thuring
25	2439	64.8	1230	8	Adk98487 B thuring

26	2437.5	64.8	1229	2	AAR54074 CryET5. 2
27	2437.5	64.8	1229	2	Aaw35259 Bacillus
28	2437.5	64.8	1229	2	Aaw17699 CryET5. 3
29	2437.5	64.8	1229	2	Aaw87633 CryET5 pr
30	2437.5	64.8	1229	2	Aay30923 B. thurin
31	2437.5	64.8	1229	8	Adk98479 B thuring
32	2437.5	62.1	488	2	Aaw44322 Bacillus
33	2335.5	62.1	488	4	Aab19947 Bacillus
34	2263.5	60.2	1228	2	AAR50955 Bacillus
35	2258.5	60.0	1209	4	Aau02094 Bacillus
36	2249.5	59.8	1227	2	Aay31990 Chimeric
37	2180.5	58.0	1227	2	Aaw44321 Bacillus
38	2180.5	58.0	1227	4	AAB19950 Bacillus
39	2171.5	57.7	1227	4	Aau02046 B. thurin
40	2156.5	57.3	1186	2	Aay16796 Amino aci
41	2141.5	56.9	1221	4	Aau00421 B. thurin
42	2127.5	56.6	1221	4	Aau00420 B. thurin
43	2101	55.8	1228	4	AAB84628 Amino aci
44	2101	55.8	1228	4	Aau02039 B. thurin
45	1923.5	51.1	643	2	Aay16797 Amino aci

ALIGNMENTS

RESULT 1  
AAB66909  
ID AAB66909 standard; protein; 719 AA.  
XX  
AC AAB66909;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa3.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 23-JUN-1999; 99GB-00015215.  
XX  
PR 23-DEC-1999; 99GB-00030536.  
XX  
(ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
XX  
PT controlling insects, and for insect-resistant transgenic plant  
XX  
PS production.  
XX  
PS Claim 14; Page 57-59; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
XX  
CC from Paecilomyces sp. (see AAB66909 to AAB66901 and AAB66913). The  
XX  
CC insecticidal proteins can be used to produce transgenic plants, which are  
XX  
CC insect-resistant. Also, the insecticidal proteins are useful for  
XX  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;

Query Match 100.0%; Score 3762; DB 4; Length 719;  
Best Local Similarity 100.0%; Pred. No. 3.4e-294;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLNHEYNVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLNHEYNVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLFIILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLFIILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLXGLGDALAVYHDSLESWGNRNTRARSVVKQSYIALELMFVKLPFAVSG 180  
 DB 121 RNKALTDLXGLGDALAVYHDSLESWGNRNTRARSVVKQSYIALELMFVKLPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGNAESWVRYNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGNAESWVRYNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPFAQRYRIRYASTDLQFHTSINGKAINQGNFSAATNRGDDLDYK 600  
 DB 541 TGTGDIRVNINPFAQRYRIRYASTDLQFHTSINGKAINQGNFSAATNRGDDLDYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 2  
 AAE36273  
 ID AAE36273 standard; protein; 719 AA.

XX AAE36273;  
 AC  
 XX  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 FN WO200298911-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 DR  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 XX  
 PS Claim 12; Page 47-50; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 XX  
 SQ Sequence 719 AA;

Query Match 100.0%; Score 3762; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-294;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLNHEYNVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLNHEYNVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLFIILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLFIILGELWPKGNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLXGLGDALAVYHDSLESWGNRNTRARSVVKQSYIALELMFVKLPFAVSG 180  
 DB 121 RNKALTDLXGLGDALAVYHDSLESWGNRNTRARSVVKQSYIALELMFVKLPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGNAESWVRYNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGNAESWVRYNQFRDMTLMVLDLVALFSDYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPFAQRYRIRYASTDLQFHTSINGKAINQGNFSAATNRGDDLDYK 600  
 DB 541 TGTGDIRVNINPFAQRYRIRYASTDLQFHTSINGKAINQGNFSAATNRGDDLDYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3  
AAU02095  
ID AAU02095 standard; protein; 719 AA.  
XX  
AC AAU02095;  
XX  
DT 07-SEP-2001 (first entry)  
XX  
DE Bacillus thuringiensis partial mutant CryIIa.  
XX  
KW Crystal protein; CryIIa; CrylBa; moth; butterfly; Colorado potato beetle;  
XW mutant; mutein.  
XX  
OS Bacillus thuringiensis.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal\_peptide  
FT Protein 20..719  
FT /label= Mature\_CryIIa  
XX  
EP1099760-A1.  
XX  
PD 16-MAY-2001.  
XX  
XX 09-NOV-1999; 99EP-00203723.  
XX  
XX 09-NOV-1999; 99EP-00203723.  
XX  
PA (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.  
XX  
PI De Maagd RA; Bosch HJ;  
XX  
DR WPI; 2001-337141/36.  
DR N-PSDB; AAS04855.  
XX  
XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural  
PT domains derived from at least 2 different crystal proteins, such as  
PT CryIIa and CrylBa, and having insecticidal activity, useful for combating  
PT insects.  
XX  
XX Example; Page 30-32; 43pp; English.  
PS  
XX The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA  
CC encoding which was mutated to allow cloning of domain III or domains I  
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
CC of the invention, having structural domains I, II and III in this order  
CC starting from the N-terminal derived from at least 2 different crystal  
CC proteins, are useful for protecting plants against pest insects, e.g.  
CC moths, butterflies and Colorado potato beetle or for combating insects  
XX  
SQ Sequence 719 AA;  
Query Match 99.8%; Score 3753; DB 4; Length 719;  
Best Local Similarity 99.7%; Pred. No. 1.8e-293;  
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFVSASTI 60  
Db 1 MKLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFVSASTI 60  
QY 61 QTGIGIAGKILGTLPVAGOVASLYSFIILGELWPKGNQWEIEMHVEEIIINQKISTYA 120  
Db 61 QTGIGIAGKILGTLPVAGOVASLYSFIILGELWPKGNQWEIEMHVEEIIINQKISTYA 120  
QY 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVKXQYIALELMFVQKLPSPAVSG 180  
Db 121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVKXQYIALELMFVQKLPSPAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISFTYNQVERAGDYSYHCVKWS 240  
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLGSSEISFTYNQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDVTMLVLDLVALFPSYDTOMYPIKTTAQLTREVVTDAI 300  
Db 241 TGLNLRGTNAESWVRYNQFRDVTMLVLDLVALFPSYDTOMYPIKTTAQLTREVVTDAI 300  
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIAEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMMW 360  
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIAEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMMW 360  
QY 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFLTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVRVYRTESLAGNLFLTQPVNGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQODSENELPPEATQOPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQODSENELPPEATQOPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRNTIIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVSWTHRSADRNTIIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTGDIRVININPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
Db 541 TGTGDIRVININPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEWYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
Db 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEWYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYANELHIERNM 719  
Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYANELHIERNM 719  
RESULT 4  
AAB66911  
ID AAB66911 standard; protein; 719 AA.  
XX  
AC AAB66911;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa5.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
XX 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
XX production.  
PS Claim 14; Page 62-64; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66911 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are



QY 601 TFRVGTTPFSELDVOSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 DB 601 TFRVGTTPFSELDVOSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFVIVKYNELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFVIVKYNELHIERNM 719

RESULT 6  
 AAB66908  
 ID AAB66908 standard; protein; 719 AA.  
 XX AAB66908;  
 XX  
 DT 12-APR-2001 (first entry)  
 XX  
 DE Insecticidal protein cryIIa2.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.  
 XX  
 OS Paecilomyces sp.  
 XX  
 PN WO200100841-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-GB002457.  
 XX  
 PR 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX  
 PA (ZENE ) ZENECA LTD.  
 XX  
 PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX  
 DR WPI; 2001-123015/13.  
 XX  
 PT Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX  
 PS Claim 14; Page 55-57; 72pp; English.  
 XX  
 CC The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;

Query Match 99.5%; Score 3743; DB 4; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFPSSNAKVDKISTDSLKNETDIELQNIHEDCLXSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFPSSNAKVDKISTDSLKNETDIELQNIHEDCLXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGDALAYHDSLESWYGNRNNTARSVVKSQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKLGDALAYHDSLESWYGNRNNTARSVVKSQYIALELMFVQKLPFAVSG 180  
 QY 181 EEVPLLPYIAQAANLHLLLRDASIFGKEMGLSSSEISTFYNROVERAGDYSYHCVKWYS 240  
 DB 181 EEVPLLPYIAQAANLHLLLRDASIFGKEMGLSSSEISTFYNROVERAGDYSYHCVKWYS 240

QY 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDAVLPSPDYDTQMPYPIKTTAQLTREVYTDAI 300  
 DB 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDAVLPSPDYDTQMPYPIKTTAQLTREVYTDAI 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMMW 360  
 DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRNSNTQYMMW 360  
 QY 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQCPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATQCPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATVNRGEDLDYK 600  
 DB 541 TGTGDIRVNNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATVNRGEDLDYK 600  
 QY 601 TFRVGTTPPSEFLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 DB 601 TFRVGTTPPSEFLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFVIVKYNELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDEFYLDKRELFVIVKYNELHIERNM 719

RESULT 7  
 AAE36272  
 ID AAE36272 standard; protein; 719 AA.  
 XX AAE36272;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 PN WO200298911-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX  
 PI Vincent JL, Viner R;  
 XX  
 DR WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-  
 PT terminus, useful as an active ingredient of a pesticide.  
 XX  
 PS Claim 12; Page 44-47; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine  
 CC motif at the amino-terminus. Polynucleotide or DNA constructs of the  
 CC invention are useful for producing plants or plant parts that are  
 CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify

CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.5%; Score 3743; DB 6; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-292;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60  
 Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTAESWVRYNQFRDMDTLMLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300  
 Db 241 TGLNLRGTAESWVRYNQFRDMDTLMLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300

QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360

QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTFGDIRYNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAITMNGEDLDYK 600  
 Db 541 TGTFGDIRYNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAITMNGEDLDYK 600

QY 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVPEVTEYAEYDFFKAQEKV 660  
 Db 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNPFSSGNEVYIDRIEFVPEVTEYAEYDFFKAQEKV 660

QY 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDFYLDKRELFEIVKYNELHIERNM 719  
 Db 661 TALFTSTNPRGLTKDVKDHYDQVSNLVESLSEDFYLDKRELFEIVKYNELHIERNM 719

RESULT 8  
 AAR08041  
 ID AAR08041 standard; protein; 719 AA.  
 XX  
 AC AAR08041;

XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 27-FEB-1991 (first entry)

XX 81 kD endotoxin deduced from DNA carried on pJH12.  
 DE Crystal; insecticide; toxin; delta endotoxin.  
 XX  
 KW  
 XX

OS Bacillus thuringiensis; JHCC 4353 and 4835.  
 XX WO9013651-A.  
 XX 15-NOV-1990.  
 XX 09-MAY-1989; 89GB-00010624.  
 XX 09-MAY-1989; 89GB-00010624.  
 XX (ICIL ) IMPERIAL CHEM IND PLC.  
 PA Blenk RG, Ely S, Tailor RH, Tippett JM;  
 PI WPI; 1990-361486/48.  
 XX N-PSDB; AAQ06636.  
 DR  
 DR Bacillus thuringiensis strains - used for producing an endotoxin for  
 PT protecting plants against insects, partic. Lepidoptera and Coleoptera.  
 XX  
 PS Claim 5; Fig 5-10; 66pp; English.  
 XX  
 CC The sequence carried on pJH12 which was isolated from B. thuringiensis  
 CC strains JHCC4353 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can  
 CC be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,  
 CC or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11  
 CC (NCIB 40275). The delta-endotoxin produced by the transformants can be  
 CC used in formulations for combatting Lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
 CC standardise OS field)

XX Sequence 719 AA;

Query Match 99.4%; Score 3741; DB 2; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.7e-292;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60  
 Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTAESWVRYNQFRDMDTLMLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300  
 Db 241 TGLNLRGTAESWVRYNQFRDMDTLMLDLVALFPSYDTQMPYPIKTTAQLTREYVTDI 300

QY 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
 Db 301 GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360

QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 Db 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 QY 601 TFRVGTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVGTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719

RESULT 9  
 ID AAB66910 standard; protein; 719 AA.  
 AC AAB66910;  
 XX  
 DT 12-APR-2001 (first entry)  
 DE Insecticidal protein cryIIa4.  
 XX  
 KW Insecticide; transgenic plant; insect-resistance.  
 XX  
 OS Paecilomyces sp.  
 XX  
 PN WO200100841-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 23-JUN-2000; 2000WO-GB002457.  
 XX  
 PR 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX  
 PA (ZENE) ZENECA LTD.  
 PA  
 PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX  
 DR WPI; 2001-123015/13.  
 XX

Novel insecticidal protein obtained from species of Paecilomyces for controlling insects, and for insect-resistant transgenic plant production.  
 PS Claim 14; Page 60-62; 72pp; English.  
 CC The present invention relates to novel insecticidal proteins obtained from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The insecticidal proteins can be used to produce transgenic plants, which are insect-resistant. Also, the insecticidal proteins are useful for controlling insects by providing them at a locus where insects feed

Sequence 719 AA;  
 Query Match 99.4%; Score 3739; DB 4; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 2.4e-292;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVASATI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEYENVEPVASATI 60  
 QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFTILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVFPAGQVASYLSFTILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLALAVYHDSLESWGNRNNTTRASVVKSQYIALELMFVQKLPSPFVSG 180  
 Db 121 RNKALTDLKGDLALAVYHDSLESWGNRNNTTRASVVKSQYIALELMFVQKLPSPFVSG 180

QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 Db 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGNTNAESWVRYNQFRDNTLMVLDLVALPSPYDTOMYPIKTAQLTREVYTDAL 300  
 Db 241 TGLNLRGNTNAESWVRYNQFRDNTLMVLDLVALPSPYDTOMYPIKTAQLTREVYTDAL 300  
 QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYNNMW 360  
 Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRMSNTQYNNMW 360  
 QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRVRESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEBNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRTNTEBNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 Db 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 QY 601 TFRVGTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVGTTPFSLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719

RESULT 10  
 ID AAE36274 standard; protein; 719 AA.  
 AC AAE36274;  
 XX

DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX Bacillus thuringiensis.

OS WO200298911-A2.  
 XX  
 PN 12-DEC-2002.  
 XX

PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX

PA (SYGN) SYNGENTA LTD.  
 XX  
 PI Vincent JL, Viner R;  
 XX

DR WPI; 2003-175137/17.  
 XX

New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

Claim 12; Page 50-53; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are

CC resistant to insects. The protein or synergistic combination is useful as  
 CC an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify  
 CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 2.4e-292;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDNTLMVLDLVALFSDYDQMPYIKTTAQLTREVTDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDNTLMVLDLVALFSDYDQMPYIKTTAQLTREVTDAI 300

QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360

QY 361 GGHKLEFRITIGTTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITIGTTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540

QY 541 TGTFGDIRVNIINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDDLYK 600  
 DB 541 TGTFGDIRVNIINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDDLYK 600

QY 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

QY 661 TALEFTSTNPRGLKTDVQVHIDQVSNLSELSDEFYLDKEKELFEIVKYANELHIERNM 719  
 DB 661 TALEFTSTNPRGLKTDVQVHIDQVSNLSELSDEFYLDKEKELFEIVKYANELHIERNM 719

RESULT 11  
 AAE36271  
 ID AAE36271 standard; protein; 718 AA.  
 XX  
 AC AAE36271;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.  
 OS  
 XX WO200298911-A2.  
 PN  
 XX 12-DEC-2002.  
 PD  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX  
 XX 07-JUN-2001; 2001GB-00013900.  
 PR  
 XX (SYGN ) SYNGENTA LTD.  
 PA  
 XX Vincent JL, Viner R;  
 PI  
 XX MPI; 2003-175137/17.  
 DR  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 XX Claim 12; Page 42-44; 67pp; English.  
 PS  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention  
 CC  
 XX Sequence 718 AA;

Query Match 99.2%; Score 3730.5; DB 6; Length 718;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-291;  
 Matches 715; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLGFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180

QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDNTLMVLDLVALFSDYDQMPYIKTTAQLTREVTDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDNTLMVLDLVALFSDYDQMPYIKTTAQLTREVTDAI 300

QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360

QY 361 GGHKLEFRITIGTTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITIGTTLNISTOGSTNTSINPVTLPFTSRDVRTESLAGLNFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540

QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYK 600  
Db 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYK 599  
QY 601 TFRVGTFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
Db 600 TFRVGTFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDDEFYLDKRELFELVYKYNELHIERNM 719  
Db 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDDEFYLDKRELFELVYKYNELHIERNM 718

RESULT 12  
AAB66907  
ID AAB66907 standard; protein; 718 AA.  
XX AC AAB66907;  
XX DT 12-APR-2001 (first entry)  
XX Insecticidal protein cryIIa1.  
XX DE Insecticide; transgenic plant; insect-resistance.  
XX KW Insecticide; transgenic plant; insect-resistance.  
XX OS Paecilomyces sp.  
XX PN WO200100841-A1.  
XX PD 04-JAN-2001.  
XX PF 23-JUN-2000; 2000WO-GB002457.  
XX PR 29-JUN-1999; 99GB-00015215.  
XX PR 23-DEC-1999; 99GB-00030536.  
XX PA (ZENE) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX Claim 14; Page 53-55; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX SQ Sequence 718 AA;  
Query Match 99.0%; Score 3724.5; DB 4; Length 718;  
Best Local Similarity 99.3%; Pred. No. 3.6e-291;  
Matches 714; Conservative 1; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHEDCLKMSEYENVEPVFSASTI 60  
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEHEDCLKMSEYENVEPVFSASTI 60  
QY 61 QTGIGIACKILGTGVFPAGQVASYLSFILGELWPKQKQWEIFMEHVVEEINQKISTYA 120  
Db 61 QTGIGIACKILGTGVFPAGQVASYLSFILGELWPKQKQWEIFMEHVVEEINQKISTYA 120  
QY 121 RNKALTDLKGJGDALAVYHDSLESWVGNNRNNTRARSVKSQYIALELMFVQKLPSFAVSG 180  
Db 121 RNKALTDLKGJGDALAVYHDSLESWVGNNRNNTRARSVKSQYIALELMFVQKLPSFAVSG 180

QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
Db 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
QY 241 TGLNLRGTHAESWVRYNQPRRDMTLMVLDLVALFPSTYDTOMYPKTKTAQLTREVYTDAL 300  
Db 241 TGLNLRGTHAESWVRYNQPRRDMTLMVLDLVALFPSTYDTOMYPKTKTAQLTREVYTDAL 300  
QY 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYISLLSRWNTQYNNMW 360  
Db 301 GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDLEQVTIYISLLSRWNTQYNNMW 360  
QY 361 GGHKLEFRTIGTGLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVNGVPR 420  
Db 361 GGHKLEFRTIGTGLNISTOGSTNTSINPVTLPFTSRDYRTESLAGLNLFLTQPVN-VPR 419  
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 420 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 479  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
Db 480 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 539  
QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYK 600  
Db 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLDYK 599  
QY 601 TFRVGTFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
Db 600 TFRVGTFTTFFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 659  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDDEFYLDKRELFELVYKYNELHIERNM 719  
Db 660 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDDEFYLDKRELFELVYKYNELHIERNM 718

RESULT 13

ADM74717  
ID ADM74717 standard; protein; 719 AA.  
XX AC ADM74717;  
XX 03-JUN-2004 (first entry)  
XX B. thuringiensis cryIIel SEQ ID NO:2.  
DE cryI; toxicity; lepidoptera; cryIIa; cryIIb; coleoptera; diptera;  
KW cryIIel.  
XX Bacillus thuringiensis.  
XX CN1401772-A.  
PD 12-MAR-2003.  
XX 20-AUG-2001; 2001CN-00124163.  
XX 20-AUG-2001; 2001CN-00124163.  
XX (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
XX Song F, Zhang J, Huang D;  
PI WPI; 2003-442339/42.  
DR N-PSDB; ADM74716.  
XX Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
PT with high-toxicity to lepidoptera pests, encoded protein, primer  
PT sequences and the shuttle vector pSV422b, useful as a pesticide.  
XX Example 3; SEQ ID NO:2; 29pp; Chinese.  
PS

XX The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
CC combination, expression vector, nucleotide sequence of the B  
CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
CC amino acid sequence of the protein encoded by it, cooperative use of the  
CC cryI gene with the expression product of cryIa or cryIb, primer  
CC sequences for expressing the genes, and the constructed shuttle vector  
CC PSX422b. The gene in combination with the cryIa or cryIb genes  
CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
CC The present sequence represents the cryIIe protein.

XX  
SQ Sequence 719 AA;

Query Match 93.9%; Score 3534; DB 7; Length 719;  
Best Local Similarity 93.2%; Pred. No. 8.3e-276;  
Matches 670; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGKQWEIFMEHVEEIIQKISTYA 120  
Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGKQWEIFMEHVEEIIQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWVGNNRNTARSVVKQYIALELMFVQKLPFAVSG 180  
Db 121 RNKALTDLKGDLAVYHDSLESWVGNNRNTARSVVKQYIALELMFVQKLPFAVSG 180

QY 181 BEVPLLPYQAANLHLLLRDASIFGKELWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
Db 181 BEVPLLPYQAANLHLLLRDASIFGKELWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSDYDQYPIKTTAQLTREVTDAI 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSDYDQYPIKTTAQLTREVTDAI 300

QY 301 GTVHPSPFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVITISLSSRWSTQYMNW 360  
Db 301 GTVHPSPFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVITISLSSRWSTQYMNW 360

QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVPR 420

QY 421 VDFHWFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHWFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480

RESULT 14  
AAB66912  
ID AAB66912 standard; protein; 719 AA.  
XX  
AC AAB66912;  
XX  
DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIb1.  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX Claim 14; Page 64-66; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed

XX Sequence 719 AA;

Query Match 93.1%; Score 3503; DB 4; Length 719;  
Best Local Similarity 92.5%; Pred. No. 2.6e-273;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60  
Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGKQWEIFMEHVEEIIQKISTYA 120  
Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGKQWEIFMEHVEEIIQKISTYA 120

QY 121 RNKALTDLKGDLAVYHDSLESWVGNNRNTARSVVKQYIALELMFVQKLPFAVSG 180  
Db 121 RNKALTDLKGDLAVYHDSLESWVGNNRNTARSVVKQYIALELMFVQKLPFAVSG 180

QY 181 BEVPLLPYQAANLHLLLRDASIFGKELWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
Db 181 BEVPLLPYQAANLHLLLRDASIFGKELWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSDYDQYPIKTTAQLTREVTDAI 300  
Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSDYDQYPIKTTAQLTREVTDAI 300

QY 301 GTVHPSPFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVITISLSSRWSTQYMNW 360  
Db 301 GTVHPSPFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVITISLSSRWSTQYMNW 360

QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDYRTESLAGNLFITQPVNGVPR 420

QY 421 VDFHWFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480  
Db 421 VDFHWFVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIWNPFAQYRVIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIWNPFAQYRVIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
DB 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANELHIERNM 719

RESULT 15

AAE36276

ID AAE36276 standard; protein; 719 AA.

AC AAE36276;

XX 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

OS WO2002298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

PR 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

PI Vincent JL, Viner R;

XX WIPI; 2003-175137/17.

PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

PS Claim 12; Page 56-58; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

Query Match

Best Local Similarity 93.1%; Score 3503; DB 6; Length 719;

Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLKNQKHQSPSSNAKVDKISTDSLKNETDIELONINHEDECKMSEYENVEPVSASTI 60

DB 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKNMNEDEYLMSEHESIDPVSASTI 60

QY 61 QTGIGIAGKILGTGVFPAGQVASYFLIGELWPKGNQWEIFMEHVEEIIINOKISTYA 120

DB 61 QTGIGIAGKILGTGVFPAGQIASLYFLIGELWPKGKSQWEIFMEHVEEIIINOKILTYA 120

Search completed: October 28, 2004, 18:19:59

Job time : 91.6903 secs

QY 121 RNKALTDLKGLDALAVYHDSLESVWGNRNTRARSVVYKSOYIALELMFVQKLPFAVSG 180  
DB 121 RNKALSDLRGLDALAVYHESLESWVENNTRARSVVQVQYIALELMFVQKLPFAVSG 180  
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSVHCWKWYS 240  
DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSASEISTFYNRQVERTRDYSCHCKWYN 240  
QY 241 TGLNLRGTNAESWVRYNQFRDRTMLVLDLVALFPSYDTOMYPIKTAQLTREVTYDAI 300  
DB 241 TGLNLRGTNAESWVRYNQFRDRTMLVLDLVALFPSYDTLVYPIKTTSTREVTYDAI 300  
QY 301 GTVHPHPSFTSTWNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYLSLSRVSNTQYMMW 360  
DB 301 GTVHPNQAFSTTWNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYLSLSRVSNTQYMMW 360  
QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPPTSRDVRTSLAGLNLFLTQPVNGVPR 420  
DB 361 GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVRTSLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQOPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFPTLPIASDNFYVLYGAGVGTQDSENELPPEATTQOPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIWNPFAQYRVIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIWNPFAQYRVIRYASTTDLOFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
DB 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANELHIERNM 719



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-56  
Perfect score: 3762  
Sequence: 1 MKLKNQDKHQSFSSNAKVYDK.....KRELFVIVKANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3743	99.5	719	17	US-10-782-020-10
2	3743	99.5	719	17	US-10-782-141-8
3	3743	99.5	719	17	US-10-782-096-10
4	3743	99.5	719	17	US-10-782-570-7
5	3459.5	92.0	710	14	US-10-428-961-42
6	2263.5	60.2	1228	16	US-10-809-953-10
7	2250.5	59.8	1207	10	US-09-988-462-7
8	2171.5	57.7	1227	14	US-10-428-961-63
9	2156.5	57.3	1186	9	US-09-826-660-23
10	2101	55.8	1228	14	US-10-428-961-38
11	2101	55.8	1228	15	US-10-614-524-2
12	1923.5	51.1	643	9	US-09-826-660-25
13	1707.5	45.4	1167	14	US-10-089-678-1

14	1678.5	44.6	653	14	US-10-428-961-6	Sequence 6, Appli
15	1655.5	44.0	1157	17	US-10-782-141-16	Sequence 16, Appli
16	1655.5	44.0	1157	17	US-10-782-096-17	Sequence 17, Appli
17	1655.5	44.0	1157	17	US-10-782-570-13	Sequence 13, Appli
18	1496	39.8	1206	13	US-10-032-717-2	Sequence 2, Appli
19	1496	39.8	1206	14	US-10-414-637-2	Sequence 2, Appli
20	1496	39.8	1206	15	US-10-606-320-2	Sequence 2, Appli
21	1496	39.8	1206	17	US-10-746-914-2	Sequence 2, Appli
22	1480	39.3	1210	13	US-10-032-717-4	Sequence 4, Appli
23	1480	39.3	1210	14	US-10-414-637-4	Sequence 4, Appli
24	1480	39.3	1210	15	US-10-606-320-4	Sequence 4, Appli
25	1480	39.3	1210	17	US-10-746-914-4	Sequence 4, Appli
26	1476.5	39.2	1156	14	US-10-099-285-72	Sequence 72, Appli
27	1476.5	39.2	1156	14	US-10-428-961-28	Sequence 28, Appli
28	1452	38.6	1155	9	US-09-756-643-2	Sequence 2, Appli
29	1452	38.6	1155	10	US-09-988-462-9	Sequence 9, Appli
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31	1452	38.6	1177	14	US-10-035-060-6	Sequence 6, Appli
32	1452	38.6	1181	10	US-09-988-462-11	Sequence 11, Appli
33	1452	38.6	1181	10	US-09-988-462-13	Sequence 13, Appli
34	1452	38.6	1181	10	US-09-988-462-15	Sequence 15, Appli
35	1452	38.6	1181	10	US-09-988-462-17	Sequence 17, Appli
36	1452	38.6	1181	10	US-09-988-462-28	Sequence 28, Appli
37	1452	38.6	1181	14	US-10-136-998A-4	Sequence 4, Appli
38	1452	38.6	1181	14	US-10-136-998A-8	Sequence 8, Appli
39	1452	38.6	1181	14	US-10-136-998A-10	Sequence 10, Appli
40	1452	38.6	1181	14	US-10-136-998A-12	Sequence 12, Appli
41	1447	38.4	1177	14	US-10-035-060-2	Sequence 2, Appli
42	1444	38.4	1177	14	US-10-102-469-24	Sequence 24, Appli
43	1428.5	38.0	1176	17	US-10-782-141-6	Sequence 6, Appli
44	1428.5	38.0	1176	17	US-10-782-096-7	Sequence 7, Appli
45	1428.5	38.0	1176	17	US-10-782-096-7	Sequence 7, Appli

## ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782.020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 99.5%; Score 3743; DB 17; Length 719;  
Best Local Similarity 99.6%; Pred. No. 3.7e-307;  
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVYDKISTDSLKNETDIELQNHEDCLXSEYENVEPFSASTI 60  
DB 1 MKLKNQDKHQSFSSNAKVYDKISTDSLKNETDIELQNHEDCLXSEYENVEPFSASTI 60  
QY 61 QTGTGIAGKILGTGLGVFPAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGTGIAGKILGTGLGVFPAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINQKISTYA 120

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QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
DB 181 EEPVLLPIYAQAANLHLLLRDASIIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240
QY 241 TGLNLRGNAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
DB 241 TGLNLRGNAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMNW 360
DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMNW 360
QY 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
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QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
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; Sequence 8, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-8

Query Match
Best Local Similarity 99.5%; Score 3743; DB 17; Length 719;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNEDCLKMSYENVEPFFVASTI 60

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DB 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINHNEDCLKMSYENVEPFFVASTI 60
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DB 61 QTGIGIAGKILGTLGVPAGQVAVSLYSFILGELWPKGNQWEIIFMEHVEIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVKQYIALELMFVQKLPFAVSG 180
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QY 241 TGLNLRGNAESWVRNQFRDMTLMVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300
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DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMNW 360
QY 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
DB 361 GGKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
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DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719

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; Sequence 10, Application US/10782096
; Publication No. US20040210964A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for its Use
; FILE REFERENCE: 045600/274148
; CURRENT APPLICATION NUMBER: US/10782,096
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,633
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-096-10

Query Match
99.5%; Score 3743; DB 17; Length 719;

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Best Local Similarity 99.6%; Pred. No. 3.7e-307;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKSEYENVEPFSASTI 60
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Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINOKISTYA 120
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Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180
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Db 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFQTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFQTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV 660
Db 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

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RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMT-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719

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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 99.5%; Score 3743; DB 17; Length 719;
Best Local Similarity 99.6%; Pred. No. 3.7e-307;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKSEYENVEPFSASTI 60
Db 1 MCLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKSEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINOKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINOKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSYHCVKWS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
Db 241 TGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFQTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFQTQPVNGVPR 420
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
Db 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV 660
Db 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

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RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US2003023711A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rel
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

```

PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: 60/153,995  
PRIOR FILING DATE: 1999-09-15  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 42  
LENGTH: 710  
TYPE: PR  
ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (200)..(200)  
OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
US-10-428-961-42

Query Match 92.0%; Score 3459.5; DB 14; Length 710;  
Best Local Similarity 92.1%; Pred. No. 3.4e-283;  
Matches 662; Conservative 16; Mismatches 32; Indels 9; Gaps 1;  
QY 1 MKLNQDQKQSFSSNAKVDKISTDSLXNETDIELQNHEDCLKYSEYENVEPVSASTI 60  
Db 1 MKSKNQNMHQSLSNATVDKNFTGSLNNTNTELOQNFH-----EGIEPFVSASTI 51  
QY 61 QTGIGIAGKILGTPAGQVAVSLYFIFLGLWPKGNQWEIFMEHVEELINQKISTYA 120  
Db 52 QTGIGIAGKILGTPAGQVAVSLYFIFLGLWPKGNQWEIFMEHVEELINQKISTYA 111  
QY 121 RNKALTDLKGLDALAVYHDSLESVGNRNTRARSVVKSYIALELMFVQKLPSPAVSG 180  
Db 112 RNKALADLKGLDALAVYHDSLESWIENRNTTRSVVKSQYITLELMFVQSLSPAVSG 171  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
Db 172 EEPVLLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSEYSDCVKWN 231  
QY 241 TGLANLGRGTNAESVRYNQFRDMTLMVLDLVALFSPYDTOMYPIKTTAQLTREYITDAI 300  
Db 232 TGLANLGRGTNAESVRYNQFRDMTLMVLDLVALFSPYDTOMYPIKTTAQLTREYITDAI 291  
QY 301 GTVHPHPSFTSTTYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
Db 292 GTVHPHPSFTSTTYNNNAPSFTIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 351  
QY 361 GGHKLEFRIGTUNISTQSTNTSINPVTLPFTSRDVRVRESLAGLNLFILTPQVNGVPR 420  
Db 352 GGHKLEFRIGTUNISTQSTNTSINPVTLPFTSRDVRVRESLAGLNLFILTPQVNGVPR 411  
QY 421 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELEPPEATGQPNYESYSHRLSHIGLIS 480  
Db 412 VDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELEPPEATGQPNYESYSHRLSHIGLIS 471  
QY 481 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 472 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531  
QY 541 TGTGDIRVNNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATNRGDDLDYK 600  
Db 532 TGTGDIRVNNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATNRGDDLDYK 591  
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 660  
Db 592 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 651  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
Db 652 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 710

RESULT 6  
US-10-809-953-10  
Sequence 10, Application US/10809953  
Publication No. US20040181825A1  
GENERAL INFORMATION:

APPLICANT: Van Mellaert, Herman  
APPLICANT: Botterman, Johan  
APPLICANT: Van Rie, Jeroen  
APPLICANT: Joos, Henk  
TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC  
TITLE OF INVENTION: CRYSTAL PROTEINS  
FILE REFERENCE: 021565-078  
CURRENT APPLICATION NUMBER: US/10/809,953  
CURRENT FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER: US/09/661,016  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: PCT/EP90/00905  
PRIOR FILING DATE: 1990-05-30  
PRIOR APPLICATION NUMBER: GB 89401499.2  
PRIOR FILING DATE: 1989-05-31  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1228  
TYPE: PR  
ORGANISM: Bacillus thuringiensis  
US-10-809-953-10

Query Match 60.2%; Score 2263.5; DB 16; Length 1228;  
Best Local Similarity 62.4%; Pred. No. 1e-181;  
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;  
QY 23 TDSLXNETDIELQNH-----EDCLKMSEYENVEPVSASTIQTGIGIAGKI 70  
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDAIEDSLCIAENNDIPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQVAVSLYFIFLGLWPKGNQWEIFMEHVEELINQKISTYARNKALTDLKG 130  
Db 62 LGVLGVPPAGQVAVSLYFIFLGLWPKGNQWEIFMEHVEELINQKISTYARNKALTDLKG 121  
QY 131 LGDALAVYHDSLESVGNRNTRARSVVKSYIALELMFVQKLPSPAVSGEVPPLPIYA 190  
Db 122 LGDSFRAYQOSLEDWLENEDDARTSRVLTQVIALELDLFLNAPLFAIRNQEVPLLMVYA 181  
QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWSYSLGLNLRGTN 250  
Db 182 QAANLHLLLRDASIFGSEFGLTSQEQRYEYERQVETRDYSDYCVENYNTGLNLRGTN 241  
QY 251 AESVRYNQFRDMTLMVLDLVALFSPYDTOMYPIKTTAQLTREYITDAICTVHPHPSFT 310  
Db 242 AASVRYNQFRDMTLMVLDLVALFSPYDTOMYPIKTTAQLTREYITDAIGAT--GVNMA 299  
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMWGCHKLEFRTI 370  
Db 300 SMWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYNNMWGCHKLEFRTI 359  
QY 371 GGTNLISQSTNTSINPVTLPFTSRDVRVRESLAGLNLF--LTQPVNGVPRVDFHWKFV 428  
Db 360 GGGLNTSTHGATNTSINPVTLPFTSRDVRVRESLAGLNLF--LTQPVNGVPRVDFHWKFV 416  
QY 429 THP-----IASDNFYPGYAGIGTQLODSENELEPPEATGQPNYESYSHRLSHIGLISASH 483  
Db 417 TNPQNSIDRTANTYQSP--YESPGQLKDESETLPETTERPNYESYSHRLSHIGLISASH 475  
QY 484 VKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTGT 543  
Db 476 VNVFVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRINTGT 535  
QY 544 FGDIRVNNINPPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSAATNRGDDLDYKTFR 603  
Db 536 FGPVIRVTNGLTQRYIRIGFRYASTVDFVFSRGTTVNNFRFLRMTNSGDELKGNFV 595  
QY 604 TVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 663  
Db 596 RRAFTTFFTQIQDIIRTSIQGLSGNEVYIDRIEFVPEVTEYAEYDFEKAQEV 655  
QY 664 FTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

Db 656 FTNTNPRRLKTDYTDYHIDQVSNLVACLSDPECLDEKRELLKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7  
; Sequence 7, Application US/09988462  
; Publication No. US20030046726A1  
; GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-No. US20030046726A1-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 59.8%; Score 2250.5; DB 10; Length 1207;  
Best Local Similarity 64.0%; Pred. No. 1.3e-180;  
Matches 440; Conservative 77; Mismatches 157; Indels 13; Gaps 5;

QY 40 EDCLKMSYENVEPFVSASTQTGTGIGIAGKILGTGVGPAGQVASLYSHLGEIWPKN 99  
Db 10 EDSLICIAEGNIDPFVSASTVGTGINAGRIAGLVGPAGQVASFVSLVGLWPRGD 69

QY 100 QWEIFMEHVEEINQKISTYARKALTDLKLGLDALAVYHDSLSWVGNNRNNTRASYVK 159  
Db 70 QWEIFLHVEQLINQITENARNTALRQLGLGDSFRAYQQSLEDWLENRDDARTSVLY 129

QY 160 SQYIALELMFVQKLPSPFAVSGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSIST 219  
Db 130 TOYIALELDFNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR 189  
QY 220 FYNROVERAGDYSYHCWKYSTGLNNLRGTNAESWRYNQFRDRLTMLVLDLVALPESYD 279  
Db 190 YERQVTRTDYSDYCVWYNTGLNSLGTNAASWRYNQFRDRLTMLVLDLVALPESYD 249  
QY 280 TOMYPIKTTAQLTREVYTDAGTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDEL 339  
Db 250 TRTYPINTSAQLTREVYTDAGT- -GVNMAWYNNAPSPSAIEAAVVRNPHLLDEL 307  
QY 340 EQVTIYSLLSRWSTQYNNMGGHKLERTIGTIGTINISTQSTNTSINPVTLPFTGRDVI 399  
Db 308 EQLTIPSSASSRWSTNTHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTGRDVI 367  
QY 400 RTESLAGLNLFP- -LTQPVNGVPRVDFHMKFVTHP- -IASDNFYYPGYAGIGTQLQDS 452  
Db 368 RTESYAGVLLWGIYLEPIHGVPTVRFNF- -TNPQNTSDRGTYANSQP-YESPGQLQKDS 423  
QY 453 ENELPPEATQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPL 512  
Db 424 ETELPPTERTPRNYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTIEPNSITQIPL 483  
QY 513 VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNPPFAQRYVRIRYASTDLQ 572  
Db 484 VKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNNPPFAQRYVRIRYASTDLQ 543  
QY 573 PHTSINGKAINQGNFSAWNGEDLDYKTFRTVGTFTFPFSLDQVSTFTIGAWNFSSGNE 632  
Db 544 FVSRGGTIVNNFRFLRTNMGDELKYNFVRAFTTPTFTQIQDIIRTSIQGLSGNGE 603  
QY 633 VYIDRIEFVPEVITYEAEYDFEKAQEKYALTFTSTNPRGLKTDVKYHIDQVSNLVESLS 692  
Db 604 VYIDKIEIIPVATFAEYDLERAQEAVALFTNTNFRRLKTDVTDVHIDQVSNLVACL 663  
QY 693 DEFYLDKRELFEIVKYANLHIERNM 719  
Db 664 DEFCLDEKRELLKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63  
; Sequence 63, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; FILE REFERENCE: MECO201--1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 63  
; LENGTH: 1227  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-63

Query Match 57.7%; Score 2171.5; DB 14; Length 1227;  
Best Local Similarity 59.0%; Pred. No. 6.2e-174;  
Matches 421; Conservative 104; Mismatches 176; Indels 13; Gaps 3;

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QY 13 SSNAKVDK1STDLSKN-----ETDIELQNHEDCLKSEYENVEPFSASTIQTGIG 65
Db 7 NENEIINALSIPAVSNHSAQMLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQVASFYSLFELGELMPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGRLGLVGVPPAGQIASFYSLFELGELMPKGRDPWEIFLEHVEQLIRQVTEENTRTAL 121
QY 126 TDLKGLGDALAVYHDSLSWVGNRNNTARSVYKSOVIALELMFVQKLPFSFVSGEEVPL 185
Db 122 ARLOGLGNSFRAYQOOSLEDWLENRRDARTSRVLYTQVIALELDLFNAMPLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQROVERAGDYSYHCVKYSTGLNN 245
Db 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEKTRREYSYCARWYNTGLNN 241
QY 246 LRGTNAESWRYNQFRDRTMLVLDLVALFPSYDTQMPYPIKTAQLTREYVTDAGTVHP 305
Db 242 LRGTNAESWRYNQFRDRTMLVLDLVALFPSYDTQMPYPIKTAQLTREYVTDAGTVHP 301
QY 306 HPSFTSTTWNNAAPSFSAIEAAVVRPHLLDFLEQVITYLSLRSWNTQYMNWGGHKL 365
Db 302 PSGFASTNWFNNAPSFSAIEAAVVRPHLLDFLEQVITYLSLRSWNTQYMNWGGHKL 361
QY 366 EFRITGTLNISTQSTNTSINPVTLPFTSRDYRTESLAGNLFLTQPVNGVPRVDFHW 425
Db 362 ESRTIRGSLSTWHTGNTSINPVTLPFTSRDYRTESLAGNLFLTQPVNGVPRVDFHW 421
QY 426 KFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVK 485
Db 422 RNPLSLRGSLLYITGYTGVTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVK 481
QY 486 ALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVRGPFGTGGDILRRNTGTGFG 545
Db 482 APVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVRGPFGTGGDILRRNTGTGFG 541
QY 606 GFTTPEFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTAFT 665
Db 602 EFPVGISASCSQ-TAGISISNAGRQTFHDXIEFIPITATLEAESDLERACKAVNALFT 660
QY 666 STNPRGLKTDVYKHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 NTNPRKLTGVTVDHIDEVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 714

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RESULT 9
US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

FEATURE:  
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-09-826-660-23

Query Match 57.3%; Score 2156.5; DB 9; Length 1186;  
Best Local Similarity 58.7%; Pred. No. 1.1e-172;  
Matches 419; Conservative 107; Mismatches 175; Indels 13; Gaps 3;

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QY 13 SSNAKVDK1STDLSKN-----ETDIELQNHEDCLKSEYENVEPFSASTIQTGIG 65
Db 7 NENEIINALSIPAVSNHSAQMLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTGVPFAGQVASFYSLFELGELMPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125
Db 62 IAGRLGLVGVPPAGQIASFYSLFELGELMPKGRDPWEIFLEHVEQLIRQVTEENTRTAL 121
QY 126 TDLKGLGDALAVYHDSLSWVGNRNNTARSVYKSOVIALELMFVQKLPFSFVSGEEVPL 185
Db 122 ARLOGLGNSFRAYQOOSLEDWLENRRDARTSRVLYTQVIALELDLFNAMPLFAIRNQEVPL 181
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQROVERAGDYSYHCVKYSTGLNN 245
Db 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEKTRREYSYCARWYNTGLNN 241
QY 246 LRGTNAESWRYNQFRDRTMLVLDLVALFPSYDTQMPYPIKTAQLTREYVTDAGTVHP 305
Db 242 LRGTNAESWRYNQFRDRTMLVLDLVALFPSYDTQMPYPIKTAQLTREYVTDAGTVHP 301
QY 306 HPSFTSTTWNNAAPSFSAIEAAVVRPHLLDFLEQVITYLSLRSWNTQYMNWGGHKL 365
Db 302 PSGFASTNWFNNAPSFSAIEAAVVRPHLLDFLEQVITYLSLRSWNTQYMNWGGHKL 361
QY 366 EFRITGTLNISTQSTNTSINPVTLPFTSRDYRTESLAGNLFLTQPVNGVPRVDFHW 425
Db 362 ESRTIRGSLSTWHTGNTSINPVTLPFTSRDYRTESLAGNLFLTQPVNGVPRVDFHW 421
QY 426 KFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVK 485
Db 422 RNPLSLRGSLLYITGYTGVTQLODSENELPPEATQPNYESYSHRLSHIGLISASHVK 481
QY 486 ALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVRGPFGTGGDILRRNTGTGFG 545
Db 482 APVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVRGPFGTGGDILRRNTGTGFG 541
QY 546 DIRVINPFAQRYRIRYASTDLOQHTSINGKAINQGNFSAIWNRGEDLDYKTERIV 605
Db 542 SMGLNFNNTSLQRYRVRYAASQTMVLRVTVGGSTTFDQGFPPSTMSANESLTSQSFRFA 601
QY 606 GFTTPEFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTAFT 665
Db 602 EFPVGISASCSQ-TAGISISNAGRQTFHDXIEFIPITATLEAESDLERACKAVNALFT 660
QY 666 STNPRGLKTDVYKHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 661 SSNQGLKTDVTDHIDRVSNLVESLSDEFCLDEKRELSEKVKHAKELSDERNL 714

```

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RESULT 10
US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

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; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 38  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-428-961-38

Query Match 55.8%; Score 2101; DB 14; Length 1228;  
 Best Local Similarity 59.2%; Pred. No. 5.7e-168;  
 Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;

QY	13	SSNAKVDKISTDLSKN-ETDIELQ-NINHEDECKMSEYENVEPFVSASTIQTGIGIAGKI	70
Db	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI	66
QY	71	LGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG	130
Db	67	LGVLGVPFAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQG	126
QY	131	LGDAVAVHDSLESWGNRNNTTRARSVVKSOYIALELMFVQKLPFAVSGEVEPLPIYA	190
Db	127	LGDSFRAYQOQSLDNLNDRDARTSVLYTQYIALELDFNAMPLFAIRNQEVPPLMYA	186
QY	191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNNLRGTN	250
Db	187	QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVWEYNTGLNSLRGTN	246
QY	251	AESWRYNQFRDMLTGLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHHPSPFT	310
Db	247	AASWRYNQFRDMLTGLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHHPSPFT	304
QY	311	STTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNWGGHKLERTI	370
Db	305	SMWYNNAPSAIEATAVIRSPHLLDFLEQVTIYLLSRWSNTQYMNWGGHKLERTI	364
QY	371	GGTINISTQGSTNTSINPVTLPFTSRDVRYSAGLNLP--LTQPVNGVPRVDVHFKV	428
Db	365	GGGLNTSTHGSTNTSINPVLSPFSDRDVYTESYAGVLLWGIYLEPIHGVPTVRNFRNP	424
QY	429	--THPIASDNFYYPYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLISASHVKA	486
Db	425	QNTFERGTANYSQP--YESPGLQKDSSETLPETTERPNYESYSHRLSHIGLISASHVKA	483
QY	487	LVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFGD	546
Db	484	PVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFGD	543
QY	547	IRVYNINPPAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGSDLDYKTERTVG	606
Db	544	MGLNFNNTSLQRYRVRVRYAASQTMVLRTVGGSTTFDQGFPTMSANESLTSQSFRFAE	603
QY	607	FTTFFSFLDVQSTFTIGAWNPFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTAFTS	666
Db	604	FPVGISASGSQ--TAGISISNAGRQTFHDKIEFIPITATFEAEYDLERAQEAVALFTN	662
QY	667	TNPRGLKTDVKDHYHDQVSNLVESLSDFEYLDKRELFELVVKYANELHIERNM	719
Db	663	TNPRGLKTDVKDHYHDQVSNLVESLSDFEYLDKRELFELVVKYANELHIERNM	715

RESULT 11  
 US-10-614-524-2  
 ; Sequence 2, Application US/10614524  
 ; Publication No. US20040016020A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arraut, Greta  
 ; APPLICANT: Boets, Annemie  
 ; APPLICANT: Damme, Nicole  
 ; APPLICANT: Mathieu, Eva

; APPLICANT: Vanneste, Stijn  
 ; APPLICANT: Van Rie, Jeroen  
 ; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.  
 ; FILE REFERENCE: NEWTSUS2  
 ; CURRENT APPLICATION NUMBER: US/10/614,524  
 ; CURRENT FILING DATE: 2003-07-08  
 ; PRIOR APPLICATION NUMBER: US/09/739,243  
 ; PRIOR FILING DATE: 2000-12-19  
 ; PRIOR APPLICATION NUMBER: 60/173387  
 ; PRIOR FILING DATE: 1999-12-28  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-614-524-2

Query Match 55.8%; Score 2101; DB 15; Length 1228;  
 Best Local Similarity 59.2%; Pred. No. 5.7e-168;  
 Matches 422; Conservative 97; Mismatches 184; Indels 10; Gaps 7;

QY	13	SSNAKVDKISTDLSKN-ETDIELQ-NINHEDECKMSEYENVEPFVSASTIQTGIGIAGKI	70
Db	7	NENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGINIAGRI	66
QY	71	LGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG	130
Db	67	LGVLGVPFAGQIASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQG	126
QY	131	LGDAVAVHDSLESWGNRNNTTRARSVVKSOYIALELMFVQKLPFAVSGEVEPLPIYA	190
Db	127	LGDSFRAYQOQSLDNLNDRDARTSVLYTQYIALELDFNAMPLFAIRNQEVPPLMYA	186
QY	191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKYSTGLNNLRGTN	250
Db	187	QAANLHLLLRDASLFGSEFGLTSQEIQRYERQVEQTRDYSYCVWEYNTGLNSLRGTN	246
QY	251	AESWRYNQFRDMLTGLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHHPSPFT	310
Db	247	AASWRYNQFRDMLTGLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHHPSPFT	304
QY	311	STTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNWGGHKLERTI	370
Db	305	SMWYNNAPSAIEATAVIRSPHLLDFLEQVTIYLLSRWSNTQYMNWGGHKLERTI	364
QY	371	GGTINISTQGSTNTSINPVTLPFTSRDVRYSAGLNLP--LTQPVNGVPRVDVHFKV	428
Db	365	GGGLNTSTHGSTNTSINPVLSPFSDRDVYTESYAGVLLWGIYLEPIHGVPTVRNFRNP	424
QY	429	--THPIASDNFYYPYAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLISASHVKA	486
Db	425	QNTFERGTANYSQP--YESPGLQKDSSETLPETTERPNYESYSHRLSHIGLISASHVKA	483
QY	487	LVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFGD	546
Db	484	PVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGFGD	543
QY	547	IRVYNINPPAQRVVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGSDLDYKTERTVG	606
Db	544	MGLNFNNTSLQRYRVRVRYAASQTMVLRTVGGSTTFDQGFPTMSANESLTSQSFRFAE	603
QY	607	FTTFFSFLDVQSTFTIGAWNPFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTAFTS	666
Db	604	FPVGISASGSQ--TAGISISNAGRQTFHDKIEFIPITATFEAEYDLERAQEAVALFTN	662
QY	667	TNPRGLKTDVKDHYHDQVSNLVESLSDFEYLDKRELFELVVKYANELHIERNM	719
Db	663	TNPRGLKTDVKDHYHDQVSNLVESLSDFEYLDKRELFELVVKYANELHIERNM	715

RESULT 12  
 US-09-826-660-25



[illegible]

```

Db      471 LIIGNTLRAPVYSWTHRSADRTNTIGPNRITQIPAVKGRFLNG-SVISGPGFTGDDVVR 529
QY      538 -RTNWTGTF---GDIRVWIN-PPFAQRYRVRIYASTTDLQFHTSINGKAINQGNFSATMN 592
Db      530 LNRNNGNIGNRGYIEVPIQFTSTSTRYRVRYASVTSTELNVNLGNSSFTNTILPATAA 589
QY      593 RGEDLDYKTFRTVGTTPFSFLDVQSTFT-----IGAWNFSSGNEVYIDRIEFVVEVT 646
Db      590 SLNQLQ-----SGDFGYVEINNAFTSATGNIVGARNFSANAEEIIDRFEFIPVTAT 640
QY      647 YEAEYDFEKAQE 658
Db      641 FEVEYDLERAQK 652

RESULT 15
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziele, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match      44.0%; Score 1655.5; DB 17; Length 1157;
Best Local Similarity 48.8%; Pred. No. 2.4e-130;
Matches 369; Conservative 97; Mismatches 233; Indels 57; Gaps 18

QY      1 MCLKNQDQHQSFSNAKVDKISTDS----LKNETDIEIQINIHEDCLKMSEYE-----N 50
Db      1 MSPNNQNEYEIIDATPST-SVSSDSNRYPPFANEPTDALQNMNRYKDYLRKMSGGENPELFGN 59
QY      51 VEPFVSASTIQIGIGIAGKILGTGVPPAGOVASLYSIFILGELWP-KGKNQWEIPEMHEVE 109
Db      60 PETFISSTIQTGIGIVGRILGALGVPPASQIASFYSFIVQLWPKSVSDIWGEIMERVE 119
QY      110 EIINQKISTYARKALTDLKLGDALAVYHDSLESWGNRNNTARSVVKVSQYIALELMF 169
Db      120 ELVDQKIEKYVKDKALAEKLGKGNALDVYQQLSDLEWLENRDARTRSVVSNQFIADLNF 179
QY      170 VQKLPSFAVSGEEVPLPIYQAQANLHLLLRDASI FQKEWGLSSSEISTFYNRQVERAG 229
Db      180 VSSIPSFAVSGHEVLLLA VYAQAVNLHLLLRDASIFGEWGETPGEISRFYNRQVQLTA 239
QY      230 DYSHYCVKMYSTGLNNLRGTNAESWVRNQFRDMDTLMLVLDLVALFPSYDTQMYPIKTTA 289
Db      240 EYSDYCVKWKYGLDKLKGTTSSWLVNHQFRREMTLLVLDLVALFPNYDTHMYPIETTA 299
QY      290 QLTREVYTDAGTGVHPHPSFTST---TWYNNNAPSFAIEAAVVRNPHLLDLFEQVTIY 345
Db      300 QLTRDRVYTDPIA---FNIVTSTGFCNPWSTHSGILFYEVENNVRPPHFLFDLSSSVEIN 355
QY      346 SLLSR-----WSNTQYMNMGGHKLKLEFR-----TIGGTINI STQGSTNTSINPVTLPFTSR 396
Db      356 T--SRGGITLNNDAYINWWSGHTLKKRYARTADSTVITYANYGRITSEKNS-----FALED 408

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QY	397	DVYRTESLAGNLF	LTQPVNGVPRVDFHFKFVTHPIASDNFY	-----YPCYAGIGTQLQD	451
Db	409	DIFEINSTVANL	ANYQKAYGPGSWFH--MVKRGTSSTTAYLYSKTHTALQGC-TQYIE		465
QY	452	SENELPPEATG	QPNYESYSHRLSHI-----GLISASHVKALVYSWTHRSADRTN	TIE	503
Db	466	SSDEIPLDRT	-VPVAESYSHRLSHITSHSFGKNG--SAYYGSFPVFWVWTHTSADLNNTIY		522
QY	504	PNSITQIPLV	KAFNLSSGAAVRGPGTGGDILRRNTGTGDIRVNIINPPFAQRYRRI		563
Db	523	SDKITQIPAV	KGDMLYLGGSVVQGGTGGDILKRINPSILGTFAVTVNGSLSORRYRRI		582
QY	564	RYASTTDLOF	HTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTTTPFSLDVQSTFTIG		623
Db	583	RYASTTDFEF	-TLYLGDTEKRNFKNTMDNGASLTETFKFASFITDFQFRETQDKILLS		641
QY	624	AMNFSGNEVY	IDRIEFVPEVTEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQ		683
Db	642	MGDFSSGQEV	IDRIEFIPVDETYEAECQDLEAKKAVNALFTNTKD-GLRPGVTIDYEVNQ		700
QY	684	VSNLVESSL	DEFYLDKEKELFEIVKYANELHIERNM		719
Db	701	AANLVECL	SDDLVPNEKRLLFDAVREAKRLSGARNL		736

Search completed: October 28, 2004, 18:41:02  
Job time : 71.6795 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-56  
Perfect score: 3762  
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3752	99.7	719	2	CAC85964
2	3743	99.5	719	1	C1AB_BACTK
3	3743	99.5	719	2	Q6X181
4	3743	99.5	719	2	AAP86782
5	3738	99.4	719	2	Q93NJ5
6	3737	99.3	719	2	O85796
7	3608	95.9	719	2	O8KV61
8	3534	93.9	719	2	Q9F0P8
9	3503	93.1	719	1	C1IB_BACTE
10	3380	89.8	719	1	C1ID_BACTU
11	3379	89.8	719	1	C1IC_BACTU
12	2437.5	64.8	1229	1	C1BB_BACTU
13	2437.5	64.8	1233	1	C1BC_BACTM
14	2263.5	60.2	1228	2	Q93T75
15	2262.5	60.1	1228	1	C1BA_BACTK
16	2254.5	59.9	1228	2	Q93NM5
17	2180.5	58.0	849	2	Q6PYW8
18	2180.5	58.0	849	2	AAS93797
19	2180.5	58.0	1227	1	C1BE_BACTU
20	2103.5	55.9	1231	2	O8KNY2
21	2098.5	55.8	1231	1	C1BD_BACTZ
22	1979.5	52.6	1215	1	C1KA_BACTM
23	1895	50.4	381	2	Q45740
24	1655.5	44.0	1157	1	C8AA_BACUK
25	1643	43.7	1144	2	Q8KZL7
26	1483	39.4	1157	1	C9CA_BACTO
27	1471.5	39.1	1169	1	C8BA_BACUK
28	1469	39.0	1167	1	C1JA_BACTU
29	1467.5	39.0	1166	1	C1GA_BACTU
30	1467	39.0	1169	1	C1FB_BACTM
31	1461	38.8	1174	2	Q45749

32	1452	38.6	1155	1	C1AB_BACTK	P06578 bacillus th
33	1452	38.6	1155	2	Q7BE98	Q7be98 bacillus th
34	1452	38.6	1155	2	Q9F296	Q9f296 bacillus th
35	1452	38.6	1155	2	AAN76494	Aan76494 bacillus
36	1452	38.6	1155	2	AAO13302	Aao13302 bacillus
37	1450	38.5	1118	2	Q9AM83	Q9am83 bacillus th
38	1447	38.5	1156	2	Q6GUA7	Q6gua7 bacillus th
39	1442	38.3	1177	2	Q6EIX3	Q6eix3 bacillus th
40	1440	38.3	1155	2	Q93T21	Q93t21 bacillus th
41	1439.5	38.3	793	2	Q6PYW7	Q6pyw7 bacillus th
42	1439.5	38.3	793	2	AAS93798	Aas93798 bacillus
43	1439.5	38.3	1180	2	Q9S5V8	Q9s5v8 bacillus th
44	1438.5	38.2	1176	2	Q7WZT9	Q7wzt9 bacillus th
45	1434.5	38.1	1181	1	C1AE_BACTL	Q03748 bacillus th

ALIGNMENTS

RESULT 1  
CAC85964 PRELIMINARY; PRT; 719 AA.  
ID CAC85964; PRELIMINARY; PRT; 719 AA.  
AC CAC85964; PRELIMINARY; PRT; 719 AA.  
DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE Delta-endotoxin.  
GN CRYIIA.  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group; Bacillus thuringiensis.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BNS3;  
RA Tounsi S., Zouari N., Jaoua S.;  
RT "Cloning and study of the expression of a novel cryIIa-type gene from  
RT Bacillus thuringiensis subsp. kurstaki.";  
RL J. Appl. Microbiol. 95:23-28(2003).  
DR EMBL; AJ315121; CAC85964.1; -.  
SQ SEQUENCE 719 AA; 81203 MW; 8676ESA6C25DAFE8 CRC64;

Query Match	99.7%	Score	3752	DB	2	Length	719
Best Local Similarity	99.9%	Pred. No.	1.7e-252				
Matches	718	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
Qy	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLMSEYENVEPFVSASTI	60				
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLMSEYENVEPFVSASTI	60				
Qy	61	QTGIGIAGKILGTILGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120				
Db	61	QTGIGIAGKILGTILGVPFAGQVASYLSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120				
Qy	121	RNKALTDLXGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPSPAVSG	180				
Db	121	RNKALTDLXGLDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPSPAVSG	180				
Qy	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNROVERAGDYSHCVKWYS	240				
Db	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNROVERAGDYSHCVKWYS	240				
Qy	241	TGLNNLRGTNAESWRYNQFRDMLVLDLVALFFSYDTOMYPKTTAQLTREVYTDAL	300				
Db	241	TGLNNLRGTNAESWRYNQFRDMLVLDLVALFFSYDTOMYPKTTAQLTREVYTDAL	300				
Qy	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVRNPHLLDFLEQVTIYSLLSRWNSNTQYMMNW	360				
Db	301	GTVHPHPSFTSTTWYNNNAPSFAIEAAVRNPHLLDFLEQVTIYSLLSRWNSNTQYMMNW	360				
Qy	361	GGHKLFRFTIGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNGVPR	420				
Db	361	GGHKLFRFTIGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNFLTPQVNGVPR	420				

QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 Db 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSLHIGLIS 480  
 QY 481 ASHKALVSWTHRSADRTNTIEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 Db 481 ASHKALVSWTHRSADRTNTIEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMRGCDLQYK 600  
 Db 541 TGTFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQNFSAATMRGCDLQYK 600  
 QY 601 TFRVVGFTTFFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 Db 601 TFRVVGFTTFFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLTKTDVYHIDQVSNLVSLSDEFYLDKRELPEIVKYANLHIERNM 719  
 Db 661 TALFTSTNPRGLTKTDVYHIDQVSNLVSLSDEFYLDKRELPEIVKYANLHIERNM 719

RESULT 2  
 CLIA\_BACTK STANDARD; PRT; 719 AA.  
 ID AC Q45752; P71092; Q45750; Q45751; Q45756;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticial crystal protein cryIIa (Insecticidal delta-endotoxin)  
 DE CryII(a) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIa; Synonyms=cryII(a), cryV, cryV1, CGCryV;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 CX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSIR732;  
 RX MEDLINE=93298009; PubMed=8517758;  
 RA Gleave A.P., Williams R., Hedges R.J.;  
 RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
 RT serotypes for the presence of cryV-like insecticidal protein genes and  
 RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
 RT kurstaki.";  
 RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JHCC4835;  
 RX MEDLINE=92269582; PubMed=1588820;  
 RA Tailor R., Tippet J., Gibb G., Pellis S., Pike D., Jordan L., Ely S.;  
 RT "Identification and characterization of a novel Bacillus thuringiensis  
 RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";  
 RL Mol. Microbiol. 6:1211-1217(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HD-1;  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 RT thuringiensis and cloning of cryV-type genes from Bacillus  
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 RT entomocidus.";  
 RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB88;  
 RX MEDLINE=96178985; PubMed=8606196;  
 RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
 RA Craig J.A., Koziel M.G., Estruch J.J.;  
 RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
 RT thuringiensis: the cryV-encoded protein is expressed early in  
 RT stationary phase.";  
 RL J. Bacteriol. 178:2141-2144(1996).

RN SEQUENCE FROM N.A.  
 RP STRAIN=61;  
 RA Selvapandian A., Bhatnagar R.K.;  
 RT "Isolation, cloning and expression of cryV gene.";  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella and Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 EMBL; M98544; AAA22354.1; -;  
 EMBL; X62821; CAA44633.1; -;  
 EMBL; L36338; AAC36999.1; -;  
 EMBL; L49391; AAB00958.1; -;  
 EMBL; Y08920; CAA70124.1; -;  
 PIR; I39815; I39815.  
 PIR; S25383; S25383.  
 HSSP; P02965; LC1Y.  
 InterPro; IPR001178; Endotoxin.  
 InterPro; IPR005638; endotoxin\_C.  
 InterPro; IPR005639; endotoxin\_N.  
 InterPro; IPR008979; Gal\_bind\_like.  
 Pfam; PF03944; Endotoxin\_C; 1.  
 Pfam; PF00555; Endotoxin\_M; 1.  
 Pfam; PF03945; Endotoxin\_N; 1.  
 Sporulation; Toxin.  
 VARIANT 159 159 K -> R (in strain 61).  
 VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 VARIANT 443 443 A -> V (in strain AB88).  
 VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
 SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;  
 Query Match 99.5%; Score 3743; DB 1; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 7.2e-252;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHECLKSEYENVEPFSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHECLKSEYENVEPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQHEIFMEHVEEIIINQISTYA 120  
 Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQHEIFMEHVEEIIINQISTYA 120  
 QY 121 RNKALTDLKLGDALAVYHDSLSWVGNNRNNTRRSVVKSOYIALELMFVKLPFAVSG 180  
 Db 121 RNKALTDLKLGDALAVYHDSLSWVGNNRNNTRRSVVKSOYIALELMFVKLPFAVSG 180  
 QY 181 BEVPLLPITVAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGYSYHCVKWS 240  
 Db 181 BEVPLLPITVAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGYSYHCVKWS 240  
 QY 241 TGLANLRGTNAESVRYNQFRDMLTLDLVALFSDYDQWPIKTTAQLTREYVTDI 300  
 Db 241 TGLANLRGTNAESVRYNQFRDMLTLDLVALFSDYDQWPIKTTAQLTREYVTDI 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVITYLSLLSRWSNTQYMNW 360

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Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420
Db 361 GGHKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGCDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDELDYK 600
Db 541 TGTGCDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDELDYK 600
QY 601 TERTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDFEKAQEKV 660
Db 601 TERTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFIIVKYANLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFIIVKYANLHIERNM 719

RESULT 3
Q6X181
ID Q6X181 PRELIMINARY; PRT; 719 AA.
AC Q6X181;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE CryII.
GN Name=cryII;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match
Best Local Similarity 99.5%; Score 3743; DB 2; Length 719;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPVSASTI 60
Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLSWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGDLALAVYHDSLSWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240

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QY 241 TGLNLRGTNAESWYRQNRDMDTLMVLDLVALFPSYDTOMYPIKTTAQLTREYTDAI 300
Db 241 TGLNLRGTNAESWYRQNRDMDTLMVLDLVALFPSYDTOMYPIKTTAQLTREYTDAI 300
QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMNW 360
QY 361 GGHKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420
Db 361 GGHKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYYPGVAGIGTQDSENELPPEATGQPNYESYSHRLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGCDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDELDYK 600
Db 541 TGTGCDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDELDYK 600
QY 601 TERTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDFEKAQEKV 660
Db 601 TERTVGTTPFSLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFIIVKYANLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFIIVKYANLHIERNM 719

RESULT 4
AAP86782
ID AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE CryII.
GN CryII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -
DR SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match
Best Local Similarity 99.6%; Score 3743; DB 2; Length 719;
Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPVSASTI 60
Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKGDLALAVYHDSLSWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180
Db 121 RNKALTDLKGDLALAVYHDSLSWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSYHCVKWS 240

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Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWYS 240  
 QY 241 TGLNLRGTNAESWVRVYQFRDMLVLDLVALFSDYDQMPYKTTAQLTREYVTDAL 300  
 Db 241 TGLNLRGTNAESWVRVYQFRDMLVLDLVALFSDYDQMPYKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSTQYNNMW 360  
 Db 301 GTVHPHPSSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFQTQPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFQTQPVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRNTIETPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHKALVYSWTHRSADRNTIETPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 Db 541 TGTGDIRVNINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 QY 601 TFRVGTFTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVGTFTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 5

Q93NJ5 ID Q93NJ5 PRELIMINARY; PRT; 719 AA.  
 AC Q93NJ5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE CryIIa.  
 GN Names=cryIIa;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Song F., Zhang J., Gu A., Huang D., Li G.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF373207; AAK66742.1;  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 81225 MW; G629DF2C44827241 CRC64;

Query Match 99.4%; Score 3738; DB 2; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.6e-251;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINIHEDCLKMSYEYENVEPFFVSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTSLKNETDIELQINIHEDCLKMSYEYENVEPFFVSASTI 60

QY 61 QTGIGIAGKILGTLPVPAQVAVSLYSLFGLWPKGNQWEIEMEHVEEIIINOKISTYA 120  
 Db 61 QTGIGIAGKILGTLPVPAQVAVSLYSLFGLWPKGNQWEIEMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGLDALAVYHDSLESWGNNRNTARSVVKSOYIALELMFVKQLPSFAVSG 180  
 Db 121 RNKALTDLKGLDALAVYHDSLESWGNNRNTARSVVKSOYIALELMFVKQLPSFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWYS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKWYS 240  
 QY 241 TGLNLRGTNAESWVRVYQFRDMLVLDLVALFSDYDQMPYKTTAQLTREYVTDAL 300  
 Db 241 TGLNLRGTNAESWVRVYQFRDMLVLDLVALFSDYDQMPYKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSTQYNNMW 360  
 Db 301 GTVHPHPSSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSTQYNNMW 360  
 QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFQTQPVNGVPR 420  
 Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGNLFQTQPVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRNTIETPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHKALVYSWTHRSADRNTIETPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 Db 541 TGTGDIRVNINPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 QY 601 TFRVGTFTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 Db 601 TFRVGTFTPFSLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDHYDQVSNLVESLSDDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 6

O85796 ID O85796 PRELIMINARY; PRT; 719 AA.  
 AC O85796;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Insecticidal protein.  
 GN Name=cryVI01;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OG Plasmid large plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SL01;  
 RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF076953; AAC26910.1;  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.

DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Plasmid.  
SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
  
Query Match  
Best Local Similarity 99.3%; Score 3737; DB 2; Length 719;  
Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFSASTI 60  
DB 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
  
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180  
  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
  
QY 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVLFPSYDTQMPYIKTTAQLTREVTYDAI 300  
DB 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVLFPSYDTQMPYIKTTAQLTREVTYDAI 300  
  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360  
  
QY 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
DB 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
  
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480  
  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
  
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
  
QY 601 TFRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
DB 601 TFRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 7  
Q8XY61 PRELIMINARY; PRT; 719 AA.  
ID Q8XY61  
AC Q8XY61;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Cry.  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Porcar M., Martinez C., Caballero P.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF278797; AAM73516.1; -.  
DR PIR; B42459; B42459.  
DR HSSP; P02965; 1CIY.  
DR CO; GO:0005102; F:receptor binding; IEA.  
DR CO; GO:0006952; P:defense response; IEA.  
DR CO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;  
  
Query Match  
Best Local Similarity 95.9%; Score 3608; DB 2; Length 719;  
Matches 689; Conservative 13; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEPFSASTI 60  
DB 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKISEYENVEPFSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
  
QY 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180  
DB 121 RNKALTDLKGGLDALAVYHDSLESWGNNRNTARSVVKSQYIALELMFVKLPSPAVSG 180  
  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWS 240  
  
QY 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVLFPSYDTQMPYIKTTAQLTREVTYDAI 300  
DB 241 TGLNNLRGTNAESWVRYNQFRDMLMVLVLFPSYDTQMPYIKTTAQLTREVTYDAI 300  
  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360  
DB 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWNSNTQYNNMW 360  
  
QY 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
DB 361 GGHKLEPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
  
QY 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS 480  
  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
  
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
  
QY 601 TFRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
DB 601 TFRTVGFTTTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 8  
Q9F0P8 PRELIMINARY; PRT; 719 AA.  
ID Q9F0P8  
AC Q9F0P8;

DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE CrvII.  
 GN Name=crvII;  
 OS Bacillus thuringiensis.  
 OG Plasmid pBTC19.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BTC007;  
 RX MEDLINE=22837682; PubMed=12957903;  
 RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,  
 HU Y., Li G., Huang D.;  
 RT "Identification of crvII-type genes from Bacillus thuringiensis  
 strains and characterization of a novel crvII-type gene";  
 RL Appl. Environ. Microbiol. 69:5207-5211(2003).  
 DR EMBL; AF211190; AG43526.1; -;  
 DR HSSP; P02965; ICIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid.  
 SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

Query Match 93.9%; Score 3534; DB 2; Length 719;  
 Best Local Similarity 93.2%; Pred. No. 2.6e-237;  
 Matches 670; Conservative 27; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 MKLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLMSEYENVEPVSASTI 60  
 DB 1 MKLKNQKHQSLSSNAKVDKIATDSLKNETDIELKNINHEFLRSEHESIDPVSASTI 60  
 QY 61 QTGICGKILGTGVPAGOVASLYSPILGELWPKGNQWEIFMEHVEELINOKISTYA 120  
 DB 61 QTGICGKILGTGVPAGOVASLYSPILGELWPKGNQWEIFMEHVEELIDOKISTYA 120  
 QY 121 RNKALTDLGLDALAVTHDSLSWGNRNTRARVSKSOYIALELMFVKLPSPAVSG 180  
 DB 121 RNIALADLGLDALAVTHESLESWKRNARATSVVKSQYIALELLFVKLPSPAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGDYSHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASVFGKEWGLSNSQISTFNNRQVERTSDYSDHCVKWS 240  
 QY 241 TGLNLRGTNAESWVRVYNOFRDMLTMLVLDLVALFPSTDTQMPYIKTTAQLTREYITDAI 300  
 DB 241 TGLNLRGTNAESWVRVYNOFRDMLTMLVLDLVALFPSTDTQMPYIKTTAQLTREYITDAI 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
 DB 301 GTVHPNASFSTWYNNNAPSFAIESAAVRNPHLLDFLEQVTIYSLLSWSNTQYNNMW 360  
 QY 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
 DB 361 GGHRLFRITGGVLTNTSQSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPR 420  
 QY 421 VDFHWKFTVTHPIASDNFFYPGYAGIGTQLQDSENEIPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFFYPGYAGIGTQLQDSENEIPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTIENPNTSQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTIENPNTSQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540

QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600  
 DB 541 TGTGDIRVNINPPFAQRYRVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDDLYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAYEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAYEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

## RESULT 9

CLIB\_BACTE  
 ID CLIB\_BACTE STANDARD; PRT; 719 AA.  
 AC Q45709;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin  
 CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;  
 OS Bacillus thuringiensis (subsp. entomocidus).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1436;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BP465;  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 thuringiensis and cloning of cryV-type genes from Bacillus  
 thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 entomocidus";  
 RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
 CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella but not on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 sporulation and is accumulated both as an inclusion and as part of  
 the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; U07642; AA02114.1; -;  
 DR EIR; 140590; 140590.  
 DR HSSP; P02965; ICIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81295 MW; E8210ABAE97688E CRC64;

Query Match 93.1%; Score 3503; DB 1; Length 719;  
 Best Local Similarity 92.5%; Pred. No. 3.7e-235;  
 Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 MKLKNQKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLMSEYENVEPVSASTI 60

Db 1 M K L N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H S I D P F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q I S T Y A 120  
Db 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K S Q W E I F M E H V E E I I N Q I S T Y A 120  
QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
Db 121 R N K A L S D L R G L G D A L A V Y H S L E S W E N R N N T R A R S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V R A G D Y S H C V K W Y S 240  
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240  
QY 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
Db 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V Y P I K T T S Q L T R E V Y T D A I 300  
QY 301 G T V H P H P F T S T T W Y N N N A P S F A I E A A V V R N P H L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
Db 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L D F L E K V T I Y S L L S R W S N T Q Y M N W 360  
QY 361 G G H K L E F R T I G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T O P V N G V P R 420  
Db 361 G G H R L E S P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G N L F L T O P V N G V P R 420  
QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
Db 421 V D F H W K F T L P I A S D N F Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
QY 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R T N 540  
Db 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R T N 540  
QY 541 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D I Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
Db 541 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D I Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
QY 601 T F R T V G F T T P F S D V O S T F T I G A M F S S G N E V Y I D R I E F V P V E Y T E A E Y D F E K A Q S K V 660  
Db 601 T F T I G T T P F S D V O S T F T I G A M F S S G N E V Y I D R I E F V P V E Y T E A E Y D F E K A Q S K V 660  
QY 661 T A L T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
Db 661 T A L T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719

RESULT 10  
CLID BACTU STANDARD; PRT; 719 AA.  
AC Q9XDL1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryII (Insecticidal delta-endotoxin  
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIId; Synonyms=cryII(d), NRcryV;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]

SEQUENCE FROM N.A.  
STRAIN=BR30;  
RX MEDLINE=20374042; PubMed=10919402;  
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
RT gene."  
RL Curr. Microbiol. 41:65-69(2000).  
CC -!-FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
CC epithelial cells of many lepidopteran larvae. Active on Plutella  
CC xylostella and on Bombyx mori.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of

CC the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF047579; AAD44366.1; -.  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal bird like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
CC Sporulation; Toxin.  
CC SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 89.8%; Score 3380; DB 1; Length 719;  
Best Local Similarity 89.4%; Pred. No. 1.4e-226;  
Matches 643; Conservative 36; Mismatches 40; Indels 0; Gaps 0;

QY 1 M K L N Q D K H Q S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
Db 1 M K S K N Q M Y R S F S S N A T V D K S F T D P L E H N T N M E L Q N S H E D C L K M S E Y E S V E P F V S V S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q I S T Y A 120  
Db 61 Q T G I G I A G K I L G N L G V P P A G Q V A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q I S T Y A 120  
QY 121 R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
Db 121 R N K A L A D L K G L G D A L A V Y H S L E S W I E N R N T R V S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V R A G D Y S H C V K W Y S 240  
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S E S E I S T F Y N Q S S Q T Q E Y S D Y C S E W Y N 240  
QY 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
Db 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T R M Y P I P T S A Q L T R E V Y T D A I 300  
QY 301 G T V H P H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
Db 301 G T V H P N A S P A S T T W Y N N N A P S F S T I E A A V V R N P H L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
QY 361 G G H K L E F R T I G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T O P V N G V P R 420  
Db 361 G G H K L E F R T I G T L N T S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T O P V N G V P R 420  
QY 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
QY 481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G F T G G D I L R T N 540  
Db 481 A S H V K A L Y S W T H R S A D R T N T I N S D S I T Q I P L V K A F N L P S G A S V V R G P G F T G G D I L Q R T N 540  
QY 541 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D I Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
Db 541 T G T F G D I R V N I N P P F A Q R Y R L R Y A S T T N L E F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
QY 601 T F R T V G F T T P F S D V O S T F T I G A M F S S G N E V Y I D R I E F V P V E Y T E A E Y D F E K A Q S K V 660  
Db 601 A F R T V G F T T P F S P N A Q S T F T I G A M F S L G N E V Y I D R I E F V P V E Y T E A E Y D L K K A Q D E I 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSEDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 661 TAMFTSTNLRRLKTNVTCHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLNIERNM 719

RESULT 11  
 C11C BACTU STANDARD; PRT; 719 AA.  
 AC 087404;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin)  
 DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIc; Synonyms=cryII(c);  
 OS Bacillus thuringiensis.  
 OG Plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C18 / Egypt;  
 RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of insects.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.

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 CC EMBL; AF056933; AAC62933.1; -.  
 CC HSSP; P02965; ICY.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin\_C.  
 CC InterPro; IPR005639; endotoxin\_N.  
 CC InterPro; IPR008979; Gal\_bind\_like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Plasmid; Sporulation; Toxin.  
 KW SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;  
 SQ

Query Match 89.8%; Score 3379; DB 1; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 1.6e-226;  
 Matches 645; Conservative 34; Mismatches 40; Indels 0; Gaps 0;

QY 1 MKLNQDKHGFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSYENVEPFSASTI 60  
 Db 1 MKLNKPKDKQTLSSNAKVDKIATDSLKNETDIELKNNEDYLRSEHESIDPFSASTI 60

QY 61 QTGIGIAGKILGTGVPFAGQVASYLSYFGLGELWPKGKNOWEIFMEHVERIINOKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSYFGLGELWPKGKNOWEIFMEHVERIINOKISTYA 120

QY 121 RNKALTDLKGLDALAVVHDSLSWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGLDALAVVHDSLSWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWEGLSSSEISTFYNROVERAGDYSYHCVKWYS 240  
 Db 181 BEVPLPIYAQAANLHLLLRDASIFGKWEGLSSSEISTFYNROVERAGDYSYHCVKWNN 240

QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLVLFPSYDTCMPYIKTKTAQLTREVTDAI 300  
 Db 241 TGLNLRATNGQSWVRYNQFRDKIDIELMVLVLRVFPSTYDILVPIKTSQLTREVTDAI 300

QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRPHLLDLEQVTTISLLSWSNTQYMMNW 360  
 Db 301 GTVDPNQALRSTTWYNNNAPSFAIEAAVVRPHLLDLEQVTTISLLSWSNTQYMMNW 360

QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYSFESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHRLSRRPIGGALNTSQGSTNTSINPVTLPFTSRDVRYSFESLAGLNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYYPGYAGIGTQDSSENELEPPATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHWKFTPLPIASDNFYYPGYAGIGTQDSSENELEPPATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 GSHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540

QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASATDLPQFTSINGKAINQGNFSATMNRGDDLYK 600  
 Db 541 SGTGHIRVNIINPPFAQRYRVRIRYASATDLPQFTSINGKAINQGNFSATMNRGDDLYK 600

QY 601 TFRVTGFTTFFSFLDVQSTFTTICAWNFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQEKV 660  
 Db 601 TFRVTGFTTFFSFLDVQSTFTTICAWNFSSGNEVYIDRIEFPVPEVTEAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSEDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHIERNM 719

## RESULT 12

C1BB BACTU STANDARD; PRT; 1229 AA.  
 ID Q1BB BACTU STANDARD; PRT; 1229 AA.  
 AC Q45739;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIBb (Insecticidal delta-endotoxin)  
 DE CryIIB(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN Name=cryIIBb; Synonyms=cryIIB(b), cryET5;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL B-21110 / EG5847;  
 RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;  
 RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins  
 RT toxic to lepidopteran insects."  
 RL Patent number US5322687, 21-JUN-1994.  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.

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 CC EMBL; L32020; AAA22344.1; -.  
 CC HSSP; P02965; ICY.  
 CC InterPro; IPR001178; Endotoxin.

DR	InterPro; IPR005638; endotoxin_C.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DR	InterPro; IPR005639; endotoxin_N.	OX	NCBI_TaxID=1441;
DR	InterPro; IPR008979; Gal bind like.	RN	[1]
DR	Pfam; PF03944; Endotoxin_C; 1.	RP	SEQUENCE FROM N.A.
DR	Pfam; PF00555; Endotoxin_M; 1.	RA	Bishop A.H., Bone E.J., Ellar D.J.;
DR	Pfam; PF03945; Endotoxin_N; 1.	RT	"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
KW	Sporulation; Toxin.	RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
SQ	SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;	CC	-!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut epithelial cells of insects.
Query Match 64.8%; Score 2437.5; DB 1; Length 1229;			
Best Local Similarity 65.4%; Pred. No. 1.3e-160;			
Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;			
QY	13 SSNAKVDKISTDSLKN-ETDIELO-NINHEDCMKSEYENVEPFVSASTIQTGIGIAGKI 70	CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
DB	7 NENEIINALSIPTVSNPSTQMNLSPPDARIEDSLCVAEVNNDPFSVASTVQTGINIAGRI 66	CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
QY	71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEELINQKISTYARNKALTDLKG 130	CC	-!- SIMILARITY: Belongs to the delta endotoxin family.
DB	67 LGVLGVPPAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQVVTENTRTAARLEG 126	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
QY	131 LGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSGEEVPLPIYA 190	DR	EMBL; Z46442; CAA86568.1; -.
DB	127 LGRGYSYQQALLETWLDNRNDARSRIILERYVALELDITTAIFLRIRNEEVPLLMVYA 186	DR	HSSP; P02965; 1CIY.
QY	191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSHCVKMYSTGLNNLRGTN 250	DR	InterPro; IPR001178; Endotoxin.
DB	187 QAAHLHLLLRDASLFGSEWGMASSDVQYQEQIRYTEESNHCQVWNTGLNNLRGTN 246	DR	InterPro; IPR005638; endotoxin_C.
QY	251 AESWVRNQFRDMDTLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDGIVTVPHPSPFT 310	DR	InterPro; IPR005639; endotoxin_N.
DB	247 AESWLRNQFRDMDTLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDGIVTVPHPSPFT 306	DR	InterPro; IPR008979; Gal bind like.
QY	311 STTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNMGHKLERTI 370	DR	Pfam; PF03944; Endotoxin_C; 1.
DB	307 STWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNMGHKLERTI 366	DR	Pfam; PF00555; Endotoxin_M; 1.
QY	371 GGTINISTQGST-NTSINPVTLPFTSRDVRVTESLAGNLFLTPQVNGVPRVDFHWKFTV 429	DR	Pfam; PF03945; Endotoxin_N; 1.
DB	367 GGTINISTQGST-NTSINPVTLPFTSRDVRVTESLAGNLFLTPQVNGVPRVDFHWKFTV 422	KW	Sporulation; Toxin.
QY	430 HPIASDNFYYPG-----YAGIGTQLQDSSENEPEATGQPNYESYSHRLSHIGLISAS 482	SQ	SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;
DB	423 --INPQNIYERGATTYSQPYQGVGIQFDSETELPETTERPNYESYSHRLSHIGLIGN 480	Query Match 64.8%; Score 2437.5; DB 1; Length 1233;	
QY	483 HVKALVSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542	Best Local Similarity 65.4%; Pred. No. 1.4e-160;	
DB	481 TRAPVSWTHRSADRTNTPNSITQIPLVKALNLHSGVTVVGPGFTGGDILRRNTG 540	Matches 469; Conservative 90; Mismatches 141; Indels 17; Gaps 6;	
QY	543 TFGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAIWMRGEDLDYKTF 602	QY	13 SSNAKVDKISTDSLKN-ETDIELO-NINHEDCMKSEYENVEPFVSASTIQTGIGIAGKI 70
DB	541 TFGDIRVNINPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSAIWMRGEDLDYKTF 600	DB	7 NENEIINALSIPTVSNPSTQMNLSPPDARIEDSLCVAEVNNDPFSVASTVQTGINIAGRI 66
QY	603 RTVGFTTFFSLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTA 662	QY	71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEELINQKISTYARNKALTDLKG 130
DB	601 RTAGFSTPFFNLNAQSTFTLGAQSPFN-QEVYIDRVFPVPAEVTFAEYDLERAQKAVNA 659	DB	67 LGVLGVPPAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQVVTENTRTAARLEG 126
QY	663 LFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYIDKEKELFEIVKYANELHIERNM 719	QY	131 LGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPSPFAVSGEEVPLPIYA 190
DB	660 LFTSTNPRGLKTDVYHIDQVSNLVESLSEDFYIDKEKELFEIVKYANELHIERNM 716	DB	127 LGRGYSYQQALLETWLDNRNDARSRIILERYVALELDITTAIFLRIRNEEVPLLMVYA 186
RESULT 13			
CIBC_BACTM STANDARD; PRT; 1233 AA.			
ID	CIBC_BACTM	AC	Q45774;
DT	30-MAY-2000 (Rel. 39, Created)	DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)	DT	05-JUL-2004 (Rel. 44, Last sequence update)
DE	Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin)	DE	Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin)
DE	CryIbC(c) (Crystalline entomocidal protoxin) (140 kDa crystal protein).	DE	CryIbC(c) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN	Name=cryIbC; Synonyms=cryIb(c), cryIbC;	GN	Name=cryIbC; Synonyms=cryIb(c), cryIbC;
OS	Bacillus thuringiensis (subsp. morrisoni).	OS	Bacillus thuringiensis (subsp. morrisoni).

```

Db 481 TLRAVYVSWTHRSADRTNTIGPNRITQPLVKALNLHSGVTVVGGPGFTGGDILRRNTIG 540
QY 543 TFGDIRVNPFPFAQRYRVIRYASTTDLQFHTSINGKALNQGNFSATWNGEDLDYKTF 602
Db 541 TFGDIRLNVPLSQRYRVIRYASTTDLQFTRINGTTVNGNFSRTWNRGNLRYRSF 600
QY 603 RTVGFTTSPFLDVQSTFTIGAMNFSNGEVYIDRIEFVPEVTEYAEYDFEKAQKVTA 662
Db 601 RTAGFSTPNFLNAQSTFTLGAQSFN-QEYVIDRVEFVPAEVTEYAEYDFEKAQKVTA 659
QY 663 LFTSTNPRGLKTDVKDHYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719
Db 660 LFTSTNPRRLKTDVTDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 716

RESULT 14
Q93T75 PRELIMINARY; PRT; 1228 AA.
AC Q93T75;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Delta-endotoxin CrylBa2.
GN Name=crylBa2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.2%; Score 2263.5; DB 2; Length 1228;
Best Local Similarity 62.4%; Pred. No. 1.8e-148;
Matches 447; Conservative 79; Mismatches 165; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQVNIH-----EDCLKMSYEYENVEPVSASTTQTGTGIGIAGKI 70
Db 2 TSNRKNEEILNAVSNHSAQMDDLDPDARIEDSLCIAEGNIDPFVSASTVQTGINIAGRI 61
QY 71 LGTLGVPEAGQVASYLSFTLGLWPKGNQWEIFMEHVEEIKNISTYARNKALTDLKG 130
Db 62 LGVLGVPPFAGQLASFYSLVGLWPRGRDQWEIFLEHVEQLNQITENARNTALRLOG 121
QY 131 LGDALAVYHDSLESWVGNNTRARSVVVKSQVIALELMFVQKLPSFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQOSLEDWLENRDDARTSVLHTQYIALELDLFLNAPLFAIRNQEVPLMVYA 181
QY 191 QAAHLHLLLRDASIFGKWLSSSESTFYNRQVERAGDYSYHCVKWYTGNNLRGTN 250
Db 182 QAAHLHLLLRDASIFGSEFGLTSQEIQRYYERQVERTRDYSYCVVEWYNTGLSLRGTN 241
QY 251 AESWRYNQFRDRLTLMVLDLVALFPSPYDTQMPYIKTAQLTREYVTDAGTVPHPSFT 310
Db 242 AASWRYNQFRDRLTLMVLDLVALFPSPYDTQMPYIKTAQLTREYVTDAGTVPHPSFT 299
QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTVISLLSRVSNSTQVYNNMGHKLFEFTI 370

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Db 300 SMWYNNAPSFSAIEAAAIRSPHLLDLEQVTVISLLSRVSNSTQVYNNMGHKLFEFTI 359
QY 371 GGTLNISTOGSTNTSINPVTLPFTSRDVTSTESLAGNLFF--LTQPVNGVPRVDFHWKFV 428
Db 360 GGGLNTSTGATNTSINPVTLPASRDVYRTSYAGVLLWGIYLEPIHGVTVRNF--- 416
QY 429 THP-----IASDNFYPGVAGICTQLQDSENLPEATQPNYESYSHRLSHIGLISASH 483
Db 417 TNPNQISDRGTANYSQP-YESQGLQKQDSELTPEPETERYESYSHRLSHIGLISASH 475
QY 484 VKALVYSWTHRSADRTNTIGPNRITQPLVKALNLHSGVTVVGGPGFTGGDILRRNTIG 543
Db 476 VNPVYVSWTHRSADRTNTIGPNRITQPLVKALNLHSGVTVVGGPGFTGGDILRRNTIG 535
QY 544 FGDIRVNPFPFAQRYRVIRYASTTDLQFHTSINGKALNQGNFSATWNGEDLDYKTF 603
Db 536 FGIPIRVTVNGPLTQRYRIGFRYASTVDFPFVSRGGTAVNFRFLRTMNSGDELKYGNFV 595
QY 604 TVGFTTSPFLDVQSTFTIGAMNFSNGEVYIDRIEFVPEVTEYAEYDFEKAQKVTA 663
Db 596 RRAFTTPTFTQIQDIIRTSIQGLSNGEYIDKIEIPVTATFEAEYDLERAQAVNAL 655
QY 664 FTSNPRGLKTDVKDHYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719
Db 656 FTNTPRRLKTDVTDYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 711

RESULT 15
C1BA_BACTK STANDARD; PRT; 1228 AA.
AC P05517; Q45731;
DT 01-NOV-1998 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein crylBa (Insecticidal delta-endotoxin CrylB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=crylBa; Synonyms=crylB(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RC MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis."
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
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DR EMBL; X06711; CAA29898.1; -
DR EMBL; X95704; CAA65003.1; -

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Query Match	Best Local Similarity	Score	DB 1;	Length
PIR; S00873; S00873.	60.1%;	2262.5;	DB 1;	Length 1228;
HSSP; P07130; IDLC.	62.4%;	Pred. No. 2.1e-148;		
InterPro; IPR001178; Endotoxin.	79;	Mismatches 165;	Indels 25;	Gaps 6;
InterPro; IPR005638; endotoxin_C.				
InterPro; IPR005639; endotoxin_N.				
InterPro; IPR008979; Gal_bind_Like.				
Pfam; PF03944; Endotoxin_C; 1.				
Pfam; PF00555; Endotoxin_M; 1.				
Pfam; PF03945; Endotoxin_N; 1.				
Spurulation; Toxin.				
VARIANT 150	150	Y -> H (in strain HD-110).		
SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;				
23	TDLKNKNETDIELQNH-----	EDCLKMSEYENVEPFVSASTQTGIGIAGKI	70	
2	TSNRKNEEIIIAVNSHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI	61		
71	LGLTGVPPAGQVASLYSFILGELWPKGKNQWEIEMEHVEEIIINOKISTYARNKALTDLKG	130		
62	LGVLGVPPAGQLASFYSLVGEUWPRGRDQWEIHFLEHVEQLINQOITENARNTALARLOG	121		
131	LGDALAVYHDSLESWGVRNNTARSVVKSQYIALELMFVKQLPSFAVSGEEVPLPIYA	190		
122	LGDSFRAYQQSLEDWLENRDDARTSRVLTQYIALELDFLNAMEPLFAIRNQEVEPLLMVYA	181		
191	QAANLHLLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSYHCVKVSTGLNNLRGYN	250		
182	QAANLHLLLLRDASLFGSEFGLTSQEIQRYYERQVERTDYSYCVIEWYNTGLNSLRGIN	241		
251	ASWVRVYNOFRDRMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVYTDAGTVHPHPST	310		
242	AASWVRVYNOFRDRDLTGLVDLVALFPSYDTQMPYIKTTAQLTREYVYTDAGTVHPHPST	299		
311	STTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNMGHKLFRTI	370		
300	SMWYNNNAPSFAIEAAAIRSRPHLLDFLEQLTIFASRWSNTRHMTYWRGHTIQSRPI	359		
371	GGTLNISTGGSTNTSINPVTLPFTSRDVRVYRTESLAGLNLF--LTQPVNGVPRVDHFHKFV	428		
360	GGGLNTSTHGATNTSINPVTLPFASRDVYRTESYAGVLLWGIYLEPIHGVPTVRFNF---	416		
429	THP-----IASDNFYPCYAGICTQLQDSENELPPEATGQPNVYESYHSLSHIGLISASH	483		
417	TNPQNISDRGTANYSQP--YESPGIQLKDSLETLPPTETTERPNVYESYHSLSHIGIILQSR	475		
484	UKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILERTNTGT	543		
476	VNVVYVSWTHRSADRTNTIGPNRITQIPMKASLPGQTTVVRGPGFTGGDILERTNTGG	535		
544	FGDIRVNIPTPAQRVRIYRISTATDLQFHTSINGKAINQGNFSATMNRGEDILDYKTFPR	603		
536	FGPIRVTVNGPLTQRYRTGFRYASTVDFFVSRGGTTVNNFRLRTMWSGDELYKGNFV	595		
604	TVGFTTPSFLDQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEKVTAL	663		
596	RRAFITPFTFTQIIDIIRTSIQGLSNGNEVYIDKIEIIPVTATFEAEYDLERAQEAVAL	655		
664	FTSTNPRGLKTDVKDYHIDQVSNLVSISLDEFYLDKEKRELFEIVKYANLHIERNM	719		
656	FTNTNPRGLKTDVYHIDQVSNLVLACLSDEFCLDEKRELLEKVKYAKRLSDERNL	711		

Search completed: October 28, 2004, 18:29:54  
Job time : 101.579 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-57

Perfect score: 3760

Sequence: 1 MKLXNQDKHQSFSSNAKVDK.....KRELFEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3756	99.9	719	1	CI1A_BACTK	Q45752 bacillus th
2	3756	99.9	719	2	A6X181	Q6x181 bacillus th
3	3756	99.9	719	2	AAP86782	AAP86782 bacillus
4	3751	99.8	719	2	Q93N35	Q93N35 bacillus th
5	3750	99.7	719	2	O85796	O85796 bacillus th
6	3748	99.7	719	2	CAC85964	CAC85964 bacillus
7	3621	96.3	719	2	O8X161	O8X161 bacillus th
8	3547	94.3	719	2	Q9F0P8	Q9F0P8 bacillus th
9	3516	93.5	719	1	CI1B_BACTE	Q45709 bacillus th
10	3393	90.2	719	1	CI1D_BACTU	Q9Xdl1 bacillus th
11	3373	89.7	719	1	CI1C_BACTU	O87404 bacillus th
12	2445.5	65.0	1229	1	CI1B_BACTU	Q45739 bacillus th
13	2445.5	65.0	1233	1	CI1C_BACTM	Q45774 bacillus th
14	2277.5	60.6	1228	2	Q93T75	Q93T75 bacillus th
15	2276.5	60.5	1228	1	CI1A_BACTK	P05517 bacillus th
16	2268.5	60.3	1228	2	Q93NM5	Q93NM5 bacillus th
17	2195.5	58.4	849	2	Q6PYW8	Q6PYW8 bacillus th
18	2195.5	58.4	849	2	AAS93797	AAS93797 bacillus
19	2195.5	58.4	1227	1	CI1E_BACTU	O85805 bacillus th
20	2111.5	56.2	1231	2	O8KNY2	O8KNY2 bacillus th
21	2106.5	56.0	1231	1	CI1D_BACTZ	Q9Zaz5 bacillus th
22	1984.5	52.8	1215	1	CI1A_BACTM	Q45715 bacillus th
23	1904	50.6	381	2	Q45740	Q45740 bacillus th
24	1669.5	44.4	1157	1	C8AA_BACUK	Q45704 bacillus th
25	1660	44.1	1144	2	O8KZL7	O8KZL7 bacillus th
26	1494	39.7	1157	1	C9CA_BACTO	Q45733 bacillus th
27	1485.5	39.5	1169	1	C8BA_BACUK	Q45705 bacillus th
28	1482.5	39.4	1166	1	CI1A_BACTU	Q45746 bacillus th
29	1482	39.4	1167	1	CI1A_BACTU	Q45738 bacillus th
30	1475	39.2	1169	1	CI1E_BACTM	O66377 bacillus th
31	1469	39.1	1174	2	Q45749	Q45749 bacillus th

32	1465	39.0	1155	1	CI1A_BACTK	P06578 bacillus th
33	1465	39.0	1155	2	Q7BE98	Q7BE98 bacillus th
34	1465	39.0	1155	2	Q9F296	Q9F296 bacillus th
35	1465	39.0	1155	2	AA76494	AA76494 bacillus
36	1465	39.0	1155	2	AAO13302	AAO13302 bacillus
37	1463	38.9	1118	2	Q9AM83	Q9AM83 bacillus th
38	1460	38.8	1156	2	Q6GUAY	Q6GUAY bacillus th
39	1458.5	38.8	1180	2	Q9S5V8	Q9S5V8 bacillus th
40	1457.5	38.8	1176	2	Q7WZT9	Q7WZT9 bacillus th
41	1455	38.7	1177	2	Q6EIX3	Q6EIX3 bacillus th
42	1453	38.6	1155	2	Q93T21	Q93T21 bacillus th
43	1452.5	38.6	793	2	Q6PYW7	Q6PYW7 bacillus th
44	1452.5	38.6	793	2	AAS93798	AAS93798 bacillus
45	1451.5	38.6	1176	2	Q45736	Q45736 bacillus th

ALIGNMENTS

RESULT 1

CI1A_BACTK	STANDARD;	PRT;	719 AA.
AC	Q45752; P71092; Q45750; Q45751; Q45756;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	05-JUL-2004 (Rel. 44, Last sequence update)		
DE	Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin)		
DE	CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).		
GN	Name=cryIIa; Synonyms=cryII(a), cryV, cryVI, CGCryV;		
OS	Bacillus thuringiensis (subsp. kurstaki).		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=29339;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=DSIR732;		
RX	MEDLINE=93298009; PubMed=8517758;		
RA	Gleave A.F., Williams R., Hedges R.J.;		
RT	"Screening by polymerase chain reaction of Bacillus thuringiensis		
RT	serotypes for the presence of cryV-like insecticidal protein genes and		
RT	characterization of a cryV gene cloned from B. thuringiensis subsp.		
RT	kurstaki."		
RL	Appl. Environ. Microbiol. 59:1683-1687(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=JHCC4835;		
RX	MEDLINE=92269582; PubMed=1588820;		
RA	Tailor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;		
RT	"Identification and characterization of a novel Bacillus thuringiensis		
RT	delta-endotoxin entomocidal to coleopteran and lepidopteran larvae."		
RL	Mol. Microbiol. 6:1211-1217(1992).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=HD-1;		
RX	MEDLINE=95314293; PubMed=7793960;		
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;		
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus		
RT	thuringiensis and cloning of cryV-type genes from Bacillus		
RT	thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.		
RT	entomocidus."		
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AB88;		
RX	MEDLINE=96178985; PubMed=8606196;		
RA	Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.;		
RT	Craig J.A., Koziel M.G., Estruch J.J.;		
RT	"Cloning of a cryV-type insecticidal protein gene from Bacillus		
RT	thuringiensis: the cryV-encoded protein is expressed early in		
RT	stationary phase."		
RL	J. Bacteriol. 178:2141-2144(1996).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=61;		

RA Selvapandian A., Bhatnagar R.K.;  
RT "Isolation, cloning and expression of cryV gene."  
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
CC epithelial cells of certain coleopteran and lepidopteran species.  
CC Active on Plutella xylostella and Bombyx mori.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M98544; AAA23354.1; -  
CC EMBL; X62821; CAA44633.1; -  
CC EMBL; L36338; AAC36999.1; -  
CC EMBL; L49391; AAB00958.1; -  
CC EMBL; Y08920; CAA70124.1; -  
CC PIR; I39815; I39815.  
CC PIR; S25383; S25383.  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal\_bind\_Like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
FT VARIANT 159 159 K -> R (in strain 61).  
FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
FT VARIANT 233 233 1).  
FT VARIANT 443 443 A -> V (in strain AB88).  
FT VARIANT 711 712 -KQ -> NE (in strain HD-1 and strain 61).  
SQ SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
  
Query Match  
Best Local Similarity 99.9%; Score 3756; DB 1; Length 719;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60  
  
QY 61 QTGIGTAGKILGTLGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEINQKISTYA 120  
DB 61 QTGIGTAGKILGTLGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEINQKISTYA 120  
  
QY 121 RNKALTDLKGIGDALAVYHDSLESWGVRNNTARSVVKVKSQYIALELMFVQKLPFAVSG 180  
DB 121 RNKALTDLKGIGDALAVYHDSLESWGVRNNTARSVVKVKSQYIALELMFVQKLPFAVSG 180  
  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSCHVKWYS 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSCHVKWYS 240  
  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREYVTDAL 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREYVTDAL 300  
  
QY 301 GTVHPSPFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRMSNTQYMNW 360  
DB 301 GTVHPSPFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRMSNTQYMNW 360  
  
QY 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFQTQVNGVPR 420

DB 361 GGHKLEFRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFQTQVNGVPR 420  
QY 421 VDFHKKFVTHPIASDNFYVGYVIGITQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHKKFVTHPIASDNFYVGYVIGITQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVXALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVGPGFTGGDILRRTN 540  
DB 481 ASHVXALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVGPGFTGGDILRRTN 540  
QY 541 TGTGDIRVNNPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 600  
DB 541 TGTGDIRVNNPPFAQRYRIRYASTDLOFHTSINGKAINQGNFSATNMGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
DB 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
  
RESULT 2  
Q6X181 PRELIMINARY; PRT; 719 AA.  
AC Q6X181;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE CryII.  
GN Name=CryII;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY262167; A286782.1; -  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_Like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
SQ SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
  
Query Match  
Best Local Similarity 99.9%; Score 3756; DB 2; Length 719;  
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLNKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60  
  
QY 61 QTGIGTAGKILGTLGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEINQKISTYA 120  
DB 61 QTGIGTAGKILGTLGVPPAGQVASYLSPILGELWPKGNQWEIFMEHVEEINQKISTYA 120  
  
QY 121 RNKALTDLKGIGDALAVYHDSLESWGVRNNTARSVVKVKSQYIALELMFVQKLPFAVSG 180  
DB 121 RNKALTDLKGIGDALAVYHDSLESWGVRNNTARSVVKVKSQYIALELMFVQKLPFAVSG 180  
  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSCHVKWYS 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSCHVKWYS 240  
  
QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREYVTDAL 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREYVTDAL 300

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QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYXNMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYXNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGEDLDYK 600
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGEDLDYK 600
QY 601 TPTVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TPTVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3
ID AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (TremBLrel. 27, Created)
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TremBLrel. 27, Last annotation update)
DE CryII.
GN CryII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T01 328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RT "Complete sequence of cry.II gene of isolate T01 328 from Bacillus
RT thuringiensis from Cubatao (SP - Brazil) soil.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 99.9%; Score 3756; DB 2; Length 719;
Best Local Similarity 99.9%; Pred. No. 1.1e-252;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCLKMEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCLKMEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120
QY 121 RNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSFAVSG 180
DB 121 RNKALTDLKLGDALAVYHDSLESWGNRNNTARSVVKSQYIALELMFVQKLPSFAVSG 180
QY 181 EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNQVERAGDYSBCHVKWYS 240
DB 181 EEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISFTYNQVERAGDYSBCHVKWYS 240

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QY 241 TGLNNLRGTNAESWVRYNQFRDMTMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300
DB 241 TGLNNLRGTNAESWVRYNQFRDMTMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300
QY 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYXNMW 360
DB 301 GTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYXNMW 360
QY 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
DB 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
QY 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
DB 421 VDFHWKFTVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGEDLDYK 600
DB 541 TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATNRGEDLDYK 600
QY 601 TPTVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TPTVTGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
ID Q93NJ5 PRELIMINARY; PRT; 719 AA.
AC Q93NJ5;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE CryIIa.
GN Name=cryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1; -.
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 99.8%; Score 3751; DB 2; Length 719;
Best Local Similarity 99.7%; Pred. No. 2.3e-252;
Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCLKMEYENVEPFSASTI 60
DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCLKMEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120

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Db 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARVSKQYIALELMFVQKLPSPFVSG 180  
 Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARVSKQYIALELMFVQKLPSPFVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKYS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMPYPIKTTAQLTREVTYDAI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMPYPIKTTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVITYLSLLSRWSNTQYMMNW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVITYLSLLSRWSNTQYMMNW 360  
 QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRITESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRITESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHKKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHKKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVITYEAYDFEKAQEKV 660  
 Db 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVITYEAYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5  
 O85796 PRELIMINARY; PRT; 719 AA.  
 AC O85796;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Insecticidal protein.  
 GN Name=cry101;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OG Plasmid large plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN=SI01;  
 RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF076993; AAC26910.1;  
 DR HSSP; P02965; ICIV.  
 DR DR GO: 0005102; F:receptor binding; IEA.  
 DR GO: 0006952; P:defense response; IEA.  
 DR GO: 0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.

KW Plasmid. 719 AA; 81230 MW; 42746D478359BBA7 CRC64;  
 SQ SEQUENCE  
 Query Match 99.7%; Score 3750; DB 2; Length 719;  
 Best Local Similarity 99.7%; Pred. No. 2.8e-252;  
 Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFFVASII 60  
 Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFFVASII 60  
 QY 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLPVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARVSKQYIALELMFVQKLPSPFVSG 180  
 Db 121 RNKALTDLKGGLDALAVYHDSLESWGNRNTRARVSKQYIALELMFVQKLPSPFVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKYS 240  
 Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMPYPIKTTAQLTREVTYDAI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSTQMPYPIKTTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVITYLSLLSRWSNTQYMMNW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVITYLSLLSRWSNTQYMMNW 360  
 QY 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRITESLAGLNLFLTQPVNGVPR 420  
 Db 361 GGHKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRITESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHKKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHKKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVITYEAYDFEKAQEKV 660  
 Db 601 TFRVGTFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVITYEAYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 6  
 CAC85964 PRELIMINARY; PRT; 719 AA.  
 AC CAC85964;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Delta-endotoxin.  
 GN CRYIIA.  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group; Bacillus thuringiensis.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=BNS3;  
 RA Tounsi S., Zouari N., Jaoua S.;

RT "Cloning and study of the expression of a novel cryIIa-type gene from  
 RT Bacillus thuringiensis subsp. kurstaki.";  
 RL J. Appl. Microbiol. 95:23-28 (2003).  
 DR EMBL; AJ315121; CAC85964.1; --  
 SQ SEQUENCE 719 AA; 81203 MW; 867655A6C25DAF8 CRC64;

Query Match 99.7%; Score 3748; DB 2; Length 719;  
 Best Local Similarity 99.6%; Pred. No. 3.8e-252;  
 Matches 716; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKSEYENVEPVSASTI 60  
 DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSYIALELMFVKLPSEFAVSG 180  
 DB 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSYIALELMFVKLPSEFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVTYDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
 DB 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
 QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 7  
 Q8KY61 PRELIMINARY; PRT; 719 AA.  
 ID Q8KY61  
 AC Q8KY61  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cry.  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Porcar M., Martinez C., Caballero P.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF278797; AAM73516.1; --  
 DR FIR; B42459; B42459.  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;

Query Match 96.3%; Score 3621; DB 2; Length 719;  
 Best Local Similarity 96.1%; Pred. No. 2.7e-243;  
 Matches 691; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKSEYENVEPVSASTI 60  
 DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSYIALELMFVKLPSEFAVSG 180  
 DB 121 RNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVVKSYIALELMFVKLPSEFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSCHVKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVTYDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALPFSYDTQMPYIKTTAQLTREVTYDAI 300  
 QY 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
 DB 301 GTVHPHPSFTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMNW 360  
 QY 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 DB 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTFFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 8  
 Q9F0P8 PRELIMINARY; PRT; 719 AA.  
 ID Q9F0P8  
 AC Q9F0P8;

DT	01-MAR-2001 (TREMELrel. 16, Created)	
DT	01-MAR-2001 (TREMELrel. 16, Last sequence update)	
DT	01-MAR-2004 (TREMELrel. 26, Last annotation update)	
DE	CryII.	
GN	Name=cryII;	
OS	Bacillus thuringiensis.	
OG	Plasmid pBTC19.	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
OX	NCBI_TaxID=1428;	
RN	[1]_	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BTC007;	
RX	MEDLINE=22837682; PubMed=12957903;	
RA	Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,	
RA	Hu Y., Li G., Huang D.;	
RT	"Identification of cryII-type genes from Bacillus thuringiensis	
RT	strains and characterization of a novel cryII-type gene."	
RL	Appl. Environ. Microbiol. 69:5207-5211(2003).	
DR	EMBL; AF211190; AAG43526.1; -.	
DR	HSSP; P02965; 1CIY.	
DR	GO; GO:0005102; F:receptor binding; IEA.	
DR	GO; GO:0006952; P:defense response; IEA.	
DR	GO; GO:0009405; P:pathogenesis; IEA.	
DR	InterPro; IPR001178; Endotoxin.	
DR	InterPro; IPR005638; endotoxin_C.	
DR	InterPro; IPR005639; endotoxin_N.	
DR	InterPro; IPR008979; Gal_bind_like.	
DR	Pfam; PF03944; Endotoxin_C; 1.	
DR	Pfam; PF00555; Endotoxin_M; 1.	
DR	Pfam; PF03945; Endotoxin_N; 1.	
KW	Plasmid.	
SQ	SEQUENCE 719 AA; 81024 MW; 7E17481922C43556 CRC64;	
Query Match 94.3%; Score 3547; DB 2; Length 719;		
Best Local Similarity 93.5%; Pred. No. 3.8e-238;		
Matches 672; Conservative 26; Mismatches 21; Indels 0; Gaps 0;		
QY	1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60	
DB	1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNINHEDFLRXSEHSIDPVSASTI 60	
QY	61 QTGIGIAGKILGTLGVPAGQVASYLFIILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120	
DB	61 QTGIGIAGKILGTLGVPAGQIASLYFIILGELWPKGKSQWEIFMEHVEEELIDQKISTYA 120	
QY	121 RNKALTDLKGLDALAVYHDSLESWGNRNTRARSVKSOYIALELMFYQKLPSFAVSG 180	
DB	121 RNIALADLGLDALAVYHESLESWKNNRNARATSVKSOYIALELLFVQKLPSFAVSG 180	
QY	181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240	
DB	181 BEVPLPIYAQAANLHLLLRDASVFGKEWGLSNQISTFYNQVERTSDYSDHCVKWYS 240	
QY	241 TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALFSDYDTOMYPIKTTAQLTREYVTDAI 300	
DB	241 TGLNLRGNTNAESWRYNQFRDMTLMVLDLVALFSDYDTLVYPIKTTSQLTREYVTDAI 300	
QY	301 GTVHPHPSFTSTWYNNNAPSFAIEAAVRNPHLLDFLEQVITYLLSRWSNTQYMNW 360	
DB	301 GTVHPNASFTSTWYNNNAPSFAIESAAVRNPHLLDFLEQVITYLLSRWSNTQYMNW 360	
QY	361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRTTESLAGNLFLTQPVNGVPR 420	
DB	361 GGHRLREFRITGGVLTSTOGSTNTSINPVTLPFTSRDVRTTESLAGNLFLTQPVNGVPR 420	
QY	421 VDFHWKFTVTHPIASDNFFYVGYGIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480	
DB	421 VDFHWKFTALPIASDNFFYVGYAGVGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480	
QY	481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPGETGGDILRRTN 540	
DB	481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPGETGGDILRRTN 540	
RESULT 9		
CLIB_BACTE	CLIB_BACTE	
ID	ID	
AC	Q45709;	
DT	30-MAY-2000 (Rel. 39, Created)	
DT	30-MAY-2000 (Rel. 39, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin	
DE	CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).	
GN	Name=cryIIb; Synonyms=cryII(b), cryV, cryV465;	
OS	Bacillus thuringiensis (subsp. entomocidus).	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
OX	NCBI_TaxID=1436;	
RN	[1]_	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BP465;	
RX	MEDLINE=95314293; PubMed=7793960;	
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;	
RT	"Distribution of cryV-type insecticidal protein genes in Bacillus	
RT	thuringiensis and cloning of cryV-type genes from Bacillus	
RT	thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.	
RT	entomocidus."	
RL	Appl. Environ. Microbiol. 61:2402-2407(1995).	
CC	!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut	
CC	epithelial cells of certain coleopteran and lepidopteran species.	
CC	Active on Plutella xylostella but not on Bombyx mori.	
CC	!- DEVELOPMENTAL STAGE: The crystal protein is produced during	
CC	sporulation and is accumulated both as an inclusion and as part of	
CC	the spore coat.	
CC	!- MISCELLANEOUS: Toxic segment of the protein is located in the N-	
CC	terminus.	
CC	!- SIMILARITY: Belongs to the delta endotoxin family.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	EMBL; U07642; AAA82114.1; -.	
DR	PIR; I40590; 140590.	
DR	HSSP; P02965; 1CIY.	
DR	InterPro; IPR001178; Endotoxin.	
DR	InterPro; IPR005638; endotoxin_C.	
DR	InterPro; IPR005639; endotoxin_N.	
DR	InterPro; IPR008979; Gal_bind_like.	
DR	Pfam; PF03944; Endotoxin_C; 1.	
DR	Pfam; PF00555; Endotoxin_M; 1.	
DR	Pfam; PF03945; Endotoxin_N; 1.	
KW	Sporulation; Toxin.	
SQ	SEQUENCE 719 AA; 81295 MW; B8210ABEA97688E CRC64;	
Query Match 93.5%; Score 3516; DB 1; Length 719;		
Best Local Similarity 92.8%; Pred. No. 5.4e-236;		
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;		
QY	1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60	

Db 1 MKLNKPDKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPFFVASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIEMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIEMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLGLGDLAVVHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180  
 Db 121 RNKALSDRLGLDALAVHESLESVGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGYSDHCVKWYS 240  
 Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGYSDHCVKWYN 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPKTTAQLTREVYTDI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTILVYPKTTAQLTREVYTDI 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
 Db 301 GTVHPNQAFSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
 QY 361 GGKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRVRESLQGLNLTQPVNGVPR 420  
 Db 361 GGKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRVRESLQGLNLTQPVNGVPR 420  
 QY 421 VDFHKKVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHKKVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGFEGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGFEGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRVTGFTTFFSFDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDEFAQEKV 660  
 Db 601 TFRVTGFTTFFSFDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDEFAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSDEFLDEKRELFEIVKAKQIHERNM 719  
 Db 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSDEFLDEKRELFEIVKAKQIHERNM 719

RESULT 10  
 ClID\_BACTU STANDARD; PRT; 719 AA.  
 AC Q9XDL1  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin  
 DE CryII(d)) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryII(d); Synonyms=cryII(d), NRcryV;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RX MEDLINE=20374042; PubMed=10919402;  
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 RL gene."  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of

CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC -----  
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 CC -----

DR EMBL; AF047579; AAD44366.1; -.  
 DR HSSP; P02965; 1CIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal bind like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;

Query Match 90.2%; Score 3393; DB 1; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 2e-227;  
 Matches 645; Conservative 35; Mismatches 39; Indels 0; Gaps 0;

QY 1 MKLNKPDKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPFFVASTI 60  
 Db 1 MKLNKPDKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPFFVASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIEMEHVEEIIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYFGLGELWPKGNQWEIEMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLGLGDLAVVHDSLESVGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180  
 Db 121 RNKALADLGLGDLAVVHESLESVGNRNTRARSVVKSOYIALELMFVKLPSPFAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGYSDHCVKWYS 240  
 Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFNNRQVERAGYSDHCVKWYN 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTOMYPKTTAQLTREVYTDI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTMYPKTTAQLTREVYTDI 300  
 QY 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
 Db 301 GTVHPNAPSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMNW 360  
 QY 361 GGKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRVRESLQGLNLTQPVNGVPR 420  
 Db 361 GGKLEFRITIGTILNISTQGSTNTSINPVTLPFTSRDVRVRESLQGLNLTQPVNGVPR 420  
 QY 421 VDFHKKVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 Db 421 VDFHKKVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHKALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGFEGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 Db 541 TGFEGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRVTGFTTFFSFDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDEFAQEKV 660  
 Db 601 TFRVTGFTTFFSFDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDEFAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSDEFLDEKRELFEIVKAKQIHERNM 719  
 Db 661 TALFTSTNPRGLKTDVVDYHIDQVSNLVSDEFLDEKRELFEIVKAKQIHERNM 719

661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 661 TAMFTSTNLRRLKTNVTDCHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 11  
 CLIC\_BACTU STANDARD; PRT; 719 AA.  
 AC 087404;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIc (Insecticidal delta-endotoxin  
 DE CryII(c) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIIc; Synonyms=cryII(c);  
 OS Bacillus thuringiensis.  
 OG Plasmid.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C18 / Egypt;  
 RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of insects.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.

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-----  
 EMBL; AF056933; AAC62933.1; -  
 HSP; P02965; 1CIY.  
 InterPro; IPR001178; Endotoxin.  
 InterPro; IPR005638; endotoxin\_C.  
 InterPro; IPR005639; endotoxin\_N.  
 InterPro; IPR008979; Gal\_bind\_Like.  
 Pfam; PF03944; Endotoxin\_C; 1.  
 Pfam; PF00555; Endotoxin\_M; 1.  
 Pfam; PF03945; Endotoxin\_N; 1.  
 Plasmid; Sporulation; Toxin.  
 SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;

Query Match 89.7%; Score 3373; DB 1; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 4.9e-226;  
 Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

1 MKLKNQDKHQSFSNAKVDKISTDLSKNETDIELQNIHEDCLKMEYENVEPFSASTI 60  
 1 MKLKNQDKHQTLSNAKVDKIADSLKNETDIELKNNEDYLRMSEHESIDPFVSASTI 60

61 QTGIGTAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120  
 61 QTGIGTAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVEEIIINQISTYA 120

121 RNKALTDLKGLDALAVHDSLSWVGNNRNTARSVVKSOVIAELMVFQKLPFAVSG 180  
 121 RNKALTDLKGLDALAVHDSLSWVGNNRNTARSVVKSOVIAELMVFQKLPFAVSG 180

181 BEVPLPIYAQAANLHLLLRDASIFGKENGSLSSSEISTFYNNQVERAGDYSDHCVKWYS 240  
 181 BEVPLPIYAQAANLHLLLRDASIFGKENGSLSSSEISTFYNNQVERAGDYSDHCVKWYS 240

241 TGLNLRGTNAESWVRVYNOFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300  
 241 TGLNLRGTNAESWVRVYNOFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVYTDAL 300

301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVYIYLLSSWSNTQYMNW 360  
 301 GTVHPHPSFTSTWYNNAPSPSAIEAAVVRNPHLLDFLEQVYIYLLSSWSNTQYMNW 360

361 GGHKLEFRITIGTLNISTQGSNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420  
 361 GGHKLEFRITIGTLNISTQGSNTSINPVTLPFTSRDVRVYTESLAGLNFLTQPVNGVPR 420

421 VDFHWKFTVTHPIASDNFYYPGVIGTQLQDSNELPPEATQPNVYESYSHRLSHIGLIS 480  
 421 VDFHWKFTVTHPIASDNFYYPGVIGTQLQDSNELPPEATQPNVYESYSHRLSHIGLIS 480

481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540

541 TGTFGDIRVNINPFAQRVVRIRYASTDLOFHTSINGKAINQGNFSAWNRGDDLDYK 600  
 541 TGTFGDIRVNINPFAQRVVRIRYASTDLOFHTSINGKAINQGNFSAWNRGDDLDYK 600

601 TFRVTGFTTFFSFLDVQSTFTICAWNFSSGNEWYIDRIEFVFEVETVEAEYDFEKAQEKV 660  
 601 TFRVTGFTTFFSFLDVQSTFTICAWNFSSGNEWYIDRIEFVFEVETVEAEYDFEKAQEKV 660

661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 12  
 C1BB\_BACTU STANDARD; PRT; 1229 AA.  
 AC Q45739;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIIB (Insecticidal delta-endotoxin  
 DE CryIIB(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN Name=cryIIB; Synonyms=cryIIB(b), cryET5;  
 OS Bacillus thuringiensis  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRRL B-21110 / EG5847;  
 RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;  
 RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins  
 RT toxic to lepidopteran insects";  
 RL Patent number US5322687, 21-JUN-1994.  
 CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.

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-----  
 EMBL; L32020; AAA22344.1; -  
 HSP; P02965; 1CIY.  
 InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;  
 Query Match 65.0%; Score 2445.5; DB 1; Length 1229;  
 Best Local Similarity 65.6%; Pred. No. 4.2e-161;  
 Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
 QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVNNDPFFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 130  
 DB 67 LGVLGVPPAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQVTTENTRTAARLEG 126  
 QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPSFAVSGEEVPLPIYA 190  
 DB 127 LGRGYSYQQALETWLDNRDARSRIILERYVALELDITTAIPLRIRNEEVPPLMVYA 186  
 QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGYSDHCVKYSTGLNNLRGTN 250  
 DB 187 QAAHLHLLLRDASLFGSEWGMASSDVNYQEQIRYTEESNHCQWYNTGLNNLRGTN 246  
 QY 251 AESWVRNQFRDRLTGLVLDVALFSPYDTQMPYIKTTAQLTREYVTDATGTVHPSPFT 310  
 DB 247 AESWLRNQFRDRLTGLVLDVALFSPYDTQMPYIKTTAQLTREYVTDATGTVHPSPFT 306  
 QY 311 STTWNNNAPSFAIEAAVVRNPRLDLEQVTIYLLSRWSNTQYMNMGHKLERTI 370  
 DB 307 STWNNNAPSFAIEAAVVRNPRLDLEQVTIYLLSRWSNTQYMNMGHKLERTI 366  
 QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRATESLAGNLFLTQPVNGVPRVDFHKKVFT 429  
 DB 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRATESLAGNLFLTQPVNGVPRVDFHKKVFT 422  
 QY 430 HPIASDNFYYPG-----YVGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLISAS 482  
 DB 423 --INPQNIYERGATTYSQYQGVIGIQLFDSSETLPETTERPNYESYSHRLSHIGLIGN 480  
 QY 483 HVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542  
 DB 481 TLRAPVVSWTHRSADRTNTEPNSITQIPLVKALNLSGTVVCGPGFTGGDILRRNTG 540  
 QY 543 TFGDIRVNINPPFAQRVRIYASTDLOPHTSINGKALNQGNSATMNRGSDLDYKTF 602  
 DB 541 TFGDIRLNINPLSQRVRIYASTDLOPHTSINGKALNQGNSATMNRGSDLDYKTF 600  
 QY 603 RTVGFTTPEFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTA 662  
 DB 601 RTAGFTTFPFLNAQSTFTLGAQSFN-QEYVIDRVEFPAEVTFAEYDLERAQKAVNA 659  
 QY 663 LFTSTNPEGLKTDVQKIDQVSNLVESLSDEFYLDKELFELVYKAKQLHIERNM 719  
 DB 660 LFTSTNPEGLKTDVQKIDQVSNLVESLSDEFYLDKELFELVYKAKQLHIERNM 716  
 RESULT 13  
 ClBC\_BACTM  
 ID ClBC\_BACTM STANDARD; PRT; 1233 AA.  
 AC Q45774;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin  
 DE CryIb(c)) (crystalline entomocidal protoxin) (140 kDa crystal protein).  
 GN Name=cryIbC; Synonyms=cryIb(c), cryIbC;  
 OS Bacillus thuringiensis (subsp. morrisoni).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1441;  
 RN SEQUENCE FROM N.A.  
 RP Bishop A.H., Bone E.J., Ellar D.J.;  
 RA "Cloning of novel Bacillus thuringiensis delta-endotoxin.";  
 RT Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 RL -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut  
 CC epithelial cells of insects.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; Z46442; CAA86568.1; --  
 DR HSSP; P02965; 1CIY.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 SQ SEQUENCE 1233 AA; 140451 MW; 7318382413529F21 CRC64;  
 Query Match 65.0%; Score 2445.5; DB 1; Length 1233;  
 Best Local Similarity 65.6%; Pred. No. 4.2e-161;  
 Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
 QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDECLMSEYENVEPFVSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVNNDPFFVSASTVQTGINIAGRI 66  
 QY 71 LGTLGVPPAGQVASYLSFILGELWPKGNQWEIFMEHVEEINQKISTYARNKALTDLKG 130  
 DB 67 LGVLGVPPAGQLASFYSFLVGLWPSGRDPWEIFLEHVEQLIRQVTTENTRTAARLEG 126  
 QY 131 LGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVKLPSFAVSGEEVPLPIYA 190  
 DB 127 LGRGYSYQQALETWLDNRDARSRIILERYVALELDITTAIPLRIRNEEVPPLMVYA 186  
 QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGYSDHCVKYSTGLNNLRGTN 250  
 DB 187 QAAHLHLLLRDASLFGSEWGMASSDVNYQEQIRYTEESNHCQWYNTGLNNLRGTN 246  
 QY 251 AESWVRNQFRDRLTGLVLDVALFSPYDTQMPYIKTTAQLTREYVTDATGTVHPSPFT 310  
 DB 247 AESWLRNQFRDRLTGLVLDVALFSPYDTQMPYIKTTAQLTREYVTDATGTVHPSPFT 306  
 QY 311 STTWNNNAPSFAIEAAVVRNPRLDLEQVTIYLLSRWSNTQYMNMGHKLERTI 370  
 DB 307 STWNNNAPSFAIEAAVVRNPRLDLEQVTIYLLSRWSNTQYMNMGHKLERTI 366  
 QY 371 GGTINISTQGST-NTSINPVTLPFTSRDVRATESLAGNLFLTQPVNGVPRVDFHKKVFT 429  
 DB 367 GGTINTSTQGLTNTSINPVTLPFTSRDVRATESLAGNLFLTQPVNGVPRVDFHKKVFT 422  
 QY 430 HPIASDNFYYPG-----YVGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLISAS 482  
 DB 423 --INPQNIYERGATTYSQYQGVIGIQLFDSSETLPETTERPNYESYSHRLSHIGLIGN 480  
 QY 483 HVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTG 542

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Db 481 TLRAVYVSWTHRSADRTNIGPNRITQIPLVKALNLSHGVTVVGGPGFTGGDILRRNTWG 540
QY 543 TFGDIRVNIWPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATNMGEDLDYKTF 602
Db 541 TFGDIRLNIWPLSQRVIRYASTTDLQFHTSINGKAINQGNFSATNMGEDLDYKTF 600
QY 603 RTVGFTTSPFLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTA 662
Db 601 RTAGFTSPFNFLNAQSTFTLGAQFSN-QEVYIDRVFVFAEVTFEAEYDLERAKAVNA 659
QY 663 LFTSNPRGLKTDVVDYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQLHIERNM 719
Db 660 LFTSTNPRRLKTDVTDYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQLHIERNM 716

RESULT 14
Q93T75 PRELIMINARY; PRT; 1228 AA.
ID Q93T75 AC Q93T75; STRAIN=HD-9;
AC Q93T75; STRAIN=HD-9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Delta-endotoxin CryIa2.
GN Name=CryIa2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 60.6%; Score 2277.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred. No. 2.1e-149;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNIH-----EDCLKMSEYENVEPFVSASTIQTGIGIAGKI 70
Db 2 TSNRKNEIINAVSNHSAQMDLLPDARIEDSLCIAFGNNIDPFVSASTVQTGINIAGKI 61
QY 71 LGTLGVPPFAQVAVSLYFTLGLWPKGNOWEIFMEHVEEILNOKISTYARNKALTDLKG 130
Db 62 LGVLGVPPFAQLAFSYFLVAGLWPRGRDQWEIFLHVEQLINQITENARTALRLOG 121
QY 131 LGDALAVYHDSLSWVGVRNNTARSVVVKSQYIALELMFVOKLPSFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQOSLEDWLENRRDARTSRVLHTQYIALELDLFLNAPLFAIRNQEVPLLMVYA 181
QY 191 QAANLHLLLRDASIFGKWLSSSEISTFYNRQVRAGDYSDCHVKWYSTGLNLRGTN 250
Db 182 QAANLHLLLRDASLFGSEFGLTSQEIQRYRQVERTRDYSYCVWEYNTGLNSLGTN 241
QY 251 AESWRYNFRDMDTLMVLDLVALFPSPYDTQMPYIKTAQLTREYVTDALGTVHPHPSFT 310
Db 242 AASWRYNFRDMDTLMVLDLVALFPSPYDTQMPYIKTAQLTREYVTDALGT--GVANA 299
QY 311 STTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMWGGHKLFRPI 370

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Db 300 SMWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMWGGHKLFRPI 359
QY 371 GGTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFF--LTQPVNGVPRVDFHWKFV 428
Db 360 GGGLNTSTGATNTSINPVTLPFTSRDVRYSAGLNLFF--LTQPVNGVPRVDFHWKFV 416
QY 429 THP-----TASDNFYYPGVVIGTQLODSENELPPEATQGNVESYSHRLSHIGLISASH 483
Db 417 INPQNISDRGTANYSQP--YESPGIQLKDSSETLPPETTERENYESYSHRLSHIGLISASH 475
QY 484 VKALVYSWTHRSADRTNIEPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILRRNTGT 543
Db 476 VNVVYVSWTHRSADRTNIEPNSITQIPLVKAPNLSGAAVVRGPGFTGGDILRRNTGT 535
QY 544 FGDIRVNIWPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATNMGEDLDYKTF 603
Db 536 FGPIRVTVNGPLTQRYRIGFRYASTVDFDFVYSGGTAVNFRFLFTMNSGDELKYGNFV 595
QY 604 TVGFTTSPFLDVQSTFTIGAMNFFSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTA 663
Db 596 RRAFTTPTFTTQIQDIIRTSIQLSGNEVYIDRIEFVPEVVEYAEYDFEKAQKVTA 655
QY 664 FTSTNPRGLKTDVVDYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQLHIERNM 719
Db 656 FTSTNPRRLKTDVTDYHIDQVSNLVESLSEFYLDEKRELFEIVKYAKQLHIERNM 711

RESULT 15
C1BA_BACTK STANDARD; PRT; 1228 AA.
ID C1BA_BACTK AC P05517; Q45731;
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIaB (insecticidal delta-endotoxin
DE CryIaB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIaB; Synonyms=cryIaB(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339; 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RX MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from
RT Bacillus thuringiensis subsp. thuringiensis."
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloid osmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X06711; CAA29898.1; -
CC EMBL; X95704; CAA65003.1; -

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DR PIR; S00873; S00873.
DR HSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
KW Sporulation; Toxin.
FT VARIANT 150 Y -> H (in strain HD-110).
SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match      60.5%; Score 2276.5; DB 1; Length 1228;
Best Local Similarity 62.7%; Pred. No. 2.5e-149;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

QY 23 TDSLKNETDIELQNINH-----EDCLKSEYENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENELINAVNSHSAQMDLLPDARIEDSLCAEGNNIDPFVSASIVQTGINIAGRI 61

QY 71 LGTLGVPPAGQVASLYSIFILGELWPKGNQWEIFMEHVEIINQKISTYARNKALTDLKG 130
Db 62 LGVLGVPPAGQLASFYSLVGLWPRGRDQWEIFLEHVEQLINQOITENARNTALARLQG 121

QY 131 LGDALAVYHDSLESWGNRNNTARSRVVKSOYIALELMFVKLPFSVSGEVEPLLPYIA 190
Db 122 LGDSFRAYQQSLEDWLENRDDARTSRVLYIQYIALELDFLNAMPLFAIRNQEVPLLMVYA 181

QY 191 QAAHLHLILLRDASIFCKEWGLSSSEISTFYNQVERAGDYSDHCVKMYSTGLNNLRGTN 250
Db 182 QAAHLHLILLRDASLFGSEFGLTSQIRYERQVETRDYDVCVEWYNTGLNSLRGTN 241

QY 251 AESWVRNQFRDMTLMVLVDLVALFSDYDQMPYIKTTAQLTREVTDAIGTVHPHPSFT 310
Db 242 AASWVRNQFRDMLTLCGLVDLVALFSDYDRTYPINTSAQLTREVTDAIGAT--GVNMA 299

QY 311 STTWYNNAPPSAIEAAVNVNPHLLDLEQVTIYSLSRWSNTQYMMNMGGHKLERTI 370
Db 300 SGNWYNNAPPSAIEAAAIKSPHLLDLEQLTISSASRWSNTHMTYWRGHTIQSEPI 359

QY 371 GGTLLNSTQGSNTSINPVTLPFTSRDVTRESLAGNLFP--LTQPVNGVPRVDFHWKFV 428
Db 360 GGGELNSTHGANTSNINPVTLPFASRDVYTESYAGVLLWGIYLEPIHGVPVTRFNF--- 416

QY 429 THP-----IASDNFYVGYVGIGTQLQDSENELPPEATGQPNYESYSHLSHIGLISASH 483
Db 417 TNPQNISDRGTANYQP-YESPGLQKXSELPETTERPNYESYSHLSHIGIILQSR 475

QY 484 VKALVYSWTHRSADRTNTIENSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRNTGT 543
Db 476 VNVFVYSWTHRSADRTNTIGENRITQIPMVKASELPQGTTVVRGPGFTGGDILRRNTGG 535

QY 544 FGDIRVNINPPAQRVRYRYASTDLOFHTSINGKAINQGNFSATNVRGEDLDYKTFR 603
Db 536 FGEIRVTWNGPLTQRYRIGFRYASTVDFDFVSRGTTVNNFRFLRTWNSGDELKYGNFV 595

QY 604 TVGFTTFPSFLDVQSTFTIGAMNFGSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVYAL 663
Db 596 RRAFTTFPTFTQIDRIITSQGLSNGEYVIDKIEIIPVTAPEAEYDLERAQEAVAL 655

QY 664 FTSTNPRGLKTDVKYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHERNM 719
Db 656 FTNTNPRRLKTDVTDHIDQVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 711

```

Search completed: October 28, 2004, 18:30:02  
Job time : 106.579 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.191 Seconds  
 (without alignments)  
 3604.811 Million cell updates/sec

Title: US-10-019-823B-57  
 Perfect score: 3760  
 Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVKAKQLHIERNM 719

Scoring table: ELOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR 79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	3756	99.9	719	2 I39815	insecticidal prote
2	3747	99.7	719	2 S25383	parasporal crystal
3	3739	99.4	719	2 I39814	insecticidal prote
4	3516	93.5	719	2 I40590	cryv465 protein -
5	2276.5	60.5	1228	2 S00873	parasporal crystal
6	1900	50.5	380	2 B42459	hypothetical prote
7	1494	39.7	1157	1 S49247	parasporal crystal
8	1482.5	39.4	1166	2 S32645	parasporal crystal
9	1472	39.1	1155	2 A26513	parasporal crystal
10	1469	39.1	1174	2 S32649	parasporal crystal
11	1465	39.0	1155	2 JD0002	parasporal crystal
12	1465	39.0	1156	2 A29125	parasporal crystal
13	1458.5	38.8	934	2 A22798	parasporal crystal
14	1457.5	38.8	1176	2 JT0241	parasporal crystal
15	1451.5	38.6	1176	2 JC2219	parasporal crystal
16	1448	38.5	1155	2 S02134	parasporal crystal
17	1447.5	38.5	1176	2 A22617	parasporal crystal
18	1447.5	38.5	1176	2 S02215	parasporal crystal
19	1447.5	38.5	1181	2 A41052	parasporal crystal
20	1444	38.4	1155	2 I39838	parasporal crystal
21	1358	36.1	1174	2 A42459	parasporal crystal
22	1353	36.0	1138	2 A48944	parasporal crystal
23	1339.5	35.6	1156	2 A29838	parasporal crystal
24	1329.5	35.4	823	2 S04181	parasporal crystal
25	1320.5	35.1	1189	2 S00944	parasporal crystal
26	1310	34.8	1154	2 S39536	parasporal crystal
27	1270	33.8	1171	2 I40572	parasporal crystal
28	1270	33.8	1171	2 A37829	parasporal crystal
29	1261	33.5	1176	2 A48970	parasporal crystal

30	1238	32.9	1160	2 S32647	parasporal crystal
31	1223.5	32.5	1165	2 S11446	parasporal crystal
32	1207.5	32.1	655	2 JC7140	protoxin - Bacillu
33	1195	31.8	1172	2 S32689	parasporal crystal
34	1186	31.5	1160	2 I40589	parasporal crystal
35	1161.5	30.9	1178	1 USBSXH	parasporal crystal
36	1161	30.9	1177	2 A49785	parasporal crystal
37	1154	30.7	652	2 A27323	parasporal crystal
38	1135	30.2	659	2 S10228	parasporal crystal
39	1104.5	29.4	652	2 I39811	parasporal crystal
40	984	26.2	649	1 JH0261	parasporal crystal
41	933	24.8	618	2 S11445	parasporal crystal
42	889	23.6	1156	2 S19306	parasporal crystal
43	827	22.0	1136	1 USBSEI	parasporal crystal
44	691.5	18.4	934	2 B29838	parasporal crystal
45	666	17.7	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I39815

insecticidal protein cryV - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 19-Jul-1996 #sequence-revision 19-Jul-1996 #text change 09-Jul-2004

C:Accession: I39815

R:Gleave, A.P.; Williams, R.; Hedges, R.J.

Appl. Environ. Microbiol. 59, 1681-1687, 1993

.A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for t

iensis subsp. kurstaki.

A:Reference number: I39815; MUID:93298009; PMID:8517758

A:Accession: I39815

A:Status: preliminary; translated from GB/EMBL/DBU

A:Molecule type: DNA

A:Residues: 1-719 <RES>

A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PIDN:AAA22354.1; PID:G142768

C:Genetics:

A:Gene: cryV

C:Superfamily: parasporal crystal protein

Query Match 99.9%; Score 3756; DB 2; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 9.8e-256;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MKLKNQDKHQSFSNAKV	KISTDSLKNETDTELQIN	NHEDCLKMSEYENVEP	PFSASTI	60
Db	1	MKLKNQDKHQSFSNAKV	KISTDSLKNETDTELQIN	NHEDCLKMSEYENVEP	PFSASTI	60
Qy	61	QTGIGIAGKILGTILGVP	FAGQVASLYSFLGELWP	KGNQWEIFMEHVEEII	NQKISTYA	120
Db	61	QTGIGIAGKILGTILGVP	FAGQVASLYSFLGELWP	KGNQWEIFMEHVEEII	NQKISTYA	120
Qy	121	RNKALTDLXGLGDALAV	YHDSLESWGNRNTRAR	SVVKSQVIALELMFVK	LPSPAVSG	180
Db	121	RNKALTDLXGLGDALAV	YHDSLESWGNRNTRAR	SVVKSQVIALELMFVK	LPSPAVSG	180
Qy	181	EEVPLLPYAAQANLHLL	LRDASIFGKEWGLSSSE	ISTFTFNQVERAGDYS	DHCVKWYS	240
Db	181	EEVPLLPYAAQANLHLL	LRDASIFGKEWGLSSSE	ISTFTFNQVERAGDYS	DHCVKWYS	240
Qy	241	TGLNNLRGTNAESWVR	YNQFRDRTLMLDLVAL	FFSYDTQMPYIKTTAQ	LTRVYTDAI	300
Db	241	TGLNNLRGTNAESWVR	YNQFRDRTLMLDLVAL	FFSYDTQMPYIKTTAQ	LTRVYTDAI	300
Qy	301	GTVHPHPSFTSTTWYNN	NAPSFSAIEAARVNRPH	LLDFLEQVTIYSLRSW	NTQVMNMW	360
Db	301	GTVHPHPSFTSTTWYNN	NAPSFSAIEAARVNRPH	LLDFLEQVTIYSLRSW	NTQVMNMW	360
Qy	361	GGHKLFRITIGGTLNIS	TQGSTNTSINPVTLPFT	SRDVRYESLAGLNFLT	QPVNGVPR	420
Db	361	GGHKLFRITIGGTLNIS	TQGSTNTSINPVTLPFT	SRDVRYESLAGLNFLT	QPVNGVPR	420

QY 421 VDFHWKFVTHPIASDNFYYPGVYVIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGVYVIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNIWNPFFAQRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 DB 541 TGTGDIRVNIWNPFFAQRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVGTTPPESFLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVGTTPPESFLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM 719

RESULT 2

S25383  
 parasporal crystal protein cryIa1 - Bacillus thuringiensis  
 N/Alternate names: delta-endotoxin; parasporal crystal protein cryV  
 C/Species: Bacillus thuringiensis  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C/Accession: S25383  
 R/Tailor, R.; Tipett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
 Mol. Microbiol. 6, 1211-1217, 1992  
 A/Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
 A/Reference number: S25383; MUID:92269582; PMID:1588820  
 A/Molecule type: DNA  
 A/Accession: S25383  
 A/Residues: 1-719 <TAI>  
 A/Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:940289; PIDN:CAA44633.1; PID:940290  
 C/Genetics:  
 A/Gene: cryV  
 C/Superfamily: parasporal crystal protein  
 C/Keywords: delta-endotoxin

Query Match 99.7%; Score 3747; DB 2; Length 719;  
 Best Local Similarity 99.7%; Pred. No. 4.2e-255;  
 Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLGDALAVYHDSLSWVGNNTRARSVVKQSYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGLGDALAVYHDSLSWVGNNTRARSVVKQSYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTAAQTREVTDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTAAQTREVTDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVLPTSDRVYRTESLAGNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVLPTSDRVYRTESLAGNLFLTQPVNGVPR 420

QY 421 VDFHWKFVTHPIASDNFYYPGVYVIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGVYVIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNIWNPFFAQRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 DB 541 TGTGDIRVNIWNPFFAQRVRIYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRVGTTPPESFLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRVGTTPPESFLDVQSTFTIGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM 719

RESULT 3

I39814  
 insecticidal protein cryVI - Bacillus thuringiensis  
 C/Species: Bacillus thuringiensis  
 C/Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
 C/Accession: I39814  
 R/Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
 Appl. Environ. Microbiol. 61, 2402-2407, 1995  
 A/Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
 A/Reference number: I39814; MUID:95314293; PMID:7793960  
 A/Accession: I39814  
 A/Status: preliminary; translated from GB/EMBL/DBD  
 A/Molecule type: DNA  
 A/Residues: 1-719 <RES>  
 A/Cross-references: GB:136338; NID:G540281; PIDN:AAC36999.1; PID:G540282  
 C/Genetics:  
 A/Gene: cryVI  
 C/Superfamily: parasporal crystal protein

Query Match 99.4%; Score 3739; DB 2; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-254;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGLGDALAVYHDSLSWVGNNTRARSVVKQSYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGLGDALAVYHDSLSWVGNNTRARSVVKQSYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGDYSYHCVKWS 240  
 DB 181 BEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFTFNQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTAAQTREVTDAI 300  
 DB 241 TGLNLRGTNAESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTAAQTREVTDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360  
 QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVLPTSDRVYRTESLAGNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVLPTSDRVYRTESLAGNLFLTQPVNGVPR 420

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Qy 421 VDFHKKFVTHPIASDNFFYYPGVYIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
Db 421 VDFHKKFVTHPIASDNFFYYPGVYIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

Qy 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

Qy 601 TFRVTGFTTPFSDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVTEAEYDEFEKAQEKV 660
Db 601 TFRVTGFTTPFSDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVTEAEYDEFEKAQEKV 660

Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 4
140590
cryV465 protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40590
R:Shin, B.S.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
Appl. Environ. Microbiol. 61, 2402-2407, 1995
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis
tomocidus.
A:Reference number: I39814; MUID:95314293; PMID:7793960
A:Accession: I40590
A>Status: preliminary; translated from CB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-719 <RES>
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g4672
C:Genetics:
A:Gene: cryV465
C:Superfamily: parasporal crystal protein

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Query Match 93.5%; Score 3516; DB 2; Length 719;
Best Local Similarity 92.8%; Pred. No. 7.1e-239;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQPSSNAKVDKISTDSLKNETDIELQINHEDECLXMEYENVEPVSASTI 60
Db 1 MKLKNQDKHQPSSNAKVDKISTDSLKNETDIELQINHEDECLXMEYENVEPVSASTI 60

Qy 61 QTGIGIAGKILGTGVPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKILTYA 120

Qy 121 RNKALTDLGLDALAVYHDSLESWYGNRNNTARSVVKSOYIALELMFVQKLPFAVSG 180
Db 121 RNKALSDRLGLDALAVYHDSLESWYGNRNNTARSVVKSOYIALELMFVQKLPFAVSG 180

Qy 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
Db 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERIDYSDHCIKWYN 240

Qy 241 TGLNLRGTNABSWRYNQFRDMLTMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI 300
Db 241 TGLNLRGTNABSWRYNQFRDMLTMLVLDLVALFPSYDTLVYIKTTSQLTREVTDAI 300

Qy 301 GTVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360
Db 301 GTVHPNQAFSTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNW 360

Qy 361 GGHKLEPRTIGTFLNISTQGSTNTSINPVTLPFTSRDVRKTESLAGLNLFLTQPVNGVPR 420
Db 361 GGHRLSPRIGGALNTSQGSTNTSINPVTLPFTSRDVRKTESLAGLNLFLTQPVNGVPR 420

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Qy 421 VDFHKKFVTHPIASDNFFYYPGVYIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480
Db 421 VDFHKKFVTHPIASDNFFYYPGVYIGTQLODSENELPPEATQPNYESYSHRLSHIGLIS 480

Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

Qy 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

Qy 601 TFRVTGFTTPFSDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVTEAEYDEFEKAQEKV 660
Db 601 TFRVTGFTTPFSDVQSTFTIGAMNFSNGNEVYIDRIEFPVVEVTEAEYDEFEKAQEKV 660

Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 5
S00873
parasporal crystal protein cryBai - Bacillus thuringiensis subsp. thuringiensis
N:Alternate names: parasporal crystal protein cryA4
C:Species: Bacillus thuringiensis subsp. thuringiensis
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S00873
R:Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t
A:Reference number: S00873; MUID:88203216; PMID:3362680
A:Accession: S00873
A:Molecule type: DNA
A:Residues: 1-1228 <BRI>
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094;
C:Genetics:
A:Gene: cryA4
A:Start codon: TTG
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

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Query Match 60.5%; Score 2276.5; DB 2; Length 1228;
Best Local Similarity 62.7%; Pred. No. 2e-151;
Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

Qy 23 TDSLKNETDIELQINH-----EDCLKMEYENVEPVSASTIQTGIGIAGKI 70
Db 2 TSNRKNENEIINAVSNHSAQMDLLPDARIEDSLCIAEGNNIDPFVSASTVQTGINIAGRI 61

Qy 71 LGTGVPPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130
Db 71 LGTGVPPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 130

Qy 121 LGVLPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121
Db 121 LGVLPFAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG 121

Qy 131 LGDALAVYHDSLESWYGNRNNTARSVVKSOYIALELMFVQKLPFAVSGEVPPLPIYA 190
Db 131 LGDALAVYHDSLESWYGNRNNTARSVVKSOYIALELMFVQKLPFAVSGEVPPLPIYA 190

Qy 181 LGDSFRAYQQSLEDWLENEDDARTSRVLYTQVIALELDLFLNAPLEFAIRNQCEVPLLMVYA 181
Db 181 LGDSFRAYQQSLEDWLENEDDARTSRVLYTQVIALELDLFLNAPLEFAIRNQCEVPLLMVYA 181

Qy 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGTN 250
Db 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGTN 250

Qy 241 QAANLHLLLRDASIFGSEFGLTSQEQRYRVERQVERTRDYSYCVWEYNTGLNLRGTN 241
Db 241 QAANLHLLLRDASIFGSEFGLTSQEQRYRVERQVERTRDYSYCVWEYNTGLNLRGTN 241

Qy 310 AESWRYNQFRDMLTMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 310
Db 310 AESWRYNQFRDMLTMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 310

Qy 299 AASWRYNQFRDMLTMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 299
Db 299 AASWRYNQFRDMLTMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSFT 299

Qy 370 STTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWCGHKLFEFTI 370
Db 370 STTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWCGHKLFEFTI 370

Qy 359 SMWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWCGHKLFEFTI 359
Db 359 SMWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMNWCGHKLFEFTI 359

Qy 428 GGTNLINISTQGSTNTSINPVTLPFTSRDVRKTESLAGLNLFLTQPVNGVPRVDFHKKFV 428
Db 428 GGTNLINISTQGSTNTSINPVTLPFTSRDVRKTESLAGLNLFLTQPVNGVPRVDFHKKFV 428

Qy 416 GGGLNTSTHGATNTSINPVTLPFTSRDVRKTESLAGLNLFLTQPVNGVPRVDFHKKFV 416
Db 416 GGGLNTSTHGATNTSINPVTLPFTSRDVRKTESLAGLNLFLTQPVNGVPRVDFHKKFV 416

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Db 709 YGHDKMKMLEAVRAAKRLSRERNL 732

## RESULT 8

S32645

parasporal crystal protein crylGal - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S32645

R:Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645

A:Accession: S32645

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1166 <LAM>

A:Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:g295861; PIDN:CAA80233.1; PID:g2958

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 39.4%; Score 1482.5; DB 2; Length 1166;  
Best Local Similarity 46.2%; Pred. No. 1.1e-95;  
Matches 326; Conservative 97; Mismatches 207; Indels 75; Gaps 16;

QY 41 DCLKMSYE---NVEPFVSASTIQGIGIAGKILGTLGVPPAGQVASILYSPILGELMPK 96

Db 13 NCLNPESEIFNARNENFGLVSQVSSGL---TRFLLEAAVPEAGFALGLDIWGL--- 66

QY 97 GKQWEIFMEHVEEIIINOKISTYARKALTDLKLGLDALAVYHDSLESVWGNNTARS 156

Db 67 GVDQWSFLRQIEQLRQEITELERNRATAILTGLSSVNLVYVEALREWENDPNPASQE 126

QY 157 VVKSQYTALELMFVQKLPFAVSGEVEVPLPIYAQAANLHLLLRDASIFGKEWGLSSE 216

Db 127 RVTRFRILTDDAIVTGLPTLAIRNLVWNLVSVYTAQAANLHLLSLRDADVFGERWGLTQAN 186

QY 217 ISFTYRQVERAGDYSDHCVKWTSTGLNLRGTNAESVRYNQPRDRLTMLVDLVALFP 276

Db 187 IEDLYRLTNSIQEYSDHCARVYNQGLNEIGGISR---RYLDFQRLTISVLDIVALFP 242

QY 277 SYDTQMPKTKTAQLTREVTDAI--GTVHPHPSFTSTTWYNNAPSAIEAAVVRNPH 334

Db 243 NYDIRTPIPTOSQLTREIYTSPPVAGNI-----NFGLSIANVLRAHP 285

QY 335 LLDPLEQVTIYLLSRNSNTQYMMWGGHKLFRITIG-GTLN-----ISTQGSTNTS 385

Db 286 LMDFIDRIVYITNSVR--STPY---WAGHEVISRTQGQGNRIFFLYGVAANAEPPTV 340

QY 386 INPVTLEFSTRDYRTES-----LAGLNLFLOTPVNGVPRVDHFKFVTHPIASDNFY 439

Db 341 IRPTGFTDEQRQWYRARSRVVSRSSGQDFSLVDVG-----FLT--IFSASVIY 388

QY 440 PGVVGIGTQLODSENLPPPEATGQPNYESYSHRLSHIGLISAS-----HVKALVYSWTHR 494

Db 389 RNCFGFNT--DTIDEPIEGTDP--FTGYSHRLCHVGFLASSPFI SQARAPIFS WTHR 443

QY 495 SADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNINPP 554

Db 444 SATLTNTIAPDVITQIPLVKAFNLHSGATIVKGPFTGGDILRRNTVSGFGDMRVNTAP 503

QY 555 FAQRYRVIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRFTVGTTPTPSFL 614

Db 504 LSQRYRVIRYASTTDLQFYTNINGTTINGNFSMTDSGDDLQYGRFRVAGFTTPTPFS 563

QY 615 DVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKVTAFTSTNPRGLKT 674

Db 564 DANSTFTIGAFGSPNNEVYIDRIEFVPAEVTFEAEYDLEKAQKAVNALFTSSNQIGLKT 623

QY 675 DVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

Db 624 DVTDYHIDQVSNLVESLSDEFCLDEKRELSEKVKHAKRLSDERNL 668

## RESULT 9

A26513

parasporal crystal protein - Bacillus thuringiensis (strain aizawai)

C:Species: Bacillus thuringiensis

C:Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004

C:Accession: A26513

R:Oeda, K.; Oshie, K.; Shinizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.

Gene 53, 113-119, 1987

A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis

A:Reference number: A26513; MUID:87248103; PMID:3297927

A:Accession: A26513

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1155 <OED>

A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 39.1%; Score 1472; DB 2; Length 1155;  
Best Local Similarity 44.4%; Pred. No. 6e-95;  
Matches 315; Conservative 113; Mismatches 227; Indels 54; Gaps 12;

QY 36 NINHEDCMKSEYENVE-PFVSASTIQG-----IGIACKILGTLGVPPAGQVASYLS 87

Db 4 NPINCEIPYCNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62

QY 88 FILGELWPKGNQWEIFMEHVEEIIINOKISTYARKALTDLKLGLDALAVYHDSLESWVG 147

Db 63 IIWGIF--GPSQWDADFVQIEQLINQRIEIEFARNQAIISRLGLESLNLYQIYAESFREWEA 119

QY 148 NRNTRARSVVKSQYIALELMFVQKLPFAVSGEVEVPLLPYQAANLHLLLRDASIFG 207

Db 120 DPTPALREEMRIQFNDMNSALTATLPLFAVQNYQVPLLSVYQAANLHLSVLRDVSFVG 179

QY 208 KEWGLSSSISITFYNRQVERAGDYSDHCVKWTSTGLNLRGTNAESVRYNQPRDRMTLM 267

Db 180 QRWGFDAATINSRYNDLTRLIGNYTHAVRWYNTGLERVWGPDSRDWRINQFRRELTLT 239

QY 268 VLDLVALFPSYDTCWYPIKTKTAQLTREVTDAIGTVHHPHPSFTSTTWYNNAPSAIEA 327

Db 240 VLDIVLSFFNYDSRTYPIRTVSQLTREIYNFV-----LENFDGSPRALAQ 285

QY 328 AV---VRNHLHLDLEQVTIYLLSR---WSTQYNNM---WGGHKLERTIGTGLNIS 377

Db 286 GIEGSIRSEPLMDILNSITITDAHRGEYVWSGHQIMASPVGSGPEFTPLYGTMGNA 345

QY 378 TQGSTNTSNPVTLPFTSRDVRVYTESLAGLNLFLOTPVNGVPRVDHFKFVTHPIASDNF 437

Db 346 PQQRIVAQIQGVYVRLSTLYRPPFNIGIN---NQQLSVLDGTETAYG-----TSSNL 396

QY 438 YYPGVVGIGTQLODSENLPPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVYS 490

Db 397 PSAVYRKSGT--VDSDLDEIPQNNVPPRQGFSHRLSHVSVFRSGFSNVSIIIRAPMFS 454

QY 491 WTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVN 550

Db 455 WIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVRGPGFTGGDILRRNTGTGDIRVN 514

QY 551 INPPAQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRFTVGFTTP 610

Db 515 ITAPLSQRVVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRFTVGFTTP 574

QY 611 FSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKVTAFTSTNPR 670

Db 575 FNFSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLEKAQKAVNELFTSSNQI 634

QY 671 GLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

Db 635 GLKTDVYHIDQVSNLVESLSDEFCLDEKRELSEKVKHAKRLSDERNL 683

## RESULT 10

S32649

parasporal crystal protein cryIpa3 - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S32649  
R/Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A/Reference number: S32645  
A/Accession: S32649  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1174 <LAM>  
A/Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295865; PIDN:CAA80235.1; PID:G29586  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 39.1%; Score 1469; DB 2; Length 1174;  
Best Local Similarity 44.8%; Pred. No. 9, 9e-95;  
Matches 325; Conservative 103; Mismatches 202; Indels 96; Gaps 17;

QY 36 NINHE---DCLRMSEYENVEPVSASTIQIGIA-GKILGTGLVPPFAGQVASYSL 90  
Db 4 NIQOCVPYNCLSNPEVILSEBSTERGLPLDISLSTRELLSEFVPGVAFGLDFLIW 63  
QY 91 GELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGIGDALAVVHDSLESWGNEN 150  
Db 64 GFITP---SEWSIFLLQIEQLIEQRIETLERNATITLRLGADSEVYLEALREWEENPN 120  
QY 151 NTRARSVKSQYIALELMFVQKLSPAVSGEVPPLPIYQAANLHLLLRDASIFGKEW 210  
Db 121 NAQUREDVIRFANTDDALITAINNFTLSTPEIPLSVYQVQAANLHLLLRDASVFGQW 180  
QY 211 GLSSEISTFYNQVERAGDYSDHCWKVYSTGLNLRGTNAESWVRYNQFRDMLTMDLD 270  
Db 181 GLDIATVNNHYNLNLHRYTEHCLDTYNGLENLGTNTQWSRFNQFRRLTLTVLD 240  
QY 271 LVALPSPDYTMPIKTAQLREVYDAIGTVPHPSPFTSTWYNNAPS-PSAIEAAV 329  
Db 241 IVALFPNDARAVPIQSSQLTREIYTSV--IEDSP-----VSANIPNGFNAEFG- 290  
QY 330 VRNPHLLDFLEQVTIYISLLRSNNTQYMMWGGHKLFRITGGTLNISTQSTNTSINPV 389  
Db 291 VRPHLMDFMN-----SLFVTAETVRSQTVMGGHLV-----SSRTAGNPI 331  
QY 390 TLFP-----TSRDVYRTESLAGLNFLTPQVNGVPRVDFHMKFVTHPIAS 434  
Db 332 NFPIYGIFFNPGGAIWAIEDPRPFYRT-----LSDFV-----FVRGGFGN 371  
QY 435 DNFFYPGVYIGTQLQ-----DSENELPPEATGQPNYESYSHRLSHI----- 476  
Db 372 PH-YVGLGLGVAFQQTGTNHTFRNSGTIDSLDEIPPDNSGAPWNDYSHVNLHVTFR 430  
QY 477 --GLISASHV-KALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGG 533  
Db 431 WPGSIAGSDSWRAPMFSWTHRSADRNTIINPNIITQIPAVKAHNLHSGTVVRGPGFTGG 490  
QY 534 DILERTNTGTGDIRVNNPPFAQRVRYRYASTDQLPHTSINGKAINQGNFSATNR 593  
Db 491 DLERTNTGTGDIRVNTGPIQSQRVRYRYASTDQLPFTTRNGTSVNGQNFQRTNR 550  
QY 594 GEDLDYKTRTGTGFTTPPSFLDVQSTFTIGAWNFSSGNEYVIDRIEFVPEVVEYAEYDF 653  
Db 551 GGNLESGNFRTAGFTSPFSNAQSTFTLGTQAFSN-QEVIIDRIEFVPAEVTFEASDL 609  
QY 654 EKAQEKVTALFTSTNPGKLDKVDYHIQVSNLVESLSDEFYLDKRELFVVKYAKQL 713  
Db 610 ERAQKAVNALFTSTQGLKNTVTGYHIDQVSNLVACLSEDFCLDKRELSKVKHAKRL 669  
QY 714 HIERNM 719  
Db 670 SDRKRL 675

JD0002  
parasporal crystal protein cryIab3 - Bacillus thuringiensis  
N/Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prot  
C/Species: Bacillus thuringiensis  
C/Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
C/Accession: A90025; A90955; S14555; A24172; A29043; JD0002  
R/Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
Agric. Biol. Chem. 51, 455-463, 1987  
A/Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
A/Reference number: A90025  
A/Accession: A90025  
A/Molecule type: mRNA  
A/Residues: 1-1155 <KON>  
A/Cross-references: UNIPROT:P06578  
A/Experimental source: subsp. kurstaki  
R/Geiser, M.; Schweitzer, S.; Grimm, C.  
Gene 48, 109-118, 1986  
A/Title: The hypervariable region in the genes coding for entomopathogenic crystal protei  
A/Reference number: A91560; MUID:87163505; PMID:3557124  
A/Accession: A91560  
A/Molecule type: DNA  
A/Residues: 1-1155 <GEI>  
A/Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124  
A/Experimental source: subsp. kurstaki  
R/Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
DNA 5, 305-314, 1986  
A/Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal  
A/Reference number: A90955; MUID:86300092; PMID:3743328  
A/Accession: A90955  
A/Molecule type: DNA  
A/Residues: 1-1155 <WAB>  
A/Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720  
A/Experimental source: subsp. berliner  
R/Chak, K.F.; Jen, J.C.  
submitted to the EMBL Data Library, October 1990  
A/Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
A/Reference number: S14555  
A/Accession: S14555  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1155 <CHA>  
A/Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:G40273  
R/Hofte, H.; de Greve, J.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerck  
Eur. J. Biochem. 161, 273-280, 1986  
A/Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri  
A/Reference number: A26461; MUID:87054026; PMID:3023091  
A/Accession: A26461  
A/Molecule type: DNA  
A/Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>  
A/Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255  
A/Experimental source: strain berliner 1715  
C/Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
C/Genetics:  
A/Gene: cry-1-2; bt2  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin  
F/82-586/Product: toxic peptide #status predicted <TXP>  
F/82-300/Region: toxic #status predicted  
F/300-586/Region: insecticidal #status predicted

Query Match 39.0%; Score 1465; DB 2; Length 1155;  
Best Local Similarity 44.5%; Pred. No. 1.8e-94;  
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;

QY 36 NINHECLKMSYENVE-PFVSASTIQTG-----IGIACKILGTGLVPPFAGQVASYLS 87  
Db 4 NPINCEIPYNCLSNPEVEVLGGRIETGTPTIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKGIGDALAVVHDSLESWVG 147  
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEBFARNQAIISRLGLSLNLYQIYAESFREWEA 119  
QY 148 NNNNTRARSVKSQYIALELMFVQKLSPAVSGEVPPLPIYQAANLHLLLRDASIFG 207

Db 120 DPTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179  
QY 208 KEWGLSSSEISFYFNQVERAGDYSCHVKWYSTGLNNLRGTNAESVWRYNQFRDRTLM 267  
Db 180 QRWGFDAAATINSRYNDLTRIGNYTHAVRWYNTGLERVWGPDSRDWIRYNQFRELTILT 239  
QY 268 VLDLVALPSPDYTMPIKTAQLTRVYTDAGTVVHPHPSFTSTTWNNNAPS-----S 323  
Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYTNPV-----LENFDSFRGSAQ 285  
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGGHKLFRFTIGTLNI 376  
Db 286 GIEGS-IRSPHLMIDLNSITTIYDAHRGEYWSGHQIMASVPGSPGPFPLPYGTMGNA 344  
QY 377 STQGSTNTSINPVTLPTFSRDVYRTESLAGNLFLTPQVNGVPRVDFHVKFVTHPIASDN 436  
Db 345 APQORIVAQLGGVYRTLSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYYPGVGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNNVPPROGFSHRLSHVSMFRSGFSNSVSIIRAPMF 453  
QY 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFTGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRNTSPQISTLRV 513  
QY 550 NINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRFTVGFTT 609  
Db 514 NITAPLSQRYRVRIRYASTTDLQFHTSIDGRPINQGNFSAATMRSGSNLQSGSFRIVGFTT 573  
QY 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVVEVYEAEDFEKAQEKVLTALFTSTNP 669  
Db 574 PFNFGSSVFTLSAHVFNSEVYIDRIEFVPAEVTFAEYDLERAKAVNELFTSSNQ 633  
QY 670 RGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 683

RESULT 12  
A29125  
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)  
C/Species: Bacillus thuringiensis subsp. kurstaki  
C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A29125  
R/Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme  
Bio/Technology 5, 807-813, 1987  
A/Title: Insect tolerant transgenic tomato plants.  
A/Reference number: A29125  
A/Accession: A29125  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-1156 <FIS>  
A/Cross-references: UNIPROT:Q9F296; UNIPROT:Q93721  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin.

Query Match 39.0%; Score 1465; DB 2; Length 1156;  
Best Local Similarity 44.5%; Pred. No. 1.9e-94;  
Matches 316; Conservative 112; Mismatches 226; Indels 56; Gaps 13;  
QY 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPPAGQVASLYS 87  
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQWEIEMEHVEEIIINQISTYARNKALTDLKGLGDALAVYHDSLESWVG 147  
Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEFAFNQAIARLEGLSNLYQIYAESFREWEA 119  
QY 148 NNNTRARSVVKSQYIALELMFVQKLPSPFAVSGEVEPLPIYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179

QY 208 KEWGLSSSEISFYFNQVERAGDYSCHVKWYSTGLNNLRGTNAESVWRYNQFRDRTLM 267  
Db 180 QRWGFDAAATINSRYNDLTRIGNYTHAVRWYNTGLERVWGPDSRDWIRYNQFRELTILT 239  
QY 268 VLDLVALPSPDYTMPIKTAQLTRVYTDAGTVVHPHPSFTSTTWNNNAPS-----S 323  
Db 240 VLDIVSLFPNYSRTYPIRTVSQLTREIYTNPV-----LENFDSFRGSAQ 285  
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLLSR-----WSNTQYMMN---WGGHKLFRFTIGTLNI 376  
Db 286 GIEGS-IRSPHLMIDLNSITTIYDAHRGEYWSGHQIMASVPGSPGPFPLPYGTMGNA 344  
QY 377 STQGSTNTSINPVTLPTFSRDVYRTESLAGNLFLTPQVNGVPRVDFHVKFVTHPIASDN 436  
Db 345 APQORIVAQLGGVYRTLSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYYPGVGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNNVPPROGFSHRLSHVSMFRSGFSNSVSIIRAPMF 453  
QY 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGTFTGDIRV 549  
Db 454 SWTHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRNTSPQISTLRV 513  
QY 550 NINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRFTVGFTT 609  
Db 514 NITAPLSQRYRVRIRYASTTDLQFHTSIDGRPINQGNFSAATMRSGSNLQSGSFRIVGFTT 573  
QY 610 PFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVVEVYEAEDFEKAQEKVLTALFTSTNP 669  
Db 574 PFNFGSSVFTLSAHVFNSEVYIDRIEFVPAEVTFAEYDLERAKAVNELFTSSNQ 633  
QY 670 RGLKTDVKDHYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 683

RESULT 13  
A22798  
parasporal crystal protein - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
C/Accession: A22798  
R/Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
Gene 34, 243-251, 1985  
A/Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuring  
A/Reference number: A22798; NUID:85232070; PMID:2989108  
A/Accession: A22798  
A/Molecule type: DNA  
A/Residues: 1-934 <SHI>  
A/Cross-references: UNIPROT:Q9SSV8; GB:M10917; NID:G143100; PIDN:AAA22552.1; PID:G551713  
C/Comment: The authors translated the codon ACA for residue 264 as Ser.  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 38.8%; Score 1458.5; DB 2; Length 934;  
Best Local Similarity 43.7%; Pred. No. 3.8e-94;  
Matches 311; Conservative 119; Mismatches 221; Indels 61; Gaps 12;  
QY 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTLGVPPAGQVASLYS 87  
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPKGNQWEIEMEHVEEIIINQISTYARNKALTDLKGLGDALAVYHDSLESWVG 147  
Db 63 IIWGIF--GPSQWDAFLVQIEQLINQRIEFAFNQAIARLEGLSNLYQIYAESFREWEA 119  
QY 148 NNNTRARSVVKSQYIALELMFVQKLPSPFAVSGEVEPLPIYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179  
QY 208 KEWGLSSSEISFYFNQVERAGDYSCHVKWYSTGLNNLRGTNAESVWRYNQFRDRTLM 267

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Db 180 QRWGFAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRLTLT 239
Qy 268 VLDLVALPFSYDTQMYPIKTTAQLTREVYTDAGTVHPHPSFTSTTWYNNAPSFSAIEA 327
Db 240 VLDLVALPFSYDTSRRYPIRTVSQLTREIYTNPV-----LENFDGSRGMAQ 285
Qy 328 AV-----VRNPHLLDFLEQVTIYLLSRWSNTQYMMWGGHKLFRITGGT---LNISTQGS 381
Db 286 RIEQNIRQPHLMDILNRIIYTDVHRG-----FNYSGHQITASVPVGSFPEFAFPLFCN 340
Qy 382 TNSINPVTLPFTSRDVRTESL-----AGNLFLTPQVNGVPRVDFHWKVFTHPI 432
Db 341 AGNAAPPVLVSLTGLIFRTLSSPLYRRIILGSGPN---NQELFVLDGTEFSASLTNNL 397
Qy 433 ASDNFPYPCYVGIGTQLQDSENELPPEATGPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQRTV-----DSLVIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRTNTEIENSIITQPLVKAFNLSSGAAVRGPFGTGGDILRRNTGTGFDI 547
Db 451 TFSWQHRSAGAEFNIIIPSSQITQIPLTKSTNLGSGTSVWVGPGFTGGDILRRNTSPGQISTL 510
Qy 548 RVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDTYKTRTVGF 607
Db 511 RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATWSSGSLNLSGSRFTVGF 570
Qy 608 TTPSFLDVQSTTTIGAWNFSSGNEVYDRIEFVPEVTEYAEYDFEKAQEKVTALFST 667
Db 571 TTPNFSNGSSVFTLSAHVNSGNEVYDRIEFVPAEVTPEAEYDLERAKAVNELFTSS 630
Qy 668 NPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIKYAKQHLIERNM 719
Db 631 NQIGLKTVDYHIDQVSNLVECLSEDFCLDEKQELSEKVKHAKLSDERNL 682

RESULT 14
JT0241
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N;Alternate names: 135K insecticidal protein
C;Species: Bacillus thuringiensis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JT0241
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein
A;Reference number: JT0241
A;Accession: JT0241
A;Molecule type: DNA
A;Residues: 1-1176 <SHI>
A;Cross-references: UNIPROT:P02965
A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.8%; Score 1457.5; DB 2; Length 1176;
Best Local Similarity 43.7%; Pred. No. 6.4e-94;
Matches 311; Conservative 118; Mismatches 222; Indels 61; Gaps 12;

Qy 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGKQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESVVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFNQAIISLEGLSNLYQIYAESFREWEA 119
Qy 148 NRNTRARVSKSQYIALELMFVQKLPSPFAYSGEEVPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTTPAFLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRDRTLM 267
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Db 180 QRWGFAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRLTLT 239
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Db 240 VLDLVALPFSYDTSRRYPIRTVSQLTREIYTNPV-----LENFDGSRGMAQ 285
Qy 328 AV-----VRNPHLLDFLEQVTIYLLSRWSNTQYMMWGGHKLFRITGGT---LNISTQGS 381
Db 286 RIEQNIRQPHLMDILNRIIYTDVHRG-----FNYSGHQITASVPVGSFPEFAFPLFCN 340
Qy 382 TNSINPVTLPFTSRDVRTESL-----AGNLFLTPQVNGVPRVDFHWKVFTHPI 432
Db 341 AGNAAPPVLVSLTGLIFRTLSSPLYRRIILGSGPN---NQELFVLDGTEFSASLTNNL 397
Qy 433 ASDNFPYPCYVGIGTQLQDSENELPPEATGPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQRTV-----DSLVIPPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
Qy 488 VYSWTHRSADRTNTEIENSIITQPLVKAFNLSSGAAVRGPFGTGGDILRRNTGTGFDI 547
Db 451 TFSWQHRSAGAEFNIIIPSSQITQIPLTKSTNLGSGTSVWVGPGFTGGDILRRNTSPGQISTL 510
Qy 548 RVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATWNRGDLDTYKTRTVGF 607
Db 511 RVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATWSSGSLNLSGSRFTVGF 570
Qy 608 TTPSFLDVQSTTTIGAWNFSSGNEVYDRIEFVPEVTEYAEYDFEKAQEKVTALFST 667
Db 571 TTPNFSNGSSVFTLSAHVNSGNEVYDRIEFVPAEVTPEAEYDLERAKAVNELFTSS 630
Qy 668 NPRGLKTDVKYHIDQVSNLVSLSDEFYLDKRELFEIKYAKQHLIERNM 719
Db 631 NQIGLKTVDYHIDQVSNLVECLSEDFCLDEKQELSEKVKHAKLSDERNL 682

RESULT 15
JC2219
parasporal crystal protein cryIAa - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2219
R;Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 58, 830-835, 1994
A;Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an
A;Reference number: JC2219; MUID:94289859; PMID:7764972
A;Accession: JC2219
A;Molecule type: DNA
A;Residues: 1-1176 <UDA>
A;Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:G506190; PIDN:BAA04468.1; PID:G5357E
C;Genetics:
A;Gene: cryIA(a)
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 38.6%; Score 1451.5; DB 2; Length 1176;
Best Local Similarity 43.5%; Pred. No. 1.7e-93;
Matches 310; Conservative 118; Mismatches 223; Indels 61; Gaps 12;

Qy 36 NINHEDECLMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPAGQVASLYS 87
Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62
Qy 88 FILGELWPKGKQWEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVYHDSLESVVG 147
Db 63 IIWGIF---GPSQWDAFLVQIEQLINQRIEFAFNQAIISLEGLSNLYQIYAESFREWEA 119
Qy 148 NRNTRARVSKSQYIALELMFVQKLPSPFAYSGEEVPLPIYAQAANLHLLLRDASIFG 207
Db 120 DPTNPALREEMRIQFNDMNSALTTPAFLFAVQNYQVPLLSVYVQAANLHLSVLDRDVSFVG 179
Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRDRTLM 267
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Db 180 QRWGFDAAATNSRYNDLRLIGNYTDYAVRWYNTGLERWVGPSDRDWRVYNQPRRELTLT 239
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Db 240 VLDLVALFSDYDSSRRYPRTVSQLTREIYNPV-----LENFDGSGFRGVAQ 285
QY 328 AV---VRNPHLLDFLEQVTIYSLLSWSNTQYMNWGGHKLFEFTIGGT---LNISTQGS 381
Db 286 RIEQNIRQPHLMDILINSITIVTDVHRG-----FNYWSGHQITASPVGSGPEFAFPLFGN 340
QY 382 TWTNSINPTLPTSRDVRTSL-----AGLNFLTQPVNGVPRVDFHKKFVTHPI 432
Db 341 AGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGN--NQELFVLDGTGTEFSPASLTNLT 397
QY 433 ASDNFYYPGYVGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLISAS-----HVKAL 487
Db 398 PSTIYRQGTV-----DSLVDVIPQDNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450
QY 488 VYSWTHRSADRTNTIBPNSITQIPLVKAENLSSGAAVVRGPGFTGGDIILRRINTGTGDI 547
Db 451 TFSWQHRSAAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDIILRRISPGQISTL 510
QY 548 RVNINPPAQRVVRIRYASTDLOPHTSINGKAINQGNFSATMNRGEBLDYKTFRTVGF 607
Db 511 RVNITAPLSQRVVRIRYASTNLOPHTSIDGRPINQGNFSATMSSGSNLSQSGSFRTVGF 570
QY 608 TTPFSFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEAEYDFEKAQEKVTLFTST 667
Db 571 TTPFNFSNGSSVFTLSAHVNSNGNEVYIDRIEFVPAEVTPEAEYDLERAQKAVNELTSS 630
QY 668 NPGRLKTDVKYHIDQVSNLVESSLDEFYLDKRELFEIVKYAKOLHIERNM 719
Db 631 NQIGLKTVDVTDYHIDQVSNLVECLSDFECLDEKQELSEKVKHAKELSDERNL 682

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Search completed: October 28, 2004, 18:31:55  
 Job time : 22.191 secs



Result No.	Query	Score	Match	Length	DB	ID	Description
1	3756	99.9	719	17	US-10-782-020-10	Sequence 10, Appl	
2	3756	99.9	719	17	US-10-782-141-8	Sequence 8, Appl	
3	3756	99.9	719	17	US-10-782-096-10	Sequence 10, Appl	
4	3756	99.9	719	17	US-10-782-570-7	Sequence 7, Appl	
5	3472.5	92.4	710	14	US-10-428-961-42	Sequence 42, Appl	
6	2377.5	60.6	1228	16	US-10-809-953-10	Sequence 10, Appl	
7	2364.5	60.2	1207	10	US-09-988-462-7	Sequence 7, Appl	
8	2186.5	58.2	1227	14	US-10-428-961-63	Sequence 63, Appl	
9	2171.5	57.8	1186	9	US-09-826-660-23	Sequence 23, Appl	
10	2115	56.2	1228	14	US-10-428-961-38	Sequence 38, Appl	
11	2115	56.2	1228	15	US-10-614-524-2	Sequence 2, Appl	
12	1932.5	51.4	643	9	US-09-826-660-25	Sequence 25, Appl	
13	1724.5	45.9	1167	14	US-10-089-678-1	Sequence 1, Appl	

QY 121 RNKALDGLGDLAVYHDSLESWVGNRNTRARSVVKSYQYIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALDGLGDLAVYHDSLESWVGNRNTRARSVVKSYQYIALELMFVQKLPSPAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYRQVERAGDSDHCVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYRQVERAGDSDHCVKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300  
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 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMW 360  
 QY 361 GGHKLEFRRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYSRLSHIGLIS 420  
 DB 361 GGHKLEFRRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYSRLSHIGLIS 420  
 QY 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIENPNTIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRNTIENPNTIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTDLQPHTSINGKAINQGNFSATWNRGDLDYK 600  
 DB 541 TGTGDIRVNINPPFAQRYRIRYASTDLQPHTSINGKAINQGNFSATWNRGDLDYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTFFSFLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDSEFYLDKRELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDSEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 2  
 US-10-782-141-8  
 ; Sequence 8, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10782,141  
 ; CURRENT FILING DATE: 2004-02-20  
 ; PRIOR APPLICATION NUMBER: 60/448,632  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-8

Query Match 99.9%; Score 3756; DB 17; Length 719;  
 Best Local Similarity 99.9%; Pred. No. 4.5e-308;  
 Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKLKNQDKHQSFSNAKVDKISTDLSKNETDIELQININHEDCLKMSYENVEPVFSASTI 60

DB 1 MKLKNQDKHQSFSNAKVDKISTDLSKNETDIELQININHEDCLKMSYENVEPVFSASTI 60  
 QY 61 QTGIGIAGKIILGTGLVFPFAGQVASYSLFGLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKIILGTGLVFPFAGQVASYSLFGLGELWPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALDGLGDLAVYHDSLESWVGNRNTRARSVVKSYQYIALELMFVQKLPSPAVSG 180  
 DB 121 RNKALDGLGDLAVYHDSLESWVGNRNTRARSVVKSYQYIALELMFVQKLPSPAVSG 180  
 QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYRQVERAGDSDHCVKWYS 240  
 DB 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISFTFYRQVERAGDSDHCVKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300  
 QY 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMW 360  
 DB 301 GTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDLEQVTIYSLSRWSNTQYMMW 360  
 QY 361 GGHKLEFRRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYSRLSHIGLIS 420  
 DB 361 GGHKLEFRRTIGTTLNISTQGSTNTSINPVTLPFTSRDVRYSRLSHIGLIS 420  
 QY 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYYPGYAGIGTQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIENPNTIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRNTIENPNTIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTDLQPHTSINGKAINQGNFSATWNRGDLDYK 600  
 DB 541 TGTGDIRVNINPPFAQRYRIRYASTDLQPHTSINGKAINQGNFSATWNRGDLDYK 600  
 QY 601 TFRVTGFTTFFSFLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
 DB 601 TFRVTGFTTFFSFLDVQSTFTICAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDSEFYLDKRELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDSEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 3  
 US-10-782-096-10  
 ; Sequence 10, Application US/10782096  
 ; Publication No. US20040210964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
 ; TITLE OF INVENTION: Methods for Its Use  
 ; FILE REFERENCE: 045600/274148  
 ; CURRENT APPLICATION NUMBER: US/10782,096  
 ; CURRENT FILING DATE: 2004-02-19  
 ; PRIOR APPLICATION NUMBER: 60/448,633  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-096-10

Query Match 99.9%; Score 3756; DB 17; Length 719;

```
Best Local Similarity 99.9%; Pred. No. 4.5e-308;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASLYSFLGELWPKGKNQWEIIFMEHVBEIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASLYSFLGELWPKGKNQWEIIFMEHVBEIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGVRNNTNRARSVVKSOYIALELMFVKLPSPFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWGVRNNTNRARSVVKSOYIALELMFVKLPSPFAVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNMW 360
QY 361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSLESLAGNLFLTPQVNGVPR 420
Db 361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSLESLAGNLFLTPQVNGVPR 420
QY 421 VDFHWKFWTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
Db 421 VDFHWKFWTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVGVFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Db 601 TFRVGVFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719
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```
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 99.9%; Score 3756; DB 17; Length 719;
Best Local Similarity 99.9%; Pred. No. 4.5e-308;
Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPVSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINIHEDCLKMSYENVEPVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASLYSFLGELWPKGKNQWEIIFMEHVBEIINQKISTYA 120
Db 61 QTGIGIAGKILGTGVPFAGQVASLYSFLGELWPKGKNQWEIIFMEHVBEIINQKISTYA 120
QY 121 RNKALTDLKGGLDALAVYHDSLESWGVRNNTNRARSVVKSOYIALELMFVKLPSPFAVSG 180
Db 121 RNKALTDLKGGLDALAVYHDSLESWGVRNNTNRARSVVKSOYIALELMFVKLPSPFAVSG 180
QY 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
Db 181 BEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYS 240
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
Db 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREVTYDAI 300
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNMW 360
Db 301 GTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYNNMW 360
QY 361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSLESLAGNLFLTPQVNGVPR 420
Db 361 GGKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRYSLESLAGNLFLTPQVNGVPR 420
QY 421 VDFHWKFWTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
Db 421 VDFHWKFWTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540
QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
Db 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600
QY 601 TFRVGVFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
Db 601 TFRVGVFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV 660
QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
```

; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 42  
 ; LENGTH: 710  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (200)..(200)  
 ; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
 US-10-428-961-42

Query Match 92.4%; Score 3472.5; DB 14; Length 710;  
 Best Local Similarity 92.4%; Pred. No. 4e-284;  
 Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;

Qy	1	MKLNQDKHOSFSSNAKVDKISTDLKNETDIELQNHEDCLKMEYENVEPFSASTI	60
Db	1	MKSKQNMHQSLSNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI	51
Qy	61	QTGIGTAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
Db	52	QTGIGTAGKILGNLGVFPFAGQVASYLSFILGELWPKGQWEIFMEHVEEIIINQKISTYA	111
Qy	121	RNKALTDLKGDLALAVYHDSLSWVGNRNTRARSVVKSQVIALELMFVQKLPFAVSG	180
Db	112	RNKALADLKGDLALAVYHDSLSWVGNRNTRARSVVKSQVITILELMFVQSLPFAVSG	171
Qy	181	BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSDHCVKWKYS	240
Db	172	BEVPLPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSKSKKEYSDHCVKWKYN	231
Qy	241	TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI	300
Db	232	TGLNLRGMNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDI	291
Qy	301	GTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYMNW	360
Db	292	GTVHPHPSFTSTTWNNNAPSFTIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYMNW	351
Qy	361	GGHKLFRFTTGGTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFITQPVNGVPR	420
Db	352	GGHKLFRFTTGGTINISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFITQPVNGVPR	411
Qy	421	VDFHWKVFTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS	480
Db	412	VDFHWKVFTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLIS	471
Qy	481	ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAPNLSGAAVVRGPGTGGDILLRRTN	540
Db	472	ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAPNLSGAAVVRGPGTGGDILLRRTN	531
Qy	541	TGTFGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAWNRGDELDYK	600
Db	532	TGTFGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAWNRGDELDYK	591
Qy	601	TERTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEVDFEKAQEV	660
Db	592	TERTVGTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEVDFEKAQEV	651
Qy	661	TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM	719
Db	652	TALFTSTNPRGLKTDVKDHYHDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM	710

## RESULT 6

US-10-809-953-10

; Sequence 10, Application US/10809953

; Publication No. US20040181825A1

; GENERAL INFORMATION:

; APPLICANT: Van Mellaert, Herman  
 ; - APPLICANT: Botterman, Johan  
 ; APPLICANT: Van Rie, Jeroen  
 ; APPLICANT: Joos, Henk  
 ; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING BT INSECTIC  
 ; TITLE OF INVENTION: CRYSTAL PROTEINS  
 ; FILE REFERENCE: 021565-078  
 ; CURRENT APPLICATION NUMBER: US/10/809,953  
 ; CURRENT FILING DATE: 2004-03-26  
 ; PRIOR APPLICATION NUMBER: US/09/661,016  
 ; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/EP90/00905  
 ; PRIOR FILING DATE: 1990-05-30  
 ; PRIOR APPLICATION NUMBER: GB 89401499.2  
 ; PRIOR FILING DATE: 1989-05-31  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-809-953-10

Query Match 60.6%; Score 2277.5; DB 16; Length 1228;  
 Best Local Similarity 62.7%; Pred. No. 8.9e-183;  
 Matches 449; Conservative 80; Mismatches 162; Indels 25; Gaps 6;

Qy	23	TDSLKNETDIELQNH-----EDCLKMSEVENVEPFSASTIQTGIGTAGKI	70
Db	2	TSNRKNEINEINAVSNHSAQMDLLDPARDIEDSLCIAEGNNIDPFVSASTVQGINIAGRI	61
Qy	71	LGTGLVFPFAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKALTDLKG	130
Db	62	LGVLPFPFAGQVASYLSFILGELWPRGRDQWEIFLEHVEQLINQITENARTALARLQ	121
Qy	131	LGDLAVYHDSLSWVGNRNTRARSVVKSQVIALELMFVQKLPSPFVSGSEVPLPIYA	190
Db	122	LGDSFRAYQQSLEDWLENRDDARTRSVLHTQYIALEDLFLNAPLFAIRNQEVLPMVYA	181
Qy	191	QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVRAGDYSDHCVKWKYSTGLNLRGTN	250
Db	182	QAANLHLLLRDASIFGSEFGLTSQEIQRYYERQVTRDYSYCVWEYNTGLNSLRGTN	241
Qy	251	ABSRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDIAGTVHPHPSFT	310
Db	242	AASVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDIAGTVHPHPSFT	299
Qy	311	STTWNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYMNWGGHKLFRFTI	370
Db	300	SMWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLLSRWSNTQYMNWGGHKLFRFTI	359
Qy	371	GGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHWKVF	428
Db	360	GGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLF--LTQPVNGVPRVDFHWKVF	416
Qy	429	THP-----IASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH	483
Db	417	TNPQNSDRGTANYSQP-YESPGQLQDSENELPPEATGQPNYESYSHRLSHIGLISASH	475
Qy	484	VKALVYSWTHRSADRTNTIEPNSITQIPLVKAPNLSGAAVVRGPGTGGDILLRRTNTGT	543
Db	476	VNVPVYSWTHRSADRTNTIEPNSITQIPLVKAPNLSGAAVVRGPGTGGDILLRRTNTGT	535
Qy	544	FGDIRVNNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAWNRGDELDYKTFR	603
Db	536	FGPIRVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTNNVNNFRFRMTNMSGDELKYGNEV	595
Qy	604	TVGFTTPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEVDFEKAQEV	663
Db	596	RRAFITPFTTQIQDIIRTSIQGLSGNCEVYIDKIEIPVTATFEAEYDLERAQAVNAL	655
Qy	664	FTSTNPRGLKTDVKDHYHDQVSNLVESLSDFFYLDEKRELFEIVKAKQLHIERNM	719

Db 656 FTNTNPRRLKTDVTDYHIDQVSNLVACLSDPCLDEKRELLEKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7  
 ; Sequence 7, Application US/09988462  
 ; Publication No. US20030046726A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kozziel, Michael G.  
 ; Desai, Nalini M.  
 ; Lewis, Kelly S.  
 ; Kramer, Vance C.  
 ; Warren, Gregory W.  
 ; Evola, Stephen V.  
 ; Crossland, Lyle D.  
 ; Wright, Martha S.  
 ; Merlin, Ellis J.  
 ; Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: NC  
 COUNTRY: USA  
 ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462  
 FILING DATE: 20-NO. US20030046726A1-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422  
 FILING DATE: 11-APR-2000  
 APPLICATION NUMBER: US 08/459,504  
 FILING DATE: 02-JUN-1995  
 APPLICATION NUMBER: US 07/951,715  
 FILING DATE: 25-SEP-1992  
 APPLICATION NUMBER: US 07/772,027  
 FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: S-188051  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919)541-8587  
 TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 60.2%; Score 2264.5; DB 10; Length 1207;  
 Best Local Similarity 64.3%; Pred. No. 1.1e-181;  
 Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

Qy 40 EDCLKVSEYENVEPVFVSTQIGIGIAGKILGTGVFPAGOVASLYSFIIGELWPKGN 99  
 Db 10 EDSLCAEGNNIDFVASTVQIGINILGVLGVFPAGQLASYSFVLGELWPKGRD 69  
 Qy 100 QWEIFMEHVETIIKISTYARNKALTDLKGDLALAVYHDSLESVWGNRNNTRARSVVK 159  
 Db 70 QWEIFLEHVQEQINQINARNTALRQLGLDSFRAYQQSLEDWLENRDDARTSVLY 129

Qy 160 SOYIALELMFVQKLPSPAVSGEEVPLLPYAOAANLHLLLRDASIFGKEWGLSSSEIST 219  
 Db 130 TQYIALELDFLNAMEPLFAIRNQEVPLLPYAOAANLHLLLRDASIFGSEFGLTSQRIOR 189  
 Qy 220 FYNQOVERAGDYSCHVKYSTGLNNLCTNAESWVRNQFRDMLVLDLVALPFSYD 279  
 Db 190 YERQVERTRDYSYCVWYNTGLNLSLGTNAASWVRNQFRDMLVLDLVALPFSYD 249  
 Qy 280 TOMPIKTTAQLTRVYVTAIGTVHPHSFTSTWYNNAPSFSAIEAAVVRNPHLLDFL 339  
 Db 250 TRTYPINTSAQLTRVYVTAIGAT - GVNMAVMWYNNAPSFSAIEAAVVRNPHLLDFL 307  
 Qy 340 EQVTIYSLSRWSNTQYMNMGHKLERTIGTTLNLTSTQSTNTSINPVLTPFTSRDVS 399  
 Db 308 EQLTIFASRRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVLTRFASRDVS 367  
 Qy 400 RTESLAGLNLFP - LTQPVNGVPRVDFHMKFVTHP - IASDNFYYPGVYIGTQLQDS 452  
 Db 368 RTESYAGVLLWGIYLEPIEGVPTVRFPF - TNPQNSDRGTANYSP - YESFGLQLKDS 423  
 Qy 453 ENELPPEATGQPNYESYSHLSHIGLISASHVKALVSWTHRSADRNTNTPNSITQIPL 512  
 Db 424 ETELPPETTERPNYESYSHLSHIGIILQSRVNVVPVYSWTHRSADRNTNTPNRIITQIPM 483  
 Qy 513 VKAFNLSSGAAVVRGPGFTGGDIILRRNTGTGDIRVNNINPPAQRVRYRYASTTDLQ 572  
 Db 484 VKASELPQGTTVVRGPGFTGGDIILRRNTGTGDIRVNVNGLPTQRYRIGFYASTVDFD 543  
 Qy 573 PHTSINGKAINQGNFSATWNRGDLDTKTRTVGFTTTPFSLDVSQSTTIGANWFFSGNE 632  
 Db 544 PFVSRGTTVNNFRFLRTMNSGDELKYGNFVRRRAFTTPTFTQIQDIIRTSIQGLSGNE 603  
 Qy 633 VYIDRIEFVPEVTEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDHYDQVSNLVESLS 692  
 Db 604 VYIDKIEIIPVTATEAEYDLERAQEAVALFTNPNRLKTDVTDYHIDQVSNLVACL 663  
 Qy 693 DEFYLDKRELFEIVKYAKOLHIERNM 719  
 Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63  
 ; Sequence 63, Application US/10428961  
 ; Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Donovan, William P.

APPLICANT: Gilmer, Amy J.

APPLICANT: Rupa, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
 ; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECO201-1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin version 3.2

SEQ ID NO 63

LENGTH: 1227

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 58.2%; Score 2186.5; DB 14; Length 1227;  
 Best Local Similarity 59.2%; Pred. No. 4.3e-175;  
 Matches 423; Conservative 105; Mismatches 173; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTDSLKN-----ETDIEQININHHEDCLKMSYENVEPFFVASTIQTIG 65  
 Db 7 NENEIINALSPAVSNHSAQMNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61  
 QY 66 IAGKILGTLGVPPFAQVAVSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125  
 Db 62 IAGRILGVLPFAQVAVSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 121  
 QY 126 TDLKGLGDALAVYHDSLESWVGNRNNTRRSVVKSQYIALELMFVQKLPSPFAVSGEEVPL 185  
 Db 122 ARLOGLGNSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAFLFAIRNQEVPL 181  
 QY 186 LPIYAQAANLHLLLRDASIFGKELWGLSSSEISTFYNRQVERAGDYSCHCVKWSYGLNN 245  
 Db 182 LMVYAQAANLHLLLRDASIFGSEFGLTSQEIORYYERQVETREYSDYCARWYNTGLNN 241  
 QY 246 LRGTNAESWVRYNQFRDRLTMLVLDLVALFPSPYDTQMPYIKTAQLTRVYTDALGTVHP 305  
 Db 242 LRGTNAESWVRYNQFRDRLTMLVLDLVALFPSPYDTQMPYIKTAQLTRVYTDALGTVHP 301  
 QY 306 HPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNWGGHKL 365  
 Db 302 PSGFASTNWFNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNWGGHKL 361  
 QY 366 EFRITGTLNISTQGSTNTSINPVTLPFTSRDVRYSLAGLNLFTQPVNGVPRVDFHW 425  
 Db 362 ESRTIGSLSTWHTGNTSINPVTLPFTSRDVRYSLAGLNLFTQPVNGVPRVDFHW 421  
 QY 426 KFTVTHPIASDNFYYPGVIGTQDSENELPPEATQPNYESYSHRSLSHIGLISASHVK 485  
 Db 422 RNPLNSLRGSLTYTIGTGVGTQFDSELPETTERPNYESYSHRSLSHIGLISASHVK 481  
 QY 486 ALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRNTGTFG 545  
 Db 482 APVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRNTGTFG 541  
 QY 546 DIRVNINPPFAQVAVSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 719  
 Db 661 NTNPRRLKGTVDYHIDEVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 714

RESULT 9  
 US-09-826-660-23  
 ; Sequence 23, Application US/09826660  
 ; Patent No. US20010026940A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cardineau, Guy A.  
 ; APPLICANT: Steelman, Steven J.  
 ; APPLICANT: Narva, Kenneth E.  
 ; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
 ; FILE REFERENCE: MA-714XC2D1  
 ; CURRENT APPLICATION NUMBER: 2001-04-05  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 09/178,252  
 ; PRIOR FILING DATE: 1998-10-23  
 ; PRIOR APPLICATION NUMBER: 60/065,215  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/076,445  
 ; PRIOR FILING DATE: 1998-03-02  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 23  
 ; LENGTH: 1186  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence

FEATURE:  
 ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
 US-09-826-660-23  
 Query Match 57.8%; Score 2171.5; DB 9; Length 1186;  
 Best Local Similarity 59.0%; Pred. No. 7.5e-174;  
 Matches 421; Conservative 108; Mismatches 172; Indels 13; Gaps 3;  
 QY 13 SSNAKVDKISTDSLKN-----ETDIEQININHHEDCLKMSYENVEPFFVASTIQTIG 65  
 Db 7 NENEIINALSPAVSNHSAQMNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61  
 QY 66 IAGKILGTLGVPPFAQVAVSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 125  
 Db 62 IAGRILGVLPFAQVAVSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 121  
 QY 126 TDLKGLGDALAVYHDSLESWVGNRNNTRRSVVKSQYIALELMFVQKLPSPFAVSGEEVPL 185  
 Db 122 ARLOGLGNSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFLNAFLFAIRNQEVPL 181  
 QY 186 LPIYAQAANLHLLLRDASIFGKELWGLSSSEISTFYNRQVERAGDYSCHCVKWSYGLNN 245  
 Db 182 LMVYAQAANLHLLLRDASIFGSEFGLTSQEIORYYERQVETREYSDYCARWYNTGLNN 241  
 QY 246 LRGTNAESWVRYNQFRDRLTMLVLDLVALFPSPYDTQMPYIKTAQLTRVYTDALGTVHP 305  
 Db 242 LRGTNAESWVRYNQFRDRLTMLVLDLVALFPSPYDTQMPYIKTAQLTRVYTDALGTVHP 301  
 QY 306 HPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNWGGHKL 365  
 Db 302 PSGFASTNWFNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMNWGGHKL 361  
 QY 366 EFRITGTLNISTQGSTNTSINPVTLPFTSRDVRYSLAGLNLFTQPVNGVPRVDFHW 425  
 Db 362 ESRTIGSLSTWHTGNTSINPVTLPFTSRDVRYSLAGLNLFTQPVNGVPRVDFHW 421  
 QY 426 KFTVTHPIASDNFYYPGVIGTQDSENELPPEATQPNYESYSHRSLSHIGLISASHVK 485  
 Db 422 RNPLNSLRGSLTYTIGTGVGTQFDSELPETTERPNYESYSHRSLSHIGLISASHVK 481  
 QY 486 ALVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRNTGTFG 545  
 Db 482 APVYSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAVRGPFGTGGDILRRNTGTFG 541  
 QY 546 DIRVNINPPFAQVAVSYFILGELWPKGNQWEIFMEHVEEIIINQKISTYARNKAL 719  
 Db 661 NTNPRRLKGTVDYHIDEVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL 714

RESULT 10  
 US-10-428-961-38  
 ; Sequence 38, Application US/10428961  
 ; Publication No. US20030237111A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baum, James A.  
 ; APPLICANT: Chu, Chih-Rei  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Gilmer, Amy J.  
 ; APPLICANT: Rupa, Mark J.  
 ; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
 ; FILE REFERENCE: MECO201--1  
 ; CURRENT APPLICATION NUMBER: 2003-05-02  
 ; PRIOR FILING DATE: 2003-05-02  
 ; PRIOR APPLICATION NUMBER: 09/661,322



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; Sequence 25, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Steelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
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US-09-826-660-25

Query Match      51.4%; Score 1932.5; DB 9; Length 643;
Best Local Similarity 57.7%; Pred. No. 4.6e-154;
Matches 371; Conservative 100; Mismatches 159; Indels 13; Gaps 3;

QY 13 SSNAKVDKISTDSLNK-----ETDILQNIHEDCLKMEYENVEPPFVSASTIQTGIG 65
DB 7 NENEINAIISIPAVSHSAQMNLSTDARI-----EDSLCIAEGNIDPFVSASTVQTGIN 61

QY 66 IAGKILGTLCVPPFAGQVAVSLYFSLGELWPKGNQWEIFMEHVEEIIQKISTYARNKAL 125
DB 62 IAGRIILGVLPFAGQVAVSLYFSLGELWPKGNQWEIFMEHVEEIIQKISTYARNKAL 121

QY 126 TDLKGLGDALAVVHDSLESVWGNRNTRARSVVKSVYALFELMFVQKLPFVAGSEVEPL 185
DB 122 ARLOGLGNSFRAYQOSLELDWLENRDDARTSVLYTQVIALBELDFNAMPFAIRNQEVPL 181

QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGDYSCHVKWYSTGLNN 245
DB 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYERQVETREYSYDVCARWNTGLNN 241

QY 246 LRGTNAESWVRYNQFRDDMTLMDLVALFPSYDTQVPIKTTAQLTREVVYTDAGTVHP 305
DB 242 LRGTNAESWVRYNQFRDDMTLMDLVALFPSYDTQVPIKTTAQLTREVVYTDAGTVHP 301

QY 306 HPSFTSTTWNNNAPSFAIAEAAVVRPHLLDFLEQVITYLLSRWNTQYMMWGGHKL 365
DB 302 PSFGFASTNFWNNNAPSFAIAEAAVVRPHLLDFLEQVITYLLSRWNTQYMMWGGHKL 361

QY 366 EFRITGGTLNISTOGSTNTSINPVLTPSTRDVRVRESLAGNLFLTPQVNGVRVDVFW 425
DB 362 ESRTIRGSLSTSGHNTNTSINPVLTPSTRDVRVRESLAGNLFLTPQVNGVRVDVFW 421

QY 426 KFTVPIASDNFYVGYGIGTQLODSENELPPEATQOPNYESYSHRLSHIGLSASHVK 485
DB 422 RNPLNSLRGSLLYTIGYGVGTQLFDSETELEPPTETPERPNYESYSHRLSHIRLSGNTLR 481

QY 486 ALVXSWTHRSADRNTWIEPNSITQIPLVKAFLNLSGGAAVVRGPGFTGGDILLRRNTGTFG 545
DB 482 APVXSWTHRSADRNTWIEPNSITQIPLVKAFLNLSGGAAVVRGPGFTGGDILLRRNTGTFG 541

QY 546 DIRVNIINPPAQRYRIRYASTDLOFHTSINGKAINQGNFSAATMRGDDLDVKTFRV 605
DB 542 SMGLNFNTSLQRYRIRYASTDLOFHTSINGKAINQGNFSAATMRGDDLDVKTFRV 601

QY 606 GFTTFFSLDQVSTFTIGAWNFSSGNEVYIDRIEFVPEVTVYE 648
DB 602 EFPVGISAGSQ-TAGISISNAGRQTFHFDEKIEFIPITATLE 643
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RESULT 13

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US-10-089-678-1
; Sequence 1, Application US/10089678
; Publication No. US20030017967A1
; GENERAL INFORMATION:
```

```
; APPLICANT: ASANO, Shinichiro
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN
; NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
; FILE REFERENCE: Q68821
; CURRENT APPLICATION NUMBER: US/10/089,678
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: JP 2000-236140
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/JP01/06660
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
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US-10-089-678-1
```

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Query Match      45.9%; Score 1724.5; DB 14; Length 1167;
Best Local Similarity 48.1%; Pred. No. 4.3e-136;
Matches 362; Conservative 125; Mismatches 220; Indels 45; Gaps 11;

QY 1 MKLKNQDKHO---SPSSNAKVDKISTDSLNKEDIELQNIHEDCLKMEYE-----NV 51
DB 1 MSPNNQNEYELDASSSTVSVDNSVRYPLANDOTTQNNMYKDYLRMSEGENPELPGNP 60

QY 52 EPPVSASTIOTGIGTAGKILGTLCVPPFAGQVAVSLYFSLGELWPKGNQWEIFMEHVEE 110
DB 61 ETFISSSTVGTGIGIVGVLPFAGQVAVSLYFSLGELWPKGNQWEIFMEHVEE 120

QY 111 IINQKISTYARNKALTDKGLGDALAVVHDSLESVWGNRNTRARSVVKSVYALFELMFV 170
DB 121 LIDQKITDSVRKTAGLQGLDGLDVYQKSLKNWLENRNDTRARSVVTQVIALELDFV 180

QY 171 OKLPSPFVAGSEVEPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGD 230
DB 181 AKIPSPFVAGSEVEPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNQVRAGD 240

QY 231 YSDHCVKWYSTGLNLRGNAESWVRYNQFRDDMTLMDLVALFPSYDTQVPIKTTA 290
DB 241 YSDYCVKWNVTGLDKLKGNAASWLKHQFRREMTLLVLDLVALFPNYDTRTYPIET 300

QY 291 LTREVVYTDAGTVHPHPSFTSTTWNNNAPSFAIAEAAVVRPHLLDFLEQVITYLLS 349
DB 301 LTREVVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLLDILSIEFYTRAG 360

QY 350 -RWSNTQYMMWGGHKLERTIGTTLNISTOGSTNTSINPVLTPSTRDVRVRESLAG 407
DB 361 LPLNNTLEYLWVGHSHIRYKNTNASSALERNYGTITSNKIKYDLANKDIPQVRSGLAD 420

QY 408 NLFLTPQVNGVRVDVFWKFTVPIASDNFYVGYGIGTQLODSENELPPEATQOPN 455
DB 421 ANYYAA-VYGVVPYASF-----TLLDKNTGSGSVGGFTYSKPHHTMQVCTQNTYNT 471

QY 456 LPPEATQOPNYESYSHRLSHIGLS-----ASHVKALVYSWTHRSADRNTWIEPNSI 507
DB 472 IPPE--NEPLSRGYSHRLSHITSYFSKXNASSPARYGNLPPFAWTHRSADRNTWIEPNSI 529

QY 508 TQIPLVKAFLNLSGGAAVVRGPGFTGGDILLRRNTGTFGDIRVNIINPPAQRYRIRYAS 567
DB 530 TQIPLVKAFLNLSGGAAVVRGPGFTGGDILLRRNTGTFGDIRVNIINPPAQRYRIRYAS 589

QY 568 TTDLOFHTSINGKAINQGNFSAATMRGDDLDVKTFRVFTVGGTTPFSLDQVOSTFTIGAWNF 627
DB 590 TTNRLFVITSGTRIYSINWNTKMGDDLTFTNTFDLATIGTAFATSNYSLSLTGADSF 649
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QY 628 SSGNEVYIDRIEVPVEVYEAEDFEKAQKVTALFTSTNPRGLKTDYKDYHIDOVNLS 687
Db 650 ASGGEVYVDKFLIPVATFEABEDLDVAKAVNGLTFSKKD-ALQTSVTDYQVQAANL 708
QY 688 VESLSDEFYLDKRELFELFEIVKAKQLHIERNM 719
Db 709 VECLSDLYPNEKRMWDAVKEAKRLVQARNL 740

RESULT 14
US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 44.7%; Score 1680.5; DB 14; Length 653;
Best Local Similarity 51.5%; Pred. No. 9.2e-133;
Matches 346; Conservative 106; Mismatches 173; Indels 47; Gaps 14;

QY 13 SSNAKVDKISTSLKN---ETDIELQNHEDCLMSEYENVEPVSASTIQTGIGIAGK 69
Db 2 NENEIINALSIPAVSNHSAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQTGINAGR 60
QY 70 ILGLGVFPAGVSLYSFILGELWPKGNOWEIMEHVEEIIINOKISTYARNKALTDLK 129
Db 61 ILGLGVFPAGVSLYSFILGELWPSGRDPWEIFLEYVEQLRQOVTENTRTAIALLE 120
QY 130 GLGDALAVYHDSLESWGNRNNTTRARSVKQYIALELMFVQKLPSPFVSGEEVPLLPY 189
Db 121 GLGRGYRYSQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRINNEEVPLLMVY 180
QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSHCVKYVSTGLNNLRGT 249
Db 181 AQANLHLLLRDASLFGSEWGMASDVNQYQEIRYTBESNHCQVQNTGLNNLRGT 240
QY 250 NAESWVRNQFRDMDTMLVLDLVALFSDYDQMPYKTKTAQLTREVVYTDALGTVHPHPSP 309
Db 241 NAESWLRYNQFRDLTLGLVLDLVALFSDYDTRYPINTSAQLTREIYTDPIGRNAPSGF 300
QY 310 TSTWYNNAPSSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNWGGHKLERT 369
Db 301 ASINWFNNAPSSAIEAAIPRPHLLDFPQLTIYSASSRWSSTQHMVWVGHRLNRP 360
QY 370 IGGTLNISTQGST-NTSINPVLFP-TSRDVRTESLAGNLFTLPQVNGVPRVDFHWKF 427
Db 361 IGGTLNTSTQGLTNTSINPVLHYSSRDVRTESNAGNLTFTTPVNGVPRVAFN--F 418
QY 428 VTHPIASDNFYFP-----GYVGIGTQLQDSENELPPEATGQPNYESYSHRLSHIG-- 477
Db 419 ITRIFMKEAPLPTVNRIRELGPNYLIQKLNHQK-----QQNDQIMNHIVIDISYR 470
QY 478 LISASHVKALVSWTHRSADRTNTIENSITQIPLVKAFNLSSGAUVVRGPGFTGGDILR 537
```

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Db 471 LIIGNTLRAPVYSWTHRSADRTNTIGPRITQIPAVKGRFLFNG-SVISGPGFTGGDVR 529
QY 538 -RTNIGTF---GDIRVNIN-PPFAQRYVRIRYASTTDLQFHTSINGKAINOGNFSATMN 592
Db 530 LNRNNGNIQNRGYIEVPIQFTSTSTRYVRVRYASVTSIELNVNGLNSSIFTNTLPATAA 589
QY 593 RGEDLDYKTRTGTFTTSPFSLDVQSTFT-----IGAWNFSGNEVYIDRIEFPVPEVT 646
Db 590 SLDNLQ-----SGDFGYVEINNAFTSATCNIVGARNFSANAEEVIDREFIPIVTAT 640
QY 647 YEAEYDFEKAQE 658
Db 641 FEVEYDLERAQK 652

RESULT 15
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match 44.4%; Score 1669.5; DB 17; Length 1157;
Best Local Similarity 49.1%; Pred. No. 1.9e-131;
Matches 371; Conservative 98; Mismatches 230; Indels 57; Gaps 18;

QY 1 MKLKNQDKHQSFSNAKVDKISTDS---LKNETDIELQNHEDCLMSEYE-----N 50
Db 1 MSPNNQNEYIIDIATPST-SVSDSNRVPFANEPTDALQNMNYKDYLMKMSGGENPELFGN 59
QY 51 VEPFVSASTIQTGIGIAGKILGTIGVPAGVSLYSFILGELWP-KGKNQWEIPEHVE 109
Db 60 PETFISSSTIQTGIGIAGVGRILGALGVPPASQIASFYSFIVGQLWPSKSVDIWGEINERVE 119
QY 110 EIIINQKISTYARNKALTDLKGLGDALAYHDSLESWGNRNNTTRARSVKQYIALELMF 169
Db 120 ELVDQKIEKYVKDKALAEKLGKGNALDVYQSLDLEWLNDRNDARTSRWSNQFIALDLNF 179
QY 170 VQKLPSFVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAG 229
Db 180 VSSISFVSGHEVLLAVYAQAANLHLLLRDASIFGEEWGTTPGEISRFYNRQVQLTA 239
QY 230 DYSRCHVKWYSTGLNNLRGTNAESWVRYNQFRDMDTMLVLDLVALFSDYDQMPYIKTTA 289
Db 240 EYSDYCVKWKYKIGLDKLTTSKSWLNHYHQFREMLLVLDLVALFPNYDTHMYPIETTA 299
QY 290 QLTREVVYTDALGTVHPHPSTST---TWYNNAPSSAIEAAVVRNPHLLDFLEQVTIY 345
Db 300 QLTREVVYTDPIA-----FNIVTSTGFCNFWSTHSGILFYEVENNVRPPLHLDLSSVEIN 355
QY 346 SLLSR-----WSNTQYMNWGGHKLFR-----TIGGTINISTQGSTINTSINPVLFPFTR 396
Db 356 T--SRGGITLNNDAYINYSWGHTLKRYRTADSTVTVTYANYGRITSEKNS-----FALEDR 408
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-57  
Perfect score: 3760  
Sequence: 1 MKLNQDKHQSFSSNAKVDK.....KRELFIVKYAKQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	3752	99.8	719	3 US-08-286-870A-8	Sequence 8, Appli
2	3472.5	92.4	710	4 US-09-661-322A-42	Sequence 42, Appli
3	3394	90.3	648	3 US-08-286-870A-4	Sequence 4, Appli
4	3373	89.7	719	2 US-09-003-217-2	Sequence 2, Appli
5	3368	89.6	719	3 US-09-218-942-2	Sequence 2, Appli
6	2800	74.5	535	3 US-08-286-870A-6	Sequence 6, Appli
7	2445.5	65.0	1229	1 US-08-100-709-4	Sequence 4, Appli
8	2445.5	65.0	1229	1 US-08-176-865-4	Sequence 4, Appli
9	2445.5	65.0	1229	1 US-08-474-038-4	Sequence 4, Appli
10	2445.5	65.0	1229	2 US-08-779-046-4	Sequence 4, Appli
11	2445.5	65.0	1229	2 US-08-881-340-4	Sequence 4, Appli
12	2340.5	62.2	488	1 US-08-448-170-10	Sequence 10, Appli
13	2340.5	62.2	488	3 US-08-961-803-10	Sequence 10, Appli
14	2264.5	60.2	1207	1 US-07-951-715A-7	Sequence 7, Appli
15	2264.5	60.2	1207	2 US-08-459-448A-7	Sequence 7, Appli
16	2264.5	60.2	1207	3 US-08-459-595A-7	Sequence 7, Appli
17	2264.5	60.2	1207	3 US-08-459-504B-7	Sequence 7, Appli
18	2264.5	60.2	1207	3 US-08-459-444-7	Sequence 7, Appli
19	2264.5	60.2	1207	3 US-09-053-549-8	Sequence 8, Appli
20	2264.5	60.2	1207	3 US-09-547-422-7	Sequence 7, Appli
21	2264.5	60.2	1207	4 US-09-988-462-7	Sequence 7, Appli
22	2263.5	60.2	1227	3 US-09-053-549-2	Sequence 2, Appli
23	2195.5	58.4	1227	1 US-08-448-170-8	Sequence 8, Appli
24	2195.5	58.4	1227	3 US-08-961-803-9	Sequence 9, Appli
25	2186.5	58.2	1227	4 US-09-661-322A-63	Sequence 63, Appli
26	2171.5	57.8	1186	3 US-09-178-252-23	Sequence 23, Appli
27	2171.5	57.8	1186	4 US-09-826-660-23	Sequence 23, Appli

Sequence 38, Appli  
Sequence 25, Appli  
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Sequence 4, Appli  
Sequence 6, Appli  
Sequence 30, Appli  
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Sequence 5, Appli  
Sequence 5, Appli  
Sequence 72, Appli  
Sequence 72, Appli

28 2115 56.2 1228 4 US-09-661-322A-38  
29 1932.5 51.4 643 3 US-09-178-252-25  
30 1932.5 51.4 643 4 US-09-826-660-25  
31 1900 50.5 380 5 PCT-US91-02560-4  
32 1680.5 44.7 653 4 US-09-661-322A-6  
33 1669.5 44.4 1157 1 US-07-876-280-30  
34 1669.5 44.4 1157 1 US-07-812-180A-2  
35 1669.5 44.4 1157 1 US-08-315-468-2  
36 1669.5 44.4 1157 3 US-07-941-650A-2  
37 1505.5 40.0 1176 1 US-08-257-999-2  
38 1494 39.7 1157 2 US-08-532-547-5  
39 1494 39.7 1157 2 US-08-379-656B-5  
40 1494 39.7 1157 3 US-08-455-838-5  
41 1494 39.7 1157 3 US-09-019-809-5  
42 1494 39.7 1157 4 US-09-471-177-5  
43 1494 39.7 1157 4 US-09-220-806-5  
44 1487.5 39.6 1156 3 US-09-002-285-72  
45 1487.5 39.6 1156 4 US-09-589-477-72

## ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

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Query Match      99.8%; Score 3752; DB 3; Length 719;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 717; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60

QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMHEVBEIINQKISTYA 120
DB 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMHEVBEIINQKISTYA 120

QY 121 RNKALTDLKGGLDALAVYHDSLSWVGNRNNTRARSVVKSQYIALELMFVQKLPFAVSG 180
DB 121 RNKALTDLKGGLDALAVYHDSLSWVGNRNNTRARSVVKSQYIALELMFVQKLPFAVSG 180

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240

QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDAL 300
DB 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDAL 300

QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMNW 360
DB 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMNW 360

QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNFLTPQVNGVPR 420
DB 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNFLTPQVNGVPR 420

QY 421 VDFHWKVFTHPIASDNFYYPGYGIGTQLODSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 421 VDFHWKVFTHPIASDNFYYPGYGIGTQLODSNELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVYSWTHRSADRNTIENPISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 481 ASHVKALVYSWTHRSADRNTIENPISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540

QY 541 TGTFGDIRVNINPPAQRVRYRYASTTDLQPHTSINGKAINQGNFSAATNRGDLDYK 600
DB 541 TGTFGDIRVNINPPAQRVRYRYASTTDLQPHTSINGKAINQGNFSAATNRGDLDYK 600

QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

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RESULT 2
US-09-661-322A-42
; Sequence 42, Application US/09661322A
; Patent No. 6593293
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruzar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo
; FILE REFERENCE: MECO201
; CURRENT APPLICATION NUMBER: US/09/661,322A
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 710
; TYPE: PRT

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; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (200)..(200)
; OTHER INFORMATION: No. 6593293-Coding
US-09-661-322A-42

Query Match      92.4%; Score 3472.5; DB 4; Length 710;
Best Local Similarity 92.4%; Pred. No. 1.8e-302;
Matches 664; Conservative 15; Mismatches 31; Indels 9; Gaps 1;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 60
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPVSASTI 51

QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMHEVBEIINQKISTYA 120
DB 52 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELMPKGNQWEIFMHEVBEIINQKISTYA 111

QY 121 RNKALTDLKGGLDALAVYHDSLSWVGNRNNTRARSVVKSQYIALELMFVQKLPFAVSG 180
DB 112 RNKALADLKGGLDALAVYHDSLSWVGNRNNTRARSVVKSQYIALELMFVQKLPFAVSG 171

QY 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 240
DB 172 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHCVKWS 231

QY 241 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDAL 300
DB 232 TGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYPIKTTAQLTREYVTDAL 291

QY 301 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMNW 360
DB 292 GTVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMNW 351

QY 361 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNFLTPQVNGVPR 420
DB 352 GGHKLEFRITGGTLNISTOGSTNTSINPVTLPFTSRDVRYSAGLNFLTPQVNGVPR 411

QY 421 VDFHWKVFTHPIASDNFYYPGYGIGTQLODSNELPPEATQPNYESYSHRLSHIGLIS 480
DB 412 VDFHWKVFTHPIASDNFYYPGYGIGTQLODSNELPPEATQPNYESYSHRLSHIGLIS 471

QY 481 ASHVKALVYSWTHRSADRNTIENPISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB 472 ASHVKALVYSWTHRSADRNTIENPISITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531

QY 541 TGTFGDIRVNINPPAQRVRYRYASTTDLQPHTSINGKAINQGNFSAATNRGDLDYK 600
DB 532 TGTFGDIRVNINPPAQRVRYRYASTTDLQPHTSINGKAINQGNFSAATNRGDLDYK 591

QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660
DB 592 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 651

QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
DB 652 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 710

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RESULT 3
US-08-286-870A-4
; Sequence 4, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN

```

ADDRESSEE: Intellectual Property Group of  
 ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/286,870A  
 FILING DATE: 05-AUG-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/520228  
 FILING DATE: 09-MAY-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 8910624.9  
 FILING DATE: 09-MAY-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PAUL N. KOKULIS  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 70608/220720  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 648 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-286-870A-4

Query Match 90.3%; Score 3394; DB 3; Length 648;  
 Best Local Similarity 99.8%; Pred. No. 1.8e-295;  
 Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLXSEYENVEPVSASTI	60
DB	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLXSEYENVEPVSASTI	60
QY	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
DB	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
QY	121	RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKQYIAELMFPVKLPSPFVSG	180
DB	121	RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKQYIAELMFPVKLPSPFVSG	180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWYS	240
DB	181	EEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWYS	240
QY	241	TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI	300
DB	241	TGLNNLRGTNAESWRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDAI	300
QY	301	GTVHPHPSTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLGRWSNTQYNNMW	360
DB	301	GTVHPHPSTSTWYNNAPSPSAIEAAVVRNPHLLDLEQVTIYSLGRWSNTQYNNMW	360
QY	361	GGHKLEFRITIGTILNISTQGSTNTSINPVLPTSDVYTESLAGNLFQTQVNGVPR	420
DB	361	GGHKLEFRITIGTILNISTQGSTNTSINPVLPTSDVYTESLAGNLFQTQVNGVPR	420
QY	421	VDPHWKVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480
DB	421	VDPHWKVTHPIASDNFYYPGVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS	480

QY	481	ASHVKALVSWTHRSADRTNTIENSIQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN	540
DB	481	ASHVKALVSWTHRSADRTNTIENSIQIPLVKAFNLSSGAAVVRGPGFTGGDIILRTN	540
QY	541	TGTFGDIRVNINPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK	600
DB	541	TGTFGDIRVNINPPPAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK	600
QY	601	TFTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTYE	648
DB	601	TFTVGTFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTYE	648

RESULT 4

US-09-003-217-2  
 ; Sequence 2, Application US/09003217  
 ; Patent No. 5986177  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia A.  
 ; APPLICANT: Mackour, Magdy A.  
 ; APPLICANT: Bulla, Lee A.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
 ; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
 ; STREET: 3605 Glenwood Ave. Suite 310  
 ; CITY: Raleigh  
 ; STATE: NC  
 ; COUNTRY: US  
 ; ZIP: 27622  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/003,217  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spruill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: 5718-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919 420 2202  
 ; TELEFAX: 919 881 3175  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 719 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-003-217-2

Query Match 89.7%; Score 3373; DB 2; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 1.6e-293;  
 Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;

QY	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLXSEYENVEPVSASTI	60
DB	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLXSEYENVEPVSASTI	60
QY	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
DB	61	QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVEEIIINQKISTYA	120
QY	121	RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKQYIAELMFPVKLPSPFVSG	180
DB	121	RNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVKQYIAELMFPVKLPSPFVSG	180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWYS	240

Db 181 BEVPLLPYAAANLHLLLRDASIFGKNGGLSASEISTFFYNQVERTRDYSYHCVKWN 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTYDTQMPYIKTTAQLTREVYTDI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTYDTQMPYIKTTAQLTREVYTDI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSPFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMNW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSPFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMNW 360  
 QY 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420  
 Db 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420  
 QY 421 VDFHKKFVTHPIASDNFYYPGYGIGTOLQDSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 Db 421 VDFHKKFVTHPIASDNFYYPGYGIGTOLQDSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTDLPHTSINGKAINQGNFSATWNRGDLGYK 600  
 Db 541 TGTGDIRVNINPPFAQRYRIRYASTDLPHTSINGKAINQGNFSATWNRGDLGYK 600  
 QY 601 TFRVTGTFPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 Db 601 TFRVTGTFPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELVDKEKELFEIVKYAKQIHERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELVDKEKELFEIVKYAKQIHERNM 719

RESULT 5

US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; FILE REFERENCE: Crv11  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; EARLIER FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRF  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 89.6%; Score 3368; DB 3; Length 719;  
 Best Local Similarity 89.7%; Pred. No. 4.5e-293;  
 Matches 645; Conservative 33; Mismatches 41; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSNAKVDKISTDLKNETDIELQNHEDCLKXSEYENVEPFFVSASTI 60  
 Db 1 MKLNQDKHQSFSNAKVDKISTDLKNETDIELKNNEDYLRSEHESIDPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
 Db 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALTDLKGLDALAVHDSLESWGNRNTRARSVVKQSVIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGLDALAVHDSLESWGNRNTRARSVVKQSVIALELMFVQKLPFAVSG 180

QY 181 BEVPLLPYAAANLHLLLRDASIFGKNGGLSASEISTFFYNQVERAGDYSDDHCVKWS 240  
 Db 181 BEVPLLPYAAANLHLLLRDASIFGKNGGLSASEISTFFYNQVERTRDYSYHCVKWN 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTYDTQMPYIKTTAQLTREVYTDI 300  
 Db 241 TGLNLRGTNAESWVRYNQFRDMTLMVLVDLVALFPSTYDTQMPYIKTTAQLTREVYTDI 300  
 QY 301 GTVHPHPSFTSTWYNNAPSPFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMNW 360  
 Db 301 GTVHPHPSFTSTWYNNAPSPFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMNW 360  
 QY 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420  
 Db 361 GGHKLEFRITGGTINISTOGSTNTSINPVTLPFTSRDVRYSAGLNLFLTPQVNGVPR 420  
 QY 421 VDFHKKFVTHPIASDNFYYPGYGIGTOLQDSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 Db 421 VDFHKKFVTHPIASDNFYYPGYGIGTOLQDSNELPPEATGQPNYESYSHRSLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 Db 481 ASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTDLPHTSINGKAINQGNFSATWNRGDLGYK 600  
 Db 541 TGTGDIRVNINPPFAQRYRIRYASTDLPHTSINGKAINQGNFSATWNRGDLGYK 600  
 QY 601 TFRVTGTFPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 Db 601 TFRVTGTFPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELVDKEKELFEIVKYAKQIHERNM 719  
 Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDELVDKEKELFEIVKYAKQIHERNM 719

RESULT 6

US-08-286-870A-6  
 ; Sequence 6, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENN, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/286,870A  
 ; FILING DATE: 05-AUG-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/520228  
 ; FILING DATE: 09-MAY-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 8910624.9  
 ; FILING DATE: 09-MAY-1989

ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-6

Query Match 74.5%; Score 2800; DB 3; Length 535;  
Best Local Similarity 99.8%; Pred. No. 2.5e-242;  
Matches 534; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKNQKHQSFPSSNAKVDKISTDSLKNETDIELQNHEDCLKSEVENVEPVSASTI 60  
DB 1 MKLKNQKHQSFPSSNAKVDKISTDSLKNETDIELQNHEDCLKSEVENVEPVSASTI 60

QY 61 QTGIGIACKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120  
DB 61 QTGIGIACKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYA 120

QY 121 RNKALTDLKLGDALAYVHDSLESWGVRNNTNRARSVVKQYIALELMFVKQLPSFAVSG 180  
DB 121 RNKALTDLKLGDALAYVHDSLESWGVRNNTNRARSVVKQYIALELMFVKQLPSFAVSG 180

QY 181 EYVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSBCHVKWYS 240  
DB 181 EYVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSBCHVKWYS 240

QY 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDAL 300  
DB 241 TGLNNLRGTNAESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDAL 300

QY 301 GTVHPHPFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360  
DB 301 GTVHPHPFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMW 360

QY 361 GGHKLEFRITIGTILNISTQGSTNTSINPVLPTFTSDVYRTESLAGNLFLTQPVNGVPR 420  
DB 361 GGHKLEFRITIGTILNISTQGSTNTSINPVLPTFTSDVYRTESLAGNLFLTQPVNGVPR 420

QY 421 VDFHWKFTVTHPIASDNFYPGYVIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTVTHPIASDNFYPGYVIGTQLQDSENELPPEATQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7  
US-08-100-709-4  
Sequence 4, Application US/08100709  
Patent No. 5322687  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia

STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/100,709  
FILING DATE: 19930729  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Egolf, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-100-709-4

Query Match 65.0%; Score 2445.5; DB 1; Length 1229;  
Best Local Similarity 65.6%; Pred. No. 6.2e-210;  
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTDSLKQ-ETDIELQ-NINHEDECLKSEVENVEPVSASTIQTGIGIAGKI 70  
DB 7 NENEINALSIPSTVSNPSPNMNLSDPDARIEDSLCAEVNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYARNKALTDLKG 130  
DB 67 LGVLGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVVEEIIINQKISTYARNKALTDLKG 126

QY 131 LGDALAVYHDSLESWGVRNNTNRARSVVKQYIALELMFVKQLPSFAVSGEVPPLPIYA 190  
DB 127 LGRGVSQYQALETWLDNENDARSITILERYVALELDITTAIPLEIRNEEVPPLMVYA 186

QY 191 QAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSBCHVKWYSTGLNNLRGTN 250  
DB 187 QAANLHLLLRDASIFGSEWGLSSSDVNOYQYQIRYTEEYNSHCVQWYNTGLNNLRGTN 246

QY 251 AESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDALGTVHPHPFT 310  
DB 247 AESWVRNQFRDMDTLMVLDLVALFPSYDTQMPYIKTTAQLTREVVYTDALGTVHPHPFT 306

QY 311 STTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMWGSHKLEFRIT 370  
DB 307 STTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYNNMWGSHKLEFRIT 366

QY 371 GGTLMISTQGST-NTSINPVLPTFTSDVYRTESLAGNLFLTQPVNGVPRVDFHWKFTV 429  
DB 367 GGTLMISTQGST-NTSINPVLPTFTSDVYRTESLAGNLFLTQPVNGVPRVDFHWKFTV 422

QY 430 HPIASDNFYPG-----YVIGTQLQDSENELPPEATQPNYESYSHRLSHIGLISAS 482  
DB 423 --INPQNIYERGATTSYQYQVIGIQLDFSETELPPETTERPNYESYSHRLSHIGLIIGN 480

QY 483 HVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 542  
DB 481 TLRPVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTGT 540

QY 543 TFGDIRVNIINPPLPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDIYKTF 602  
DB 541 TFGDIRVNIINPPLPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDIYKTF 600

QY 603 RTVGFTTFFSLDVGQSTFTIGAMNFFSSGNEVYIDRIEVPVVEYEADEFEKAQKAVTA 662  
DB 601 RTAGFTTFFFLNAQSTFTLGAQSFNS-QEYVIDRVERVPAEVTFFEAEDLERAQKAVNA 659



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match      65.0%; Score 2445.5; DB 1; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.2e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTSLKN-ETDLEQ-NINHEDCIKSEYENVEPFFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEENNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLIFGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQLASFYFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAIARLEG 126

QY 131 LGDALAVYHDSLESWVGNNRNTARSVVKSOYIALELMFVQKLPFAVSGEEVPLPIYA 190
Db 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSHVCVQWYNTGLNNLRGTN 246

QY 251 AESWRYNQFRDRMTLMDLVALFPSTYDQMPYIKTKTAQLTREYVYTDATGTVHPHPSFT 310
Db 247 AESWRYNQFRDRMTLMDLVALFPSTYDQMPYIKTKTAQLTREYVYTDATGTVHPHPSFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMWGKHLEPRTI 370
Db 307 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMWGKHLEPRTI 366

QY 371 GGTINLTSTQGST-NTSINPVTLPFTSRDYRTESLAGNLELTQPVNGVPRVDFHWKFVT 429
Db 367 GGTINLTSTQGST-NTSINPVTLPFTSRDYRTESLAGNLELTQPVNGVPRVDFHWKFVT 422

QY 430 HPIASDNFYYPG-----YVGIGTQLQDSNEHLPPEATGQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQPYQGVIGIQLFDSSETLPETTERPNYESYSHRLSHIGLIGN 480

QY 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTG 542
Db 481 TLRAPIYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTG 540

; QUERY CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match      65.0%; Score 2445.5; DB 2; Length 1229;
Best Local Similarity 65.6%; Pred. No. 6.2e-210;
Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;

QY 13 SSNAKVDKISTSLKN-ETDLEQ-NINHEDCIKSEYENVEPFFVSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEENNIDPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLIFGELWPKGNQWEIFMEHVEEIIINOKISTYARNKALTDLKG 130
Db 67 LGVLGVFPAGQLASFYFLVGLWPSGRDPWEIFLEHVEQLIRQQVTENTRTAIARLEG 126

QY 131 LGDALAVYHDSLESWVGNNRNTARSVVKSOYIALELMFVQKLPFAVSGEEVPLPIYA 190
Db 127 LGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186

QY 191 QAAHLHLLLRDASIFGKEWGLSSSEISTFYNQVERAGDYSDHCVKWYSTGLNNLRGTN 250
Db 187 QAAHLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSHVCVQWYNTGLNNLRGTN 246

QY 251 AESWRYNQFRDRMTLMDLVALFPSTYDQMPYIKTKTAQLTREYVYTDATGTVHPHPSFT 310
Db 247 AESWRYNQFRDRMTLMDLVALFPSTYDQMPYIKTKTAQLTREYVYTDATGTVHPHPSFT 306

QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMWGKHLEPRTI 370
Db 307 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYNNMWGKHLEPRTI 366

QY 371 GGTINLTSTQGST-NTSINPVTLPFTSRDYRTESLAGNLELTQPVNGVPRVDFHWKFVT 429
Db 367 GGTINLTSTQGST-NTSINPVTLPFTSRDYRTESLAGNLELTQPVNGVPRVDFHWKFVT 422

QY 430 HPIASDNFYYPG-----YVGIGTQLQDSNEHLPPEATGQPNYESYSHRLSHIGLISAS 482
Db 423 --INPQNIYERGATTYSQPYQGVIGIQLFDSSETLPETTERPNYESYSHRLSHIGLIGN 480

QY 483 HVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTG 542
Db 481 TLRAPIYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTG 540

; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYETS
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

```

QY 543 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTF 602  
 DB 541 TFGDIRVNINPLSQRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTF 600  
 QY 603 RTVGFTTFFSFLDVOSTFTIGAMNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKAVTA 662  
 DB 601 RTAGFSTPFNPLNAQSTFTLGAQFSN-QEVIYIDRVEFVPAEVTFEAYDLERAQKAVNA 659  
 QY 663 LFTSTNPRGLKTDVYDHYDIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 660 LFTSTNPRGLKTDVYDHYDIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 11

US-08-881-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-881-340-4

Query Match 65.0%; Score 2445.5; DB 2; Length 1229;  
 Best Local Similarity 65.6%; Pred. No. 6.2e-210;  
 Matches 470; Conservative 92; Mismatches 138; Indels 17; Gaps 6;  
 QY 13 SSNAKVDTSTSLKN-ETDIELQ-NINHEBCLKMEYENVEPFSASTGTGTGIAGKI 70  
 DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVNIDPFVSASTVGTGINIAGRI 66  
 QY 71 LGTLGVFPAGQVASYLSIFLGLWPKGNQWEIFMEHVEEILNOKISTYARNKALTDLKG 130  
 DB 67 LGVLGVFPAGQLASFYSFLVGLWPKGRDPWEIFLEHVEQIRQQVTEVNTNTAARLEG 126  
 QY 131 LGDALAVYHDSLSWVGNRNNTARSVVKQSVYALSLMFVQKLPFAVSGEEVPLPIYA 190

DB 127 LGRGYSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEEVPLLMVYA 186  
 QY 191 QANLHLLLDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSGLNLRGTN 250  
 DB 187 QANLHLLLDASIFGSEWGMASDVNOYQEQIRYEEYSNHCQWYNTGLNLRGTN 246  
 QY 251 AESWRYNQFRDMTLMVLDLVALFPSTQYQYPIKTTAQLTREVYTDAGTGWPHPSFT 310  
 DB 247 AESWRYNQFRDLTLGVLDLVALFPSTQYQYPIKTTAQLTREVYTDAGTGWPHPSFT 306  
 QY 311 STTWYNNAPSFSAIEAAVVRNPHLLDLEQVITYSLSRWSNTQYNNMVGKHLFRTI 370  
 DB 307 STNWFNNAPSFSAIEAAIFRPPHLLDLEQVITYSLSRWSNTQYNNMVGKHLFRTI 366  
 QY 371 GGTLANISTQGST-NTSINPVTLPFTSRDVTYRTESLAGLNLFLTQPVNGVPRVDEHWFVT 429  
 DB 367 GGTLANISTQGST-NTSINPVTLPFTSRDVTYRTESLAGLNLFLTQPVNGVPRVDEHWFVT 422  
 QY 430 HPIASDNFYYPG-----YVGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLISAS 482  
 DB 423 --INPQNIYERGATTYSQPYQGVIGIQLFDSBELPPEATGQPNYESYSHRLSHIGLISAS 480  
 QY 483 HVKALVYSWTHRSADRTNIEPNSITQPLVKAFNLSSGAUVVRGPGFTGGDLIRRTNG 542  
 DB 481 TLRAPVYSWTHRSADRTNIEPNSITQPLVKAFNLSSGAUVVRGPGFTGGDLIRRTNG 540  
 QY 543 TFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTF 602  
 DB 541 TFGDIRVNINPLSQRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTF 600  
 QY 603 RTVGFTTFFSFLDVOSTFTIGAMNFSSGNEVYIDRIEFVPEVYEAEDFEKAQKAVTA 662  
 DB 601 RTAGFSTPFNPLNAQSTFTLGAQFSN-QEVIYIDRVEFVPAEVTFEAYDLERAQKAVNA 659  
 QY 663 LFTSTNPRGLKTDVYDHYDIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 660 LFTSTNPRGLKTDVYDHYDIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 716

RESULT 12

US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Stelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424

TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jay M. Sanders  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,803  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: ~ US 08/069,902  
FILING DATE: 01-JUNE-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/759,247  
FILING DATE: 13-SEPT-1991  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/448,170  
FILING DATE: 23-MAY-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: M/S 102DCD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
SEQUENCE CHARACTERISTICS:  
SEQUENCE FOR SEQ ID NO: 10:  
LENGTH: 488 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SS-08-961-803-10

[illegible]

QY	181	EEVPLLP	IYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNROVERAGDYSDHCVKWYS	240
			: : :       :	
D6	172	EEVPLLP	IYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRSGKSKEYSDHCWKVIN	231
QY	241	TGLNLRGT	NAESWVRYNQFRDRMTLMVLDLVALPFSYDTOMYPKITTAQLTREVTDAI	300
D6	232	TGLNRLMG	NAESWVRYNQFRDRMTLMVLDLVALPFSYDTOMYPKITTAQLTREVTDAI	291
QY	301	GTIVHPSP	FSTTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRSWNTQYMNMW	360
D6	292	GTIVHPSP	FSTTTWYNNAPSFTTIAA VVRNPHLLDLEQVTIYSLLSRSWNTQYMNMW	351

QY 361 GGKLFRTTIGTTLNISTQSTNTSINPVTLPFTSRDVTSTESLAGLNFLTPQVNGVPR 420  
 Db 352 GGKLFRTTIGTTLNISTQSTNTSINPVTLPFTSRDVTSTESLAGLNFLTPQVNGVPR 411  
 QY 421 VDFHWKFTVTHPIASDNFYPCYGVGIGTQLODSENELPPEATGPNYESYSHRSLSHIGLIS 480  
 Db 412 VDFHWKFTVTHPIASDNFYPCYGVGIGTQLODSENELPPEATGPNYESYSHRSLSHIGLIS 471  
 QY 481 ASHVKALVYSWTHRSAD 497  
 Db 472 ASHVKALVYSWTHRSAD 488

RESULT 14

US-07-951-715A-7  
 ; Sequence 7, Application US/07951715A  
 ; Patent No. 5625136  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Marcha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.  
 ; APPLICANT: Suttie, Janet L.  
 ; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 ; NUMBER OF SEQUENCES: 94  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CIBA-GEIGY Corporation  
 ; STREET: 7 Skyline Drive  
 ; CITY: Hawthorne  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10532  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/951,715A  
 ; FILING DATE: 25-SEP-1992  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/772,027  
 ; FILING DATE: 04-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Spruill, W. Murray  
 ; REGISTRATION NUMBER: 32,943  
 ; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8615  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1207 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-951-715A-7

Best Local Similarity 64.3%; Pred. No. 1e-193;  
 Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;  
 QY 40 EDCMKSEYENVEFPVSASTIQTGIGIAGKILGTGVPAGQVASFILGELWPKGKN 99  
 Db 10 EBSLCAEGNNIDPFVSASTVQTGINIAGRIILGVLCVPAGQLASFISFLVCELWPKGRD 69  
 QY 100 QWEIFMEHVEEIIKISTVARNKALTDLKGGLDALAVVHDSLESWGNRNNTAASVVK 159  
 Db 70 QWEIFLHVHVEOLINQOITENARNTALARLOGLGDSFRAYQQSLEDWLENRDDARTSVLY 129  
 QY 160 SQVIALELMFYQKLPFAVSGSEVEPLLPIYAQAANLHLLIRDASIFGKENGSLSSSEIST 219  
 Db 130 TOYIALELDFLNAFLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGTQSQEIQR 189  
 QY 220 FYNQVERAGDYSCHCKVYSTGLNNLRGTNAESWVRVYQFRDMTLMVLVALPFSYD 279  
 Db 190 YVERQVETRDYSDYCVWYNTGLNSLRGTNAASWVRVYQFRDRLTLGVLDLVALPFSYD 249  
 QY 280 TOMYPIKTAQLTRVYTDAGTGVHHPHPTSTTWYNNNAPSFAIEAAVVRNPHLLDFL 339  
 Db 250 TETYPINTSAQLTRVYTDAGAT--GVNWSMKNWYNNNAPSFAIEAAATRSPLHLLDFL 307  
 QY 340 EQVTIYSLLSWSNTQYNNMNGGKLEFRTIGTLNISTQSTNTSINPVTLPFTSRDYY 399  
 Db 308 EQLTIFSASSWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFASRDYV 367  
 QY 400 RTESLAGLNLF--LTQPVNGVPRVDFHWKFTVTHP-----IASDNFYPCYGVGIGTQLODS 452  
 Db 368 RTESYAGVLLWGIYLEPIHGVPVTRFNP---TNPQNSDRGTANYSQP-YESPLQLODS 423  
 QY 453 ENELPPEATGPNYESYSHRSLSHIGLISASHVKALVYSWTHESADRTNTIENSITQIPL 512  
 Db 424 ETELPPETTERPNYESYSHRSLSHIGLILQSRVNVVYSWTHESADRTNTIGPNRITQIPM 483  
 QY 513 VKAFNLSSGAHVWCPGFTGGDILRRNTGTGDIRVNNPFAQVVRVRYASTDLQ 572  
 Db 484 VKASELPQGTTVVRGPGFTGGDILRRNTGTGFGPIRVTVNGPLTQRYRIGFRYASTVDFD 543  
 QY 573 FHTSINGKALNQGNSATMNRGEDLDYKTRFTVGTTPPFDVQSTFTTIGAWNTSSGNE 632  
 Db 544 FFVSRGTTVNNFRFLRTMNSGDELKYGNFVRAFTTPTFTQIIDIIRTSIQGLSGNGE 603  
 QY 633 VYIDRIEFVPEVTEAEYDFEKAQKVYALFTSTNPRGLKTDVHDYHIDQVSNLVESLS 692  
 Db 604 VYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS 663  
 QY 693 DEFYLDKRELFEIVKAKQLHIERNM 719  
 Db 664 DEFCLDEKRELLEKVKYAKRLSDERNL 690

RESULT 15

US-08-459-448A-7  
 ; Sequence 7, Application US/08459448A  
 ; Patent No. 5859336  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 ; NUMBER OF SEQUENCES: 94  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: No. 5859336artis Corporation  
 ; STREET: Patent & Trademark Dept., 520 White Plains  
 ; STREET: Rd., POB 2005  
 ; CITY: Tarrytown  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10591-9005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/459,448A  
 ; FILING DATE: 02-JUN-1995  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/951,715  
 ; FILING DATE: 25-SEP-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/772,027  
 ; FILING DATE: 04-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pace, Gary M.  
 ; REGISTRATION NUMBER: 40403  
 ; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIVA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919)541-8582  
 ; TELEFAX: (919)541-8689  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1207 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-459-448A-7

Query Match 60.2%; Score 2264.5; DB 2; Length 1207;  
 Best Local Similarity 64.3%; Pred. No. 1e-193;  
 Matches 442; Conservative 78; Mismatches 154; Indels 13; Gaps 5;

QY	40	EDCLKMSVENVEPFVASTIQTGIGTAGKILGTGVPFAGQVASLYSFILGELWPKGN	99
Db	10	EDSLCIAEGNNIDPFVASTVQTGINIAGRIIGLVGVPFAGQLASFYSFLVGLWPRGRD	69
QY	100	QWEIFMEHVEEIIINOKISTYARNKALTDLGLGDALAVYHDSLESWVGNNENTFARSVVK	159
Db	70	QWEIFLEHVEQLINQITENARNALTALQGLGDSFRAYQOSLEDWLENRDDARTRSVLY	129
QY	160	SOYIALELMFVQKLPSFAVSGBEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEIST	219
Db	130	TOYIALELDFLNAMPFLAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQR	189
QY	220	FYNQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQPRDRMTLMVLDLVALFPSYD	279
Db	190	YERQVERTRDYSYCVWEYNTGLNSLRGTNAASWRYNQPRDRMTLMVLDLVALFPSYD	249
QY	280	TMVPIKTTAQLTREVYTDAGTGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFL	339
Db	250	TRTPINTSAQLTREVYTDAGTAT--GVNMAWMWYNNNAPSFAIEAAVVRNPHLLDFL	307
QY	340	EQVTIYSLSRWNTQYNNMWGKHLEFRTIGGLTNTSTCGSTNTSINPVTLPFTSRDYY	399
Db	308	EQLTIFSSASSRWSNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDYY	367
QY	400	RTESLAGLNLFP--LTQPVNCGVPRVDFHWKFTVHP-----TASDNFYYPGVIGTQLQDS	452
Db	368	RTESYAGVLLWGLIYLEPIHGVPVRFNF--TNPQNISDRGTANTYSP-YESPGIQLKDS	423

QY	453	ENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTTIEPNSITQIPL	512
Db	424	ETELPPEATERPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTTIEPNSITQIPL	483
QY	513	VKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNINPPFAQBYRVIRYASTTDLQ	572
Db	484	VKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNINPPFAQBYRVIRYASTTDLQ	543
QY	573	FHTSINGKAINQGNFSAATMNRGDDLDYKTRFTVGTTPPFSFLDVOSTFTTICAWNFSSGNE	632
Db	544	FFVSEGGTIVNFRFLRTMNSGDELKYNFVRRAFTTPTTQIQDIIRTSIQGLSGNGE	603
QY	633	VYIDRIEFVPEVTEAYEYDFEKAQEKVLTALFTSTNPRGLTVDVXHYHIDQVSNLVESLS	692
Db	604	VYIDRIEIIPTVATFEAYEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLS	663
QY	693	DEFYLDKRELEFEIVKYAKQLHIERNM	719
Db	664	DEFCLDEKRELEKVKYAKRLSDERNL	690

Search completed: October 28, 2004, 18:34:18  
 Job time : 24.3343 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-57  
Perfect score: 3760  
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELPEIVKYAKQLHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Genesep23Sep04: \*  
1: Genesep1980s: \*  
2: Genesep1990s: \*  
3: Genesep2000s: \*  
4: Genesep2001s: \*  
5: Genesep2002s: \*  
6: Genesep2003as: \*  
7: Genesep2003bs: \*  
8: Genesep2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3760	100.0	719	4	AAB66910 Insectici
2	3760	100.0	719	6	AAB36274 B. thurin
3	3756	99.9	719	4	AAB66908 Insectici
4	3756	99.9	719	6	AAB36272 B. thurin
5	3747	99.7	719	4	AAU02095 Bacillus
6	3745	99.6	719	4	AAB66911 Insectici
7	3745	99.6	719	6	AAB36275 B. thurin
8	3739	99.4	719	4	AAB66909 Insectici
9	3739	99.4	719	6	AAB36273 B. thurin
10	3735	99.3	719	2	AAR08041 81 kD end
11	3724.5	99.1	718	6	AAB36271 B. thurin
12	3718.5	98.9	718	4	AAB66907 Insectici
13	3547	94.3	719	7	ADM74717 B. thurin
14	3516	93.5	719	4	AAB66912 Insectici
15	3516	93.5	719	6	AAB36276 B. thurin
16	3472.5	92.4	710	4	AAU02041 B. thurin
17	3393	90.2	719	3	ABB07073 Bacillus
18	3373	89.7	719	2	AAW49089 Bacillus
19	3287	87.4	1217	4	AAU02092 Bacillus
20	2730	72.6	1208	4	AAU02093 Bacillus
21	2447	65.1	1230	8	ADK98484 B thuring
22	2447	65.1	1230	8	ADK98489 B thuring
23	2447	65.1	1230	8	ADK98481 B thuring
24	2447	65.1	1230	8	ADK98491 B thuring
25	2447	65.1	1230	8	ADK98487 B thuring

ALIGNMENTS

RESULT 1

AAB66910  
ID AAB66910 standard; protein; 719 AA.  
XX  
AC AAB66910;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa4.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
(ZENE ) ZENECA LTD.  
PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
controlling insects, and for insect-resistant transgenic plant  
production.  
XX  
PS Claim 14; Page 60-62; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
from Paecilomyces sp. (see AAB66910 and AAB66913). The  
insecticidal proteins can be used to produce transgenic plants, which are  
insect-resistant. Also, the insecticidal proteins are useful for  
controlling insects by providing them at a locus where insects feed  
Sequence 719 AA;  
XX

Query Match 100.0%; Score 3760; DB 4; Length 719;  
Best Local Similarity 100.0%; Pred. No. 1.2e-290;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
 D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120  
 QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S H R L S H I G L I S 240  
 D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S H R L S H I G L I S 240  
 QY 241 T G L N L R G T N A E S W R V R N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R V R N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P H P S T S T T W Y N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
 D b 301 G T V H P H P S T S T T W Y N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
 QY 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F V T H P I A S D N F Y P G V Y G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G V Y G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S G A A V V R G P G T G G I L R R T N 540  
 D b 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S G A A V V R G P G T G G I L R R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R V R I A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T V G T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 D b 601 T F R T V G T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719

RESULT 2  
 AAE36274  
 ID AAE36274 standard; protein; 719 AA.  
 XX  
 AC AAE36274;  
 XX  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 KW Bacillus thuringiensis.  
 XX  
 OS WO200298911-A2.  
 XX  
 PN 12-DEC-2002.  
 PD  
 XX 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 FT  
 XX  
 PS Claim 12; Page 50-53; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 XX  
 SQ Sequence 719 AA;  
 Query Match 100.0%; Score 3760; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-290;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
 D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E I I N Q K I S T Y A 120  
 QY 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L G D A L A V H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S H R L S H I G L I S 240  
 D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N Q V E R A G D Y S H R L S H I G L I S 240  
 QY 241 T G L N L R G T N A E S W R V R N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R V R N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P H P S T S T T W Y N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
 D b 301 G T V H P H P S T S T T W Y N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360  
 QY 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G G T L N I S T G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F V T H P I A S D N F Y P G V Y G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G V Y G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S G A A V V R G P G T G G I L R R T N 540  
 D b 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S G A A V V R G P G T G G I L R R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R V R I A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T V G T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 D b 601 T F R T V G T T P F S F L D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q L H I E R N M 719

RESULT 3	
ID	AAB66908
XX	AAB66908 standard; protein; 719 AA.
XX	AC AAB66908;
DT	12-APR-2001 (first entry)
XX	Insecticidal protein cryIIa2.
DE	Insecticide; transgenic plant; insect-resistance.
XX	Paecilomyces sp.
XX	WO200100841-A1.
PN	04-JAN-2001.
PD	23-JUN-2000; 2000WO-GB002457.
PF	29-JUN-1999; 99GB-00015215.
PR	23-DEC-1999; 99GB-00030536.
XX	(ZENE ) ZENECA LTD.
PA	Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
XX	Vincent JL, Lee MD;
PI	WPI; 2001-123015/13.
DR	Novel insecticidal protein obtained from species of Paecilomyces for
XX	controlling insects, and for insect-resistant transgenic plant
PT	production.
PT	Claim 14; Page 55-57; 72pp; English.
XX	The present invention relates to novel insecticidal proteins obtained
XX	from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC	insecticidal proteins can be used to produce transgenic plants, which are
CC	insect-resistant. Also, the insecticidal proteins are useful for
CC	controlling insects by providing them at a locus where insects feed
XX	Sequence 719 AA;
SQ	Query Match 99.9%; Score 3756; DB 4; Length 719;
	Best Local Similarity 99.9%; Pred. No. 2.5e-290;
	Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 MRLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCMKSEYENVEPVFASTI 60
DB	1 MRLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCMKSEYENVEPVFASTI 60
QY	61 QTGIGIACKILGTLGVFPAGQVASYLSFILGELWPKGKNQWEIEMEHEVEIINQKISTYA 120
DB	61 QTGIGIACKILGTLGVFPAGQVASYLSFILGELWPKGKNQWEIEMEHEVEIINQKISTYA 120
QY	121 RNKALTDLKGDLALAVYHDSLESVGNRRNTRARSVKQVIALELMFVQKLPSPFVSG 180
DB	121 RNKALTDLKGDLALAVYHDSLESVGNRRNTRARSVKQVIALELMFVQKLPSPFVSG 180
QY	181 EEPVLLPIYAQANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSHCVKWYS 240
DB	181 EEPVLLPIYAQANLHLLLRDASIFGKEWGLSSSISTFYNRQVERAGDYSHCVKWYS 240
QY	241 TGLNLRGTNAESWVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTRVYTDAL 300
DB	241 TGLNLRGTNAESWVRVYQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTRVYTDAL 300
QY	301 GTVHPHPGFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYMNW 360
DB	301 GTVHPHPGFTSTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTIYSLLSRWNSNTQYMNW 360

QY	361	GGHKLFEFTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR	420
DB	361	GGHKLFEFTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVPR	420
QY	421	VDPHWKFTVTHPIASDNFYYPGYGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS	480
DB	421	VDPHWKFTVTHPIASDNFYYPGYGIGTQLQDSNELPPEATGQPNYESYSHRLSHIGLIS	480
QY	481	ASHVKALVYSWTHRSADRTNTIEPNS:TOIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
DB	481	ASHVKALVYSWTHRSADRTNTIEPNS:TOIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN	540
QY	541	TGTFGDIRVNIINPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGDLDYK	600
DB	541	TGTFGDIRVNIINPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGDLDYK	600
QY	601	TFRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV	660
DB	601	TFRTVGFTTFFSFLDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKV	660
QY	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM	719
DB	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKRELFEIVKYAKQLHIERNM	719

RESULT 4

AAE36272

ID AAE36272 standard; protein; 719 AA.

XX AAE36272;

AC AAE36272;

DT 26-JUN-2003 (first entry)

XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.

DE Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

OS WO200298911-A2.

PN 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

PF 07-JUN-2001; 2001GB-00013900.

PR (SYGN ) SYNGENTA LTD.

PA Vincent JL, Viner R;

PI	WPI; 2003-175137/17.
DR	New insecticidal protein comprising an X-glycine motif at the amino-
XX	terminus, useful as an active ingredient of a pesticide.
PT	Claim 12; Page 44-47; 67pp; English.
PS	The invention relates to insecticidal protein comprising an X-glycine
XX	motif at the amino-terminus. Polynucleotide or DNA constructs of the
CC	invention are useful for producing plants or plant parts that are
CC	resistant to insects. The protein or synergistic combination is useful as
CC	an active ingredient of a pesticide or for controlling insects.
CC	Antibodies raised to the insecticidal proteins can be used to identify
CC	other proteins with insecticidal activity. The present sequence is
CC	Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This
XX	sequence is used in the invention
SQ	Sequence 719 AA;
	Query Match 99.9%; Score 3756; DB 6; Length 719;
	Best Local Similarity 99.9%; Pred. No. 2.5e-290;
	Matches 718; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI	60
Db	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI	60
QY	61	QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEIINQKISTYA	120
Db	61	QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEIINQKISTYA	120
QY	121	RNKALTDLGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG	180
Db	121	RNKALTDLGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG	180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYS	240
Db	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYS	240
QY	241	TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREYITDAI	300
Db	241	TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREYITDAI	300
QY	301	GTVPHPSTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
Db	301	GTVPHPSTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
QY	361	GGHKLFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR	420
Db	361	GGHKLFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR	420
QY	421	VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS	480
Db	421	VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS	480
QY	481	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNSGAAVVRGPGTGGDILRRTN	540
Db	481	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNSGAAVVRGPGTGGDILRRTN	540
QY	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
Db	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK	600
QY	601	TFRVGTFTPFSLDQVSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	660
Db	601	TFRVGTFTPFSLDQVSTFTTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV	660
QY	661	TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDEFYLDKEKRELFEIVKAKQLHIERNM	719
Db	661	TALFTSTNPRGLTKDVKYHIDQVSNLVESLSDEFYLDKEKRELFEIVKAKQLHIERNM	719

RESULT 5

ID	AAU02095	standard; protein; 719 AA.
XX	AAU02095;	
AC	AC	
XX	XX	
DT	07-SEP-2001	(first entry)
XX	XX	
DE	Bacillus thuringiensis partial mutant CryIIa.	
XX	XX	
KW	Crystal protein; CryIIa; CryIIa; moth; butterfly; Colorado potato beetle;	
KW	mutant; mutein.	
XX	XX	
OS	Bacillus thuringiensis.	
XX	XX	
FT	Key	Location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= Signal_peptide
FT	Protein	20..719
FT	Protein	/label= Mature_CryIIa
XX	XX	
PN	EP1099760-A1.	
XX	XX	

PD	16-MAY-2001.	
XX	XX	
PF	09-NOV-1999;	99EP-00203723.
XX	XX	
PR	09-NOV-1999;	99EP-00203723.
XX	XX	
PA	(CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.	
XX	XX	
PI	De Maagd RA, Bosch HJ;	
XX	XX	
DR	WPI; 2001-337141/36.	
XX	N-PSDB; AAS04855.	
XX	XX	
PT	New hybrid Bacillus thuringiensis hybrid toxins comprising structural	
PT	domains derived from at least 2 different crystal proteins, such as	
PT	CryIIa and CryIIb, and having insecticidal activity, useful for combating	
PT	insects.	
PS	Example; Page 30-32; 43pp; English.	
XX	XX	
CC	The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA	
CC	encoding which was mutated to allow cloning of domain III or domains I	
CC	and II, to make the hybrid protoxins of the invention. The hybrid toxins	
CC	of the invention, having structural domains I, II and III in this order	
CC	starting from the N-terminal derived from at least 2 different crystal	
CC	proteins, are useful for protecting plants against pest insects, e.g.	
CC	moths, butterflies and Colorado potato beetle or for combating insects	
XX	XX	
SQ	Sequence 719 AA;	
Query Match	99.7%;	Score 3747; DB 4; Length 719;
Best Local Similarity	99.7%;	Pred. No. 1.3e-289;
Matches	717; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
Db	1	MKLKQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60
QY	61	QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEIINQKISTYA 120
Db	61	QTGIGIAGKILGTGVPAGQVASYLSFILGELWPKGNQWEIFMEHVEIINQKISTYA 120
QY	121	RNKALTDLGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180
Db	121	RNKALTDLGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180
QY	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYS 240
Db	181	EEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKYS 240
QY	241	TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREYITDAI 300
Db	241	TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTOMYPIKTTAQLTREYITDAI 300
QY	301	GTVPHPSTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
Db	301	GTVPHPSTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360
QY	361	GGHKLFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
Db	361	GGHKLFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420
QY	421	VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480
Db	421	VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENEPPEATGQPNYESYSHRLSHIGLIS 480
QY	481	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNSGAAVVRGPGTGGDILRRTN 540
Db	481	ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFLNSGAAVVRGPGTGGDILRRTN 540
QY	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600
Db	541	TGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600

QY 601 TFRVGTTPFPFLDVQSTFTIGAMNFSSGNEVYIDRIEFPVPEVYEAEDFEKAQEKV 660  
DB 601 TFRVGTTPFPFLDVQSTFTIGAMNFSSGNEVYIDRIEFPVPEVYEAEDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDVYLDKRELFEIVKAKQLHIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDVYLDKRELFEIVKAKQLHIERNM 719

RESULT 6  
ID AAB66911 standard; protein; 719 AA.  
XX AAB66911;  
DT 12-APR-2001 (first entry)  
DE Insecticidal protein cryIIa5.  
XX Insecticide; transgenic plant; insect-resistance.  
OS Paecilomyces sp.  
PN WO200100841-A1.  
PD 04-JAN-2001.  
PF 23-JUN-2000; 2000WO-GB002457.  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
PI Griffin J; Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX Claim 14; Page 62-64; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;

Query Match 99.6%; Score 3745; DB 4; Length 719;  
Best Local Similarity 99.4%; Pred. No. 1.9e-289;  
Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLKNQDKHQSFPSSNAKYDKISTDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60  
DB 1 MLKNQDKHQSFPSSNAKYDKISTDSLKNETDIELQINHEDECLKMSEYENVEPVSASTI 60  
QY 61 QTGIGIACKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
DB 61 QTGIGIACKILGTGVFPAGQVASYLSFILGELWPKGNQWEIFMEHVBEIINQKISTYA 120  
QY 121 RNKALTDLKGDLAVPHDSLESWGNRNTRNSVRSQYIALELMFVQKLPSPFVSG 180  
DB 121 RNKALTDLKGDLAVPHDSLESWGNRNTRNSVRSQYIALELMFVQKLPSPFVSG 180  
QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTPNRQVERAGDYSCHVKWYS 240  
DB 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTPNRQVERAGDYSCHVKWYS 240

RESULT 7  
ID AAE36275 standard; protein; 719 AA.  
XX AAE36275;  
XX AC

DT 26-JUN-2003 (first entry)  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.  
XX WO200298911-A2.  
PD 12-DEC-2002.  
XX 30-MAY-2002; 2002WO-GB002666.  
PR 07-JUN-2001; 2001GB-00013900.  
PA (SYGN ) SYNGENTA LTD.  
XX Vincent JL, Viner R;  
XX WPI; 2003-175137/17.  
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

Claim 12; Page 53-56; 67pp; English.

The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify

CC other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
 CC sequence is used in the invention

XX SQ Sequence 719 AA;

Query Match 99.6%; Score 3745; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.9e-289;  
 Matches 715; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MKLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI	60
Db	1	MKLKNDKQKQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI	60
Qy	61	QTGIGIAGKILGTLPAGQVAVSLYFILGELWPKGNQWEIFMEHVEIINQKISTYA	120
Db	61	QTGIGIAGKILGTLPAGQVAVSLYFILGELWPKGNQWEIFMEHVEIINQKISTYA	120
Qy	121	RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG	180
Db	121	RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG	180
Qy	181	EEVPLPIYAQAANLHLLLRDASI FGEWGLSSSEISTFYNQVERAGDYSDHCVKWYS	240
Db	181	EEVPLPIYAQAANLHLLLRDASI FGEWGLSSSEISTFYNQVERAGDYSDHCVKWYS	240
Qy	241	TGLNLRGNTNAESWVRVYQFRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL	300
Db	241	TGLNLRGNTNAESWVRVYQFRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL	300
Qy	301	GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
Db	301	GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW	360
Qy	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTQPVNGVPR	420
Db	361	GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTQPVNGVPR	420
Qy	421	VDFHWKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS	480
Db	421	VDFHWKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS	480
Qy	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN	540
Db	481	ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN	540
Qy	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLPFTSINGKAINQGNFSAATMNRGDLDYK	600
Db	541	TGTFGDIRVNINPPFAQRYRIRYASTTDLPFTSINGKAINQGNFSAATMNRGDLDYK	600
Qy	601	TFRVGTFTTFFSFLDVQSTFTGAWNFGSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV	660
Db	601	TFRVGTFTTFFSFLDVQSTFTGAWNFGSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV	660
Qy	661	TALFTSTNPRGLTKDVKDYHIDQVSNLVSDEFLDKRELFIIVKAKQLHIERNM	719
Db	661	TALFTSTNPRGLTKDVKDYHIDQVSNLVSDEFLDKRELFIIVKAKQLHIERNM	719

RESULT 8  
 AAB66909

ID AAB66909 standard; protein; 719 AA.

XX AC AAB66909;

XX DT 12-APR-2001 (first entry)

XX DE Insecticidal protein cryIIa3.

XX KW Insecticide; transgenic plant; insect-resistance.

XX OS Paecilomyces sp.

PN WO200100841-A1.  
 PD 04-JAN-2001.  
 XX PF 23-JUN-2000; 2000WO-GB002457.  
 XX PR 29-JUN-1999; 99GB-00015215.  
 XX PR 23-DEC-1999; 99GB-00030536.  
 XX PA (ZENE ) ZENECA LTD.

XX XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.

XX PT Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.

XX PS Claim 14; Page 57-59; 72pp; English.

XX CC The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed

XX SQ Sequence 719 AA;

Query Match 99.4%; Score 3739; DB 4; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 5.7e-289;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60

Qy 61 QTGIGIAGKILGTLPAGQVAVSLYFILGELWPKGNQWEIFMEHVEIINQKISTYA 120  
 Db 61 QTGIGIAGKILGTLPAGQVAVSLYFILGELWPKGNQWEIFMEHVEIINQKISTYA 120

Qy 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180  
 Db 121 RNKALTDLKGDLAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180

Qy 181 EEVPLPIYAQAANLHLLLRDASI FGEWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240  
 Db 181 EEVPLPIYAQAANLHLLLRDASI FGEWGLSSSEISTFYNQVERAGDYSDHCVKWYS 240

Qy 241 TGLNLRGNTNAESWVRVYQFRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 Db 241 TGLNLRGNTNAESWVRVYQFRRDMLVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300

Qy 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 Db 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360

Qy 361 GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTQPVNGVPR 420  
 Db 361 GGHKLFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTQPVNGVPR 420

Qy 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480  
 Db 421 VDFHWKFVTHPIASDNFYYPGVAGIGTQLODSENELPPEATGQPNYESYSHRSLSHIGLIS 480

Qy 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
 Db 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540

Qy 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLPFTSINGKAINQGNFSAATMNRGDLDYK 600  
 Db 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLPFTSINGKAINQGNFSAATMNRGDLDYK 600

QY 601 TFRVGTTPFGLDVOSTFTIGAMFSSGNEVYIDRIEFVPPVEVYEAEDFEKAQKV 660  
 DB 601 TFRVGTTPFGLDVOSTFTIGAMFSSGNEVYIDRIEFVPPVEVYEAEDFEKAQKV 660  
 QY 661 TALFTSTNPRGLKTDVNDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVNDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 9  
 AAE36273  
 ID AAE36273 standard; protein; 719 AA.  
 XX AAE36273;  
 AC  
 DT 26-JUN-2003 (first entry)  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 OS Bacillus thuringiensis.  
 PN WO2002298911-A2.  
 PD 12-DEC-2002.  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 PA Vincent JL, Viner R;  
 PI WPI; 2003-175137/17.  
 DR New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Claim 12; Page 47-50; 67pp; English.  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

Query Match 99.4%; Score 3739; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 5.7e-289;  
 Matches 715; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVASATI 60  
 DB 1 MCLKNDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVASATI 60  
 QY 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPAGQVAVSLYSFILGELWPKGNQWEIFMEHVEEIIQKISTYA 120  
 QY 121 RNKALTDLKLGLDALAVYHDSLESWGVRNTRARVSVKQYIALELMFVKLPFAVSG 180  
 DB 121 RNKALTDLKLGLDALAVYHDSLESWGVRNTRARVSVKQYIALELMFVKLPFAVSG 180  
 QY 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240

DB 181 EEVPLLPYAAQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300  
 DB 241 TGLNLRGTNAESWVRYNQFRDWTMLVLDLVALFPSYDTQMPYPIKTTAQLTREVTDAI 300  
 QY 301 GTVHPHPSSTSTTWNNAAPSFAIEAAVVRNPPLLDLEQVTIYSLSRWSNTQYMMNW 360  
 DB 301 GTVHPHPSSTSTTWNNAAPSFAIEAAVVRNPPLLDLEQVTIYSLSRWSNTQYMMNW 360  
 QY 361 GGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTILNISTQGSTNTSINPVTLPFTSRDVYRTESLAGINLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLQDSNELPPEATQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 DB 541 TGTGDIRVININPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
 QY 601 TFRVGTTPFGLDVOSTFTIGAMFSSGNEVYIDRIEFVPPVEVYEAEDFEKAQKV 660  
 DB 601 TFRVGTTPFGLDVOSTFTIGAMFSSGNEVYIDRIEFVPPVEVYEAEDFEKAQKV 660  
 QY 661 TALFTSTNPRGLKTDVNDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVNDYHIDQVSNLVESLSDEFYLDKRELFEIVKAKQLHIERNM 719

RESULT 10  
 AAR08041  
 ID AAR08041 standard; protein; 719 AA.  
 XX AAR08041;  
 AC  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 27-FEB-1991 (first entry)  
 XX 81 kD endotoxin deduced from DNA carried on pJH12.  
 XX Crystal; insecticide; toxin; delta endotoxin.  
 OS Bacillus thuringiensis; JHCC 4353 and 4835.  
 XX WO9013651-A.  
 PN 15-NOV-1990.  
 PD 09-MAY-1989; 89GB-00010624.  
 PF 09-MAY-1989; 89GB-00010624.  
 PR (ICIL ) IMPERIAL CHEM IND PLC.  
 PA Blenk RG, Ely S, Tailor RH, Tippet JM;  
 PI WPI; 1990-361486/48.  
 XX N-PSDB; RAO06636.  
 DR Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.  
 XX Claim 5; Fig 5-10; 66pp; English.  
 CC The sequence carried on pJH12 which was isolated from B. thuringiensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can

CC be used to produce transformants E.coli strain MCI2022/pJH12 (NCIB 40278,  
 CC or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11  
 CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be  
 CC used in formulations for combatting Lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 719 AA;

Query Match 99.3%; Score 3735; DB 2; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-288;  
 Matches 715; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGNRNNTRARSVVKSYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNRNNTRARSVVKSYIALELMFVQKLPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 DB 301 GTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFQTQVNGVPR 420  
 DB 361 GGKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFQTQVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVYNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 DB 541 TGTGDIRVYNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLKY 600  
 QY 601 TFRVTGFTTFFSLDVQSTFTTIGAWNPNSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV 660  
 DB 601 TFRVTGFTTFFSLDVQSTFTTIGAWNPNSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKV 660  
 QY 661 TALFTSTNPRGLTKDVKDHYIDQVSNLVESLSDEFYLDKEKELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLTKDVKDHYIDQVSNLVESLSDEFYLDKEKELFEIVKAKQLHIERNM 719

RESULT 11  
 AAE36271 standard; protein; 718 AA.  
 ID AAE36271  
 XX  
 AC AAE36271;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.  
 OS WO200298911-A2.  
 PN 12-DEC-2002.  
 PD 30-MAY-2002; 2002WO-GB002666.  
 XX 07-JUN-2001; 2001GB-00013900.  
 XX (SYGN ) SYNGENTA LTD.  
 PA Vincent JL, Viner R;  
 PI WPI; 2003-175137/17.  
 DR  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT Claim 12; Page 42-44; 67pp; English.  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 SQ Sequence 718 AA;

Query Match 99.1%; Score 3724.5; DB 6; Length 718;  
 Best Local Similarity 99.4%; Pred. No. 8.2e-288;  
 Matches 715; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60  
 DB 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGNRNNTRARSVVKSYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNRNNTRARSVVKSYIALELMFVQKLPFAVSG 180  
 QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
 DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFFYNQVERAGDYSYHCVKWS 240  
 QY 241 TGLNLRGNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 DB 241 TGLNLRGNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTDAL 300  
 QY 301 GTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 DB 301 GTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDFLEQVTIYSLLSWSNTQYMNW 360  
 QY 361 GGKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFQTQVNGVPR 420  
 DB 361 GGKLEFRITIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFQTQVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAENLSSGAAVVRGPGTGGDILRRTN 540

QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDDLDYK 600  
DB 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDDLDYK 599  
QY 601 TFRVTGTFPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660  
DB 600 TFRVTGTFPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 659  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 12  
AAB66907  
ID AAB66907 standard; protein; 718 AA.  
XX AAB66907;  
AC AAB66907;  
DT 12-APR-2001 (first entry)  
XX Insecticidal protein cryIIa1.  
DE Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB0002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENEGA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX Claim 14; Page 53-55; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 718 AA;  
Query Match 98.9%; Score 3718.5; DB 4; Length 718;  
Best Local Similarity 99.3%; Pred. No. 2.5e-287;  
Matches 714; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVFVASTI 60  
DB 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVFVASTI 60  
QY 61 QTGIGIAGKILGTIGVPFAGQVASYLGFILGELWPXGKNOWEIFMEHVBEIINOKISTYA 120  
DB 61 QTGIGIAGKILGTIGVPFAGQVASYLGFILGELWPXGKNOWEIFMEHVBEIINOKISTYA 120  
QY 121 RNKALTDLKGDLALAVYHDSLESVWGNRNNTRARSVVKVSOYIAELMFVKLPSFAVSG 180  
DB 121 RNKALTDLKGDLALAVYHDSLESVWGNRNNTRARSVVKVSOYIAELMFVKLPSFAVSG 180

QY 181 EEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
DB 181 EEVPLLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
QY 241 TGLNNLRGNAESWVRVYNQFRDMDTLMVLDLVALFPSYDTOMYPIKTTAQLTREYVTDAL 300  
DB 241 TGLNNLRGNAESWVRVYNQFRDMDTLMVLDLVALFPSYDTOMYPIKTTAQLTREYVTDAL 300  
QY 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMMNMW 360  
DB 301 GTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDLEQVTTIYSLLSRWSNTQYMMNMW 360  
QY 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFILTPQVNGVPR 420  
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFILTPQVNGVPR 419  
QY 421 VDFHWKFVTHPIASDNFYYPGVGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 420 VDFHWKFVTHPIASDNFYYPGVGIGTQLOQSENELPPEATGQPNYESYSHRLSHIGLIS 479  
QY 481 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 540  
DB 480 ASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRTN 539  
QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDDLDYK 600  
DB 540 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDDLDYK 599  
QY 601 TFRVTGTFPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 660  
DB 600 TFRVTGTFPPSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKV 659  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 719  
DB 660 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDDEFYLDKRELFEIVKYAKQLHIERNM 718

RESULT 13  
ADM74717  
ID ADM74717 standard; protein; 719 AA.  
XX ADM74717;  
AC ADM74717;  
DT 03-JUN-2004 (first entry)  
XX B. thuringiensis cryIIel SEQ ID NO:2.  
DE B. thuringiensis cryIIel  
XX cryI; toxicity; lepidoptera; cryIaB; coleoptera; diptera;  
KW cryIIel.  
XX Bacillus thuringiensis.  
OS CN1401772-A.  
XX CN1401772-A.  
XX 12-MAR-2003.  
XX 20-AUG-2001; 2001CN-00124163.  
XX 20-AUG-2001; 2001CN-00124163.  
XX (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
XX Song F, Zhang J, Huang D;  
XX WPI; 2003-442339/42.  
DB N-PSDB; ADM74716.  
XX Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
PT with high-toxicity to lepidoptera pests, encoded protein, primer  
PT sequences and the shuttle vector pSXV422b, useful as a pesticide.  
XX Example 3; SEQ ID NO 2; 29pp; Chinese.

XX The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
 CC combination, expression vector, nucleotide sequence of the B  
 CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
 CC amino acid sequence of the protein encoded by it, cooperative use of the  
 CC cryI gene with the expression product of cryIaB or cryIaC, primer  
 CC sequences for expressing the genes, and the constructed shuttle vector  
 CC pSX422b. The gene in combination with the cryIaB or cryIaC genes  
 CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
 CC The present sequence represents the cryIIc protein.  
 XX  
 SQ Sequence 719 AA;  
 Query Match 94.3%; Score 3547; DB 7; Length 719;  
 Best Local Similarity 93.5%; Pred. No. 1.2e-273;  
 Matches 672; Conservative 26; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 MRLKQDQKHSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPFSASTI 60  
 DB 1 MRLKQDQKHSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSYLSPILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVAVSYLSPILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGNVNNTRARSVVKQVQVIAELMFPVKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNVNNTRARSVVKQVQVIAELMFPVKLPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFNNRQVERAGYSDHCVKWS 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFNNRQVERAGYSDHCVKWS 240  
 QY 241 TGLNLRGNAESWVRVYQFRDMTLMVLDLVALFSDYDTQMPYKTTAQLTREYVTDI 300  
 DB 241 TGLNLRGNAESWVRVYQFRDMTLMVLDLVALFSDYDTQMPYKTTAQLTREYVTDI 300  
 QY 301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPPLDLEQVITYSLLSRWSNTQYMNW 360  
 DB 301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPPLDLEQVITYSLLSRWSNTQYMNW 360  
 QY 361 TFRVGFTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 361 TFRVGFTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
 QY 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLKY 600  
 QY 601 TFRVGFTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 660  
 DB 601 TFRVGFTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 660  
 QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKAKQLHIERNM 719  
 RESULT 14  
 AAB66912  
 ID AAB66912 standard; protein; 719 AA.  
 XX  
 AC AAB66912;  
 XX  
 DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIb1.  
 DE  
 XX Insecticide; transgenic plant; insect-resistance.  
 KW  
 XX Paecilomyces sp.  
 OS  
 XX WO200100841-A1.  
 PN  
 XX 04-JAN-2001.  
 PD  
 XX 23-JUN-2000; 2000WO-GB002457.  
 PF  
 XX 29-JUN-1999; 99GB-00015215.  
 PR  
 XX 23-DEC-1999; 99GB-00030536.  
 PR  
 XX (ZENE ) ZENECA LTD.  
 PA  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 PI  
 XX WPI; 2001-123015/13.  
 DR  
 XX Novel insecticidal protein obtained from species of Paecilomyces for  
 PT controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PT  
 XX Claim 14; Page 64-66; 72pp; English.  
 PS  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB6699 to AAB6901 and AAB6913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 CC  
 XX Sequence 719 AA;  
 SQ  
 Query Match 93.5%; Score 3516; DB 4; Length 719;  
 Best Local Similarity 92.8%; Pred. No. 3.5e-271;  
 Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 MRLKQDQKHSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPFSASTI 60  
 DB 1 MRLKQDQKHSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMEYENVEPFSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVAVSYLSPILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVAVSYLSPILGELWPKGKQWEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALTDLKGDLAVYHDSLESWGNVNNTRARSVVKQVQVIAELMFPVKLPFAVSG 180  
 DB 121 RNKALTDLKGDLAVYHDSLESWGNVNNTRARSVVKQVQVIAELMFPVKLPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFNNRQVERAGYSDHCVKWS 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFNNRQVERAGYSDHCVKWS 240  
 QY 241 TGLNLRGNAESWVRVYQFRDMTLMVLDLVALFSDYDTQMPYKTTAQLTREYVTDI 300  
 DB 241 TGLNLRGNAESWVRVYQFRDMTLMVLDLVALFSDYDTQMPYKTTAQLTREYVTDI 300  
 QY 301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPPLDLEQVITYSLLSRWSNTQYMNW 360  
 DB 301 GTVHPHPSFTTWNNAAPSFAIEAAVVRNPPLDLEQVITYSLLSRWSNTQYMNW 360  
 QY 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFVTHPIASDNFYYPGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
DB 601 TFRIGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 15

AAE36276  
ID AAE36276 standard; protein; 719 AA.

AC AAE36276;

DT 26-JUN-2003 (first entry)

XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

XX WO200298911-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

XX Vincent JL, Viner R;

XX WPI; 2003-175137/17.

XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.

XX Claim 12; Page 56-58; 67pp; English.

XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
XX Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention

XX Sequence 719 AA;

Query Match 93.5%; Score 3516; DB 6; Length 719;  
Best Local Similarity 92.8%; Pred. No. 3.5e-271;  
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPFVSASTI 60

DB 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFFVSASTI 60

QY 61 QTGIGIAGKITLGTGVFAGQVASLYSIFLGLWPKGKNQWEIFMEHVEIINQISTYA 120

DB 61 QTGIGIAGKITLGTGVFAGQIASLYSIFLGLWPKGKSQWEIFMEHVEIINQILTVA 120

QY 121 RNKALTDLKGLDALAVVHDSLESWGNRNNTPARSVVYKQVIALELMFVOKLPSEAVSG 180  
DB 121 RNKALSDDLRLGDLALAVHESLESWVENNNTPARSVVYKQVIALELMFVOKLPSEAVSG 180  
QY 181 BEVPLLPPIVAAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCWKWYS 240  
DB 181 BEVPLLPPIVAAANLHLLLRDASIFGKEWGLSSASEISTFYNRQVERTRDYSHCWKWYN 240  
QY 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYPIKTAQLTREVYTDAL 300  
DB 241 TGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAL 300  
QY 301 GTVHPHPSFTSTTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYLSLSRWSNTQYNNMW 360  
DB 301 GTVHPNQAFASTTWYNNNAPSFAIAEAAVIRSHPHLLDFLEKVTIYLSLSRWSNTQYNNMW 360  
QY 361 GGHKLEFRTIGGTLNISTOGSTNTSINPVTLPTSTRDYRTESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHRLLESRIIGGALNTSTOGSTNTSINPVTLQFTSRDYRTESLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHWKFVTHPIASDNFYVGYGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFPTLPIASDNFYVGYAGVGTQLODSENELPPEATTGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
QY 601 TFRVTGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
DB 601 TFRIGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Search completed: October 28, 2004, 18:20:02  
Job time : 89.6903 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19.191 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MCLKNQDKHOSFSSNAKVDK.....KRELFIVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3724	99.0	719	2 I39814	insecticidal prote
2	3724	99.0	719	2 I39815	insecticidal prote
3	3715	98.8	719	2 S25383	parasporal crystal
4	3484	92.6	719	2 I40590	cryv465 protein -
5	2248.5	59.8	1228	2 S00873	parasporal crystal
6	1872	49.8	380	2 B42459	hypothetical prote
7	1466	39.0	1157	1 S49247	parasporal crystal
8	1458.5	38.8	1166	2 S32645	parasporal crystal
9	1450	38.6	1155	2 A26513	parasporal crystal
10	1449	38.5	1174	2 S32649	parasporal crystal
11	1443	38.4	1155	2 JD0002	parasporal crystal
12	1443	38.4	1156	2 A29125	parasporal crystal
13	1434	38.1	1155	2 I39838	parasporal crystal
14	1430.5	38.0	934	2 A22798	parasporal crystal
15	1429.5	38.0	1176	2 JT0241	parasporal crystal
16	1426	37.9	1155	2 S02134	parasporal crystal
17	1425.5	37.9	1181	2 A41052	parasporal crystal
18	1423.5	37.8	1176	2 JC2219	parasporal crystal
19	1419.5	37.7	1176	2 A26217	parasporal crystal
20	1419.5	37.7	1176	2 S02215	parasporal crystal
21	1338	35.6	1174	2 A42459	parasporal crystal
22	1324	35.2	1138	2 A48944	parasporal crystal
23	1315.5	35.0	1156	2 A29838	parasporal crystal
24	1304.5	34.7	823	2 S04181	parasporal crystal
25	1295.5	34.4	1189	2 S00944	parasporal crystal
26	1281	34.1	1154	2 S39536	parasporal crystal
27	1248	33.2	1171	2 I40572	parasporal crystal
28	1248	33.2	1171	2 A37829	parasporal crystal
29	1235	32.8	1176	2 A48970	parasporal crystal

30	1208	32.1	1160	2 S32647	parasporal crystal
31	1193.5	31.7	1165	2 S11446	parasporal crystal
32	1188.5	31.6	655	2 JC7140	protoxin - Bacillu
33	1172	31.2	1172	2 S32689	parasporal crystal
34	1154	30.7	1160	2 I40589	parasporal crystal
35	1139.5	30.3	1178	1 USBSXH	parasporal crystal
36	1139	30.3	1177	2 A49785	parasporal crystal
37	1137	30.2	652	2 A27323	parasporal crystal
38	1113	29.6	659	2 S10228	parasporal crystal
39	1080.5	28.7	652	2 I39811	parasporal crystal
40	966	25.7	649	1 JH0261	parasporal crystal
41	917	24.4	618	2 S11445	parasporal crystal
42	881	23.4	1156	2 S19306	parasporal crystal
43	800	21.3	1136	1 USBS8I	parasporal crystal
44	693.5	18.4	934	2 B29838	parasporal crystal
45	645	17.1	1180	2 I39870	parasporal crystal

ALIGNMENTS

RESULT 1

I39814  
insecticidal protein cryv1 - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C:Accession: I39814  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis ?  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7793960  
A:Accession: I39814  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: GB:I36338; NID:g540281; PIDN:AAC36999.1; PID:g540282  
C:Genetics:  
A:Gene: cryv1  
C:Superfamily: parasporal crystal protein

Query Match 99.0%; Score 3724; DB 2; Length 719;  
Best Local Similarity 99.4%; Pred:No. 2.4e-254;  
Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY	1	MCLKNQDKHOSFSSNAKVDKISTDLSKNETDIELQINNHEDCLKMSYENVEPFSASTI	60
DB	1	MCLKNQDKHOSFSSNAKVDKISTDLSKNETDIELQINNHEDCLKMSYENVEPFSASTI	60
QY	61	QTGIGIAGKILGTLGVPPAGQVASYLSFTLGELWPKGNQWELFMEHVEE-INOKISTY	119
DB	61	QTGIGIAGKILGTLGVPPAGQVASYLSFTLGELWPKGNQWELFMEHVEE-INOKISTY	119
QY	120	ARNKALTDLKGLDALAVYHDSLESWVGNNRNTARSVVSQVIALELMFVOKLPSPAVS	179
DB	120	ARNKALTDLKGLDALAVYHDSLESWVGNNRNTARSVVSQVIALELMFVOKLPSPAVS	179
QY	180	GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDSDHCWKY	239
DB	180	GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDSDHCWKY	239
QY	240	STGLNLRGNTAESWRYNQFRDMLTDLVALFPPSYDTQMPYPIKTAQLTREVYTD	299
DB	240	STGLNLRGNTAESWRYNQFRDMLTDLVALFPPSYDTQMPYPIKTAQLTREVYTD	299
QY	300	IGTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM	359
DB	300	IGTVHPHPSFTSTTWNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMM	359
QY	360	WGCHKLEFRTIGTGLNISTOGSTNTSINPVTLPFTSRDVRVTESLAGNLFQPNVNGVP	419
DB	360	WGCHKLEFRTIGTGLNISTOGSTNTSINPVTLPFTSRDVRVTESLAGNLFQPNVNGVP	419

QY 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLODSENEIPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLODSENEIPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINOGNFSATMNRGDDLY 599  
 Db 540 NTGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINOGNFSATMNRGDDLY 599  
 QY 600 KTFRTVGFTTFFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 Db 600 KTFRTVGFTTFFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFPIVKYANLHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFPIVKYANLHIERNM 719

## RESULT 2

I39815  
 insecticidal protein cryV - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I39815  
 R:Gleave, A.P.; Williams, R.; Hedges, R.J.  
 Appl. Environ. Microbiol. 59, 1683-1687, 1993  
 A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
 iensis subsp. kurstaki.  
 A:Reference number: I39815; MUID:93238009; PMID:8517758  
 A:Accession: I39815  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-719 <RES>  
 A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PID:AAA22354.1; PID:G142768  
 C:Genetics:  
 A:Gene: cryV  
 C:Superfamily: parasporal crystal protein

Query Match 99.0%; Score 3724; DB 2; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 2.4e-254;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKSEYENVEPVSASTI 60  
 Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEILFMEHVVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEILFMEHVVEE-INQKISTY 119  
 QY 120 ARNKALTDLKGDLAVYHDSLESWGVRNNTARSVTSQYIALELMFVKLPSPFAVS 179  
 Db 120 ARNKALTDLKGDLAVYHDSLESWGVRNNTARSVTSQYIALELMFVKLPSPFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 QY 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTD 299  
 Db 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTD 299  
 QY 300 IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359  
 Db 300 IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359  
 QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP 419  
 Db 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP 419

QY 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLODSENEIPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDHFKFVTHPIASDNFYYPGAGIGTQLODSENEIPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHVKALVSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINOGNFSATMNRGDDLY 599  
 Db 540 NTGTFGDIRVNIINPPFAQRYRIRYASTDLOFHTSINGKAINOGNFSATMNRGDDLY 599  
 QY 600 KTFRTVGFTTFFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 Db 600 KTFRTVGFTTFFSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFPIVKYANLHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSEDFYLDKRELFPIVKYANLHIERNM 719

## RESULT 3

S25383  
 parasporal crystal protein cryIIa1 - Bacillus thuringiensis  
 N:Alternate names: delta-endotoxin; parasporal crystal protein cryV  
 C:Species: Bacillus thuringiensis  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C:Accession: S25383  
 R:Tailor, R.; Tippet, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
 Mol. Microbiol. 6, 1211-1217, 1992  
 A:Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
 A:Reference number: S25383; MUID:92269582; PMID:1588820  
 A:Accession: S25383  
 A:Molecule type: DNA  
 A:Residues: 1-719 <TAI>  
 A:Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PID:CAA44633.1; PID:G40290  
 C:Genetics:  
 A:Gene: cryV  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 98.8%; Score 3715; DB 2; Length 719;  
 Best Local Similarity 99.2%; Pred. No. 1.1e-253;  
 Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKSEYENVEPVSASTI 60  
 Db 1 MKLNQDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDECLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEILFMEHVVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGKNQWEILFMEHVVEE-INQKISTY 119  
 QY 120 ARNKALTDLKGDLAVYHDSLESWGVRNNTARSVTSQYIALELMFVKLPSPFAVS 179  
 Db 120 ARNKALTDLKGDLAVYHDSLESWGVRNNTARSVTSQYIALELMFVKLPSPFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 QY 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTD 299  
 Db 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALFPSTYDTQMPYIKTTAQLTREVYTD 299  
 QY 300 IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359  
 Db 300 IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359  
 QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP 419  
 Db 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFLTQPVNGVP 419

QY 420 RVDFAHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDFAHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
DB 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
QY 600 KTFRTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
DB 600 KTFRTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQIHIERNM 719  
RESULT 4  
I40590  
cryV465 protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I40590  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis tonocidus.  
A:Reference number: 139814; MUID:95314293; PMID:7793960  
A:Accession: I40590  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:G467234; PIDN:AAA82114.1; PID:G4672  
C:Genetics:  
A:Gene: cryV465  
C:Superfamily: parasporal crystal protein

Query Match 92.6%; Score 3484; DB 2; Length 719;  
Best Local Similarity 92.2%; Pred. No. 2e-237;  
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;  
QY 1 MRLKNQDKHQSFSSNAKVDKIATDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
DB 1 MRLKNPDKHQSSNAKVDKIATDSLKNETDIELKNNEDYLRNHEHESIDPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPAGQVASYLFGILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTGVPAGQIASLYSFLGELWPKGKQWEI-FMEHVEEIIINQKILTY 119  
QY 120 ARNKALTDLKLGLDALAVYHDSLESWGNRNNTARSVRQYIALELMFVQKLPSFAVS 179  
DB 120 ARNKALSDRLGLDALAVYHESLESWGNRNNTARSVRQYIALELMFVQKLPSFAVS 179  
QY 180 GEEVPLLPYQAQANLHLLLRDASIFGKEWGLSSSISITFYNRQVERAGDYSKVKWY 239  
DB 180 GEEVPLLPYQAQANLHLLLRDASIFGKEWGLSASISITFYNRQVERTRDYSKVKWY 239  
QY 240 STGLNNLRGNAESWVRYNQFRDMTLMVLDLVALFPSSYDTQMPYIKTTAQLTREYVTD 299  
DB 240 NTGLNNLRGNAESWVRYNQFRDMTLMVLDLVALFPSSYDTLVPYIKTTAQLTREYVTD 299  
QY 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYMMN 359  
DB 300 IGTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEQVITYSLLSWSNTQYMMN 359  
QY 360 WGGHKLFRIGTIGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTPQVNGVP 419  
DB 360 WGGHRLSRPIGALNTSTQGSTNTSINPVTLPFTSRDVRYESLAGNLFLTPQVNGVP 419

QY 420 RVDFAHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
DB 420 RVDFAHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
DB 480 SASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
DB 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599  
QY 600 KTFRTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
DB 600 KTFRTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVEYAEYDFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYANELHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDFFYLDEKRELFEIVKYAKQIHIERNM 719  
RESULT 5  
S00873  
parasporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis  
N:Alternate names: parasporal crystal protein cryA4  
C:Species: Bacillus thuringiensis subsp. thuringiensis  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S00873  
R:Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A:Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A:Reference number: S00873; MUID:88203216; PMID:3362680  
A:Accession: S00873  
A:Molecule type: DNA  
A:Residues: 1-1228 <BRI>  
A:Cross-references: UNIPROT:P05517; EMBL:X06711; NID:G40264; PIDN:CAA29898.1; PID:G58094;  
C:Genetics:  
A:Gene: cryA4  
A:Start codon: TTG  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 59.8%; Score 2248.5; DB 2; Length 1228;  
Best Local Similarity 62.5%; Pred. No. 5.7e-150;  
Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;  
QY 23 TDSLKNETDIELQNH-----EDCLKSEYENVEPVSASTIOTGIGIAGKI 70  
DB 2 TSNRKNNEIINAVSNHSAQMDLLPDARIEDSLCIAEGNIDPFVSASTVQTGINIAGRI 61  
QY 71 LGTLGVPPAGQVASYLFGILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129  
DB 62 LGVLGVPPAGQIASLYSFLGELWPKGRQWEI-FLEHVEQLINQITENARNALALRLQ 120  
QY 130 GLGDALAVYHDSLESWGNRNNTARSVRQYIALELMFVQKLPSFAVSGEVPPLPIY 189  
DB 121 GUGDSFRAYQQSLEDWLENRDDARTSRVLYQYIALELDFLANMPLFAIRNQEVPLLMVY 180  
QY 190 AQAANLHLLLRDASIFGKEWGLSSSISITFYNRQVERAGDYSKVKWYSTGLNNLRGT 249  
DB 181 AQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVERTRDYSYCVWEYNTGLNSLRGT 240  
QY 250 NAESWVRYNQFRDMTLMVLDLVALFPSSYDTQMPYIKTTAQLTREYVTDALGTAVHPHPSF 309  
DB 241 NAASWVRYNQFRDRLTLGLDLVALFPSSYDTRTPINTSAQLTREYVTDALGT--GVNM 298  
QY 310 TSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLLSWSNTQYMMNMGHKLFPRT 369  
DB 299 ASMNWNNNAAPSFAIEAAAIRSPHLLDFLEQLTIFSSRWSNTRHMTYWRGHTIOSRP 358  
QY 370 IGTGLNISTQGSTNTSINPVTLPFTSRDVRYESLAGNLFL--LTQPVNCGVPRVDFHKKF 427  
DB 359 IGGGLNTSTHGATNTSINPVTLPFRASRDVVRYESVAGVLLMGVLEPIHGVPVRFNEF-- 416



Db 708 QYGHDKMMLLEAVRAAKRLSRNL 732

RESULT 8  
S32645  
parasporal crystal protein crylGal - Bacillus thuringiensis  
C/Species: Bacillus thuringiensis  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S32645  
R/Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A/Reference number: S32645  
A/Accession: S32645  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1166 <LAM>  
A/Cross-references: UNIPROT:Q45746; EMBL:Z22510; NID:q295861; PIDN:CAA80233.1; PID:q295861  
C/Suprafamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match		38.8%;	Score 1458.5;	DB 2;	Length 1166;
Best Local Similarity		46.2%;	Pred. No. 2.5e-94;		
Matches 326;		Conservative 97;	Mismatches 206;	Indels 77;	Gaps 19;
QY	41	DCLKMEYE----	NVEPFVSASTIQGIGIAGKILGTLGVFPFAGQVASYFELGELMPK	96	
Db	13	NCLNPESEIFNARNSEFLYSQVSSGL---	TRFLEAAVPEAGFALGFLDIWGAL---	66	
QY	97	GKQWEILFMEHVEE--	INQKISTYARNKALTDKLGGLDALAVYHDSLESWVGRNNTAR	155	
Db	67	GVDQMS--LFLRQIEQLRQIE	TELELRNATAILTGLSSSYLYVEALREWENDPNNPASQ	125	
QY	156	SVVRSQYIALELMFVQKLP	SPFAVSGEVEPLPIYAQAANLHLLLRDASIFGKEWGLSSS	215	
Db	126	ERVTRFRALTDDAIVTG	LFTLAIRNLEVNLSVYTOAANLHLLLRDASYFGERWGLTQA	185	
QY	216	EISTFYNQVERAGDYSDHC	VKMYSTGLNNLRGTNAESWRYNQPRRDMLVLDLVALF	275	
Db	186	NIEDLYRLTSNIQEYSDH	CAWYNOGLNEIGGISR---RYLDFQRDLTISVLIDVALF	241	
QY	276	PSYDTQMPYIKTAQLTREV	YTDAL--GTVHPHPSSTSTWYNNNAPSIAEAAVVRNP	333	
Db	242	PNYDIRTEIPTQSOLTR	EIYTSFVAGNI-----NFGLSIANVLRAAP	284	
QY	334	HLDPLEQVTIYSLLSRNS	NTQYMMWGGHKLFRITIG--GFLN-----ISTQGSTNT	384	
Db	285	HLMDIFIDRIYVNSVR--	STPY---WAGHEVISRRTGGOGNEIRFPPLYGVAANAEPV	339	
QY	385	SINPVTLPFTSRDVRVTE	S-----LAGLNLELTQPVNGVPRVDFHWKVFVTHPIASDNFY	438	
Db	340	TIRPTGFTDEQRYARSR	VSVFRSSGQDFSLVDVAG-----FUT--IFSASVY	388	
QY	439	YPGYAGIGTQLQDSENE	LPPEATGQPNYESYSHRLSHIGLISAS-----HVKALVYSWTH	493	
Db	389	RNGF--GFNT---DTIDE	IPIEGTDPP--FTGYSHRLCHVGFLLASSPFIQYARAPIFSWTH	442	
QY	494	RSADRTNTEPNSTQIPL	VKAFNLSSGAAVVRGPGTGGDILRRNTGTGFDIRVNINP	553	
Db	443	RSATLNTAPDVITQIPL	VKAFNLHSGATIVKPGTGGDILRRNTVSGFGDMRVNITA	502	
QY	554	PFAQRYVRIRYASTTDL	QFHTSINGKAINQGNFSAATMNRGDDLYKTRFTVGTTPPSF	613	
Db	503	PLSQRYVRIRYASTTDL	QFYTINGITINIGNFSSTMDSGDDLQYGRFRVAGFTTPTTF	562	
QY	614	LDVQSTFTTICAWNFSS	SGNEVIYDRIEFVPEVTEYAEYDFEKAQEKVLTFTSTNPRGLK	673	
Db	563	SDANSTFTTICAFGSP	NNVEIYDRIEFVPAEVTFAEYDYDLERAQKAVNALETSSNQIGLK	622	
QY	674	TDVKDYHIDQVSNLVE	SLSDEFYLDKRELFEIVKYANELHIERNM	719	
Db	623	TDVTDYHIDKVSNLVE	CLSDDEFCLDEKRELSEKVKAKRLSDERNL	668	

RESULT 9  
A26513

parasporal crystal protein - Bacillus thuringiensis (strain aizawai)  
C/Species: Bacillus thuringiensis  
C/Date: 11-Mar-1988 #sequence\_revision 11-Mar-1988 #text\_change 09-Jul-2004  
C/Accession: A26513  
R/Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.  
Gene 53, 113-119, 1987  
A/Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis  
A/Reference number: A26513; MUID:87248103; PMID:3297927  
A/Accession: A26513  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1155 <OED>  
A/Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099  
C/Suprafamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match		38.6%;	Score 1450;	DB 2;	Length 1155;
Best Local Similarity		44.1%;	Pred. No. 9.8e-94;		
Matches 313;		Conservative 110;	Mismatches 232;	Indels 54;	Gaps 12;
QY	36	NINHEDECLKMEYENVE--	PFVSASTIQG-----IGIAGKILGTLGVFPFAGQVASYLS	87	
Db	4	NPNINECIPYCNCLSNPE	VEVLGGERIEGYTTPIDISLSLTQPLLSEF--VPGAGFVLGLVD	62	
QY	88	FILGELMPKGNQWEILFM	EHVEEINQKISTYARNKALTDKLGGLDALAVYHDSLESWVG	147	
Db	63	IIWGIF---GPSQMDAFL	VQIEQLINQRIEFPARNQAIISRLGLESLNYQIYAESFREWEA	119	
QY	148	NRNNTFARSVVRSOYIA	LELMFVQKLPFAVSGEVEPLPIYAQAANLHLLLRDASIFG	207	
Db	120	DPTNPALREEMRIQFND	MNSALITAIPLFAVQYQVPLLSVYVQAANLHLSVLRDVSFVG	179	
QY	208	KEWGLSSSEISTFYNQ	VERAGDYSDHCVKMYSTGLNNLRGTNAESWRYNQPRRDMLTLM	267	
Db	180	QRWGFDAATINSRYND	LTRLIGNYTDHVRVNTGLERWVGDPDRDRIYQFRRELT	239	
QY	268	VLDLVALFPDYDTQMP	YIKTAQLTREVYTDALGTVHPHPSSTSTWYNNNAPSIAE	327	
Db	240	VLDIVSLFPYVDSRTY	PVRTVSQLTREIYNPV-----LENFDGSFRALAQ	285	
QY	328	AV---VRNPHLLDFLEQ	VTIYSLLSR-----WSNTQYMMN---WGGHKLFRITIGTILNIS	377	
Db	286	GIEGSTRSPHLMIDL	INSITITDAHGEYVWSGHQIMASPVGFSGPFTFPLYGTWGNAA	345	
QY	378	TQGSTINTSINPVTLP	FPTSRDVRVTESLAGLNLELTQPVNGVPRVDFHWKVFVTHPIASDNF	437	
Db	346	POQRIVAQLGOGVYRT	LSLTYRRPFNIGN---NQQLSVLDGCTEFAYG-----TSSNL	396	
QY	438	YPGYAGIGTQLQDSE	NELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVYS	490	
Db	397	PSAVYRKSGT--VDSL	DEIPQNNVPPRQGFHRLSHVSMFRSGFSSSVSIIRAPMFS	454	
QY	491	WTHRSADRTNTEPN	STQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTGTGFDIRVN	550	
Db	455	WTHRSAEFNNIIPSS	QITQIPLTKSTNLGSGTSVVGFGTGGDILRRNTSPGQISTLRVN	514	
QY	551	INPPFAQRYVRIRY	ASTTDLQFHTSINGKAINQGNFSAATMNRGDDLYKTRFTVGTTP	610	
Db	515	ITAPLSQRYVRIRY	ASTTNLQFHTSIDGRPINQGNFSAATMSSGSLQSGSFRFTVGTTP	574	
QY	611	FSFLDVQSTFTTIC	AWNFSSSGNEVIYDRIEFVPEVTEYAEYDEKAQEKVLTFTSTNPR	670	
Db	575	FNFSNGSSVFTLSA	HVFNSSGNEVIYDRIEFVPAEVTFAEYDYDLERAQKAVNALETSSNQI	634	
QY	671	GLKTDVKDYHIDQ	VSNLVECLSDDEFYLDKRELFEIVKYANELHIERNM	719	
Db	635	GLKTDVTDYHIDQ	VSNLVECLSDDEFCLDEKRELSEKVKAKRLSDERNL	683	

RESULT 10  
S32649

paraspore crystal protein crylFa3 - Bacillus thuringiensis  
 C:Species: Bacillus thuringiensis  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: S32649  
 R:Lambert, B.  
 submitted to the EMBL Data Library, April 1993  
 A:Reference number: S32645  
 A:Accession: S32649  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1174 <LAM>  
 A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:G295865; PIDN:CAA80235.1; PID:G295865  
 C:Superfamily: paraspore crystal protein  
 C:Keywords: delta-endotoxin

Query Match 38.5%; Score 1449; DB 2; Length 1174;  
 Best Local Similarity 44.5%; Pred. No. 1.2e-93;  
 Matches 323; Conservative 100; Mismatches 207; Indels 96; Gaps 17;

QY 36 NINHE---DCLKSEYENVEPVFVSASTIQTGIGIA-GKILGTGVFPFAGQVASYSLFIL 90  
 Db 4 NIQNCVPYNCLSNPEVEILSEERSTGLPLDISLTLRFLSEFPVGVGVAFLGLDLIW 63

QY 91 GELWPKGKQWEILFMEHVEEINQKISTYARKALTDLKGGLDALAVYHDSLESVGNRN 150  
 Db 64 GFITP---SEWSFLQIEQLIEQRIETLERNRAITLRLGLADSYEVLEALREWEENPN 120

QY 151 NTRARSVRSQYIALELMFVQKLPFAVSVEEPLPIYAQAANLHLLLRDASIFGKEW 210  
 Db 121 NAQLREDVRIRFANTDDALITANNFTLTSFEPLSVYVQAANLHLLLRDASVFGQGW 180

QY 211 GLSSSEITFYNRQVERAGDYSCHVWYSTGLNLRGTNAESVRYNQFRRLDMLVLD 270  
 Db 181 GLDIATVNNHYNRLINLHRYTHECLDTYNOGLENLRTNQWRFNQFRRLTLVLD 240

QY 271 LVALPPSYDTOMYPIKTTAQLTREYVYDAIGTVHPHSFTSTTWNNAAPS-FSAIEAAV 329  
 Db 241 IVALFPNDARAYPIQTSQLTREIYTSV--IEDSP-----VSANIPNGFNRAEFG- 290

QY 330 VRNPHLLDFLEQVITYISLSRWSNTQYMMWCGHKLFRITGGTLNISTGTSVTSINPV 389  
 Db 291 VRPPLMDFMN-----SLFVTAETVRQTVMGHVL-----SSRNTAGNPI 331

QY 390 TLPP-----TSRDVYRESLAGLNLFLTPQVNGVPRVDFHMKFVTHPIAS 434  
 Db 332 NFPIYGIFFNGGAIWIADEDPFPYR-----LSDPV-----FVRGGFGN 371

QY 435 DNFFYPGYAGIGTQLQ-----DSENLPPATGQPNYESYSHRLSHI----- 476  
 Db 372 PH-YVLGLRGVAFQQTGNTHTFRNSGTIDSLDEIPQDNGSGAPWNDYSHVNLHVTFR 430

QY 477 --GLISASHV-KALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGG 533  
 Db 431 WPGIAGSDSWRAPMFSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGG 490

QY 534 DILRTNTGTFGDIRVNIAPPQAVRIRYASTDQLQFTSINGKAINQGNFSATMNR 593  
 Db 491 DLRLRTNTGTFADIRVNIAPPQAVRIRYASTDQLQFTSINGKAINQGNFSATMNR 550

QY 594 GEDLDYKTFRTVGTFTTPSFELDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDF 653  
 Db 551 GGNLESGNFRTAGFTSTPFSFNAQSTFTLGTQAFSN-QEVYIDRIEFVPEVTEAEYDF 609

QY 654 EXAQEKVATLFTSTNPGKLTVDKVDHIDQVSNLVESLSDEFYIDKRELFEIVKYANEL 713  
 Db 610 ERAQKAVNALFTSTSQLGLKNTVGYHIDQVSNLVACLSDEFYIDKRELFEIVKYANEL 669

QY 714 HIERNM 719  
 Db 670 SDRKEL 675

JD00002  
 paraspore crystal protein crylAb3 - Bacillus thuringiensis  
 N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal protein  
 C:Species: Bacillus thuringiensis  
 C>Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004  
 C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD00002  
 R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.  
 Agric. Biol. Chem. 51, 455-463, 1987  
 A>Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from  
 A:Reference number: A90025  
 A:Accession: A90025  
 A:Molecule type: mRNA  
 A:Residues: 1-1155 <KON>  
 A:Cross-references: UNIPROT:P06578  
 A:Experimental source: subsp. kurstaki  
 R:Geiser, M.; Schweitzer, S.; Grimm, C.  
 Gene 48, 109-118, 1986  
 A>Title: The hypervariable region in the genes coding for entomopathogenic crystal protei  
 A:Reference number: A91560; MUID:87163505; PMID:3557124  
 A:Accession: A91560  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <GEI>  
 A:Cross-references: GB:M15271; NID:G143123; PIDN:AAA22561.1; PID:G143124  
 A:Experimental source: subsp. kurstaki  
 R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.  
 DNA 5, 305-314, 1986  
 A>Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product analy  
 A:Reference number: A90955; MUID:86300092; PMID:3743328  
 A:Accession: A90955  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <WAB>  
 A:Cross-references: GB:M13898; NID:G142719; PIDN:AAA22330.1; PID:G142720  
 A:Experimental source: subsp. berliner  
 R:Chak, K.F.; Jen, J.C.  
 submitted to the EMBL Data Library, October 1990  
 A:Description: Complete nucleotide sequence and expression in Escherichia coli of a cry  
 A:Reference number: S14555  
 A:Accession: S14555  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1155 <CHA>  
 A:Cross-references: EMBL:X54939; NID:G40272; PIDN:CAA38701.1; PID:G40273  
 R:Hofte, H.; de Greve, H.; Seurinck, J.; Janssens, S.; Mahillon, J.; Ampe, C.; Vandekerck  
 Eur. J. Biochem. 161, 273-280, 1986  
 A>Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thuri  
 A:Reference number: A26461; MUID:87054026; PMID:3023091  
 A:Accession: A26461  
 A:Molecule type: DNA  
 A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>  
 A:Cross-references: GB:X04698; NID:G40254; PIDN:CAA28405.1; PID:G40255  
 A:Experimental source: strain berliner 1715  
 C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
 C:Genetics:  
 A:Gene: cry-1-2; bt2  
 C:Superfamily: paraspore crystal protein  
 C:Keywords: delta-endotoxin  
 F;82-586/Product: toxic peptide #status predicted <TXP>  
 F;82-300/Region: toxic #status predicted  
 F;300-586/Region: insecticidal #status predicted

Query Match 38.4%; Score 1443; DB 2; Length 1155;  
 Best Local Similarity 44.2%; Pred. No. 3.1e-93;  
 Matches 314; Conservative 109; Mismatches 231; Indels 56; Gaps 13;

QY 36 NINHECLKMSYENVE-PFVSASTIQTG-----IGIAGKILGTGVFPFAGQVASYLS 87  
 Db 4 NPNINECIPYNCLSNPEVEVLGGERTGTGTIDTSLTLQFLSEF-VPGAGVFLGLVD 62

QY 88 FILGELWPKGKQWEILFMEHVEEINQKISTYARKALTDLKGGLDALAVYHDSLESVWG 147  
 Db 63 IIVGIF---GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGSLNLYQIYAESFREWEA 119

QY 148 NNNTRARSVRSQYIALELMFVQKLPFAVSVEEPLPIYAQAANLHLLLRDASIFG 207

Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAANLHLSVLDRDVSFG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267  
Db 180 QRWGFDAAATINSRYNDLTRIGNYTDHVRWYNTGLERWGPDSRDWIRYNQFRRELTLT 239  
QY 268 VLDLVALPFSYDTQMPYIKTTAQLTRVYTDAGTVHPHPSFTSTTWYNNAPSF-----S 323  
Db 240 VLDIVSLFPYDSRTPIRTVSQLTRITYNPV-----LENFDGSRGSAQ 285  
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLSR-----WSNTQYMMN---WGHKLEFRTIGTGLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITITDAHRGEYWSGHQIMASPVGSGPFTFPPLYGTWMA 344  
QY 377 STQGSTNTSINPVTLPFTSRDVRYSLAGLNLFLTPQVNGVPRVDFHVKFVTHPIASDN 436  
Db 345 APOQRIVAQLGQGVYRTLSLTYRRPNFINIGN---NQQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFHRLSHVSMFRSGFNSVSIIRAPMF 453  
QY 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPFTGGDILRRINTGTGDIRV 549  
Db 454 SWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRISPGQISTLRV 513  
QY 550 NINPFFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYKTRTVGFTT 609  
Db 514 NITAPLSQRYVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFTT 573  
QY 610 PFSFLDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKVTALFTSTNP 669  
Db 574 PFNPSNGSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633  
QY 670 RGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVECLSDDEFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 12  
A29125  
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)  
C:Species: Bacillus thuringiensis subsp. kurstaki  
C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A29125  
R/Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme  
Bio/Technology 5, 807-813, 1987  
A>Title: Insect tolerant transgenic tomato plants.  
A/Reference number: A29125  
A/Accession: A29125  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-1156 <FIS>  
A/Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 38.4%; Score 1443; DB 2; Length 1156;  
Best Local Similarity 44.2%; Pred. No. 3.1e-93;  
Matches 314; Conservative 109; Mismatches 231; Indels 56; Gaps 13;

QY 36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGVFPAGQVSLYS 87  
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPCKGNQWELFMHVEEINQKISTYARNKALTDKLGDLALAVYHDSLESWVG 147  
Db 63 IIWGI--GPSQWDAFLVQIEQLINQRIEFPARNQAIISRLGSLNLYQIYAESFREWEA 119  
QY 148 NRNNTPARSVRSQYIALMLFMVQKLPFAVSGEEVPLLPYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAANLHLSVLDRDVSFG 179

QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267  
Db 180 QRWGFDAAATINSRYNDLTRIGNYTDHVRWYNTGLERWGPDSRDWIRYNQFRRELTLT 239  
QY 268 VLDLVALPFSYDTQMPYIKTTAQLTRVYTDAGTVHPHPSFTSTTWYNNAPSF-----S 323  
Db 240 VLDIVSLFPYDSRTPIRTVSQLTRITYNPV-----LENFDGSRGSAQ 285  
QY 324 AIEAAVVRNPHLLDFLEQVTIYSLSR-----WSNTQYMMN---WGHKLEFRTIGTGLNI 376  
Db 286 GIEGS-IRSPHLMIDLINSITITDAHRGEYWSGHQIMASPVGSGPFTFPPLYGTWMA 344  
QY 377 STQGSTNTSINPVTLPFTSRDVRYSLAGLNLFLTPQVNGVPRVDFHVKFVTHPIASDN 436  
Db 345 APOQRIVAQLGQGVYRTLSLTYRRPNFINIGN---NQQLSVLDGTEFAYG-----TSSN 395  
QY 437 FYYPGYAGIGTQLODSNELPPEATGQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
Db 396 LPSAVYRKSGT--VDSLDEIPQNNVPPRQGFHRLSHVSMFRSGFNSVSIIRAPMF 453  
QY 490 SWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVRGPFTGGDILRRINTGTGDIRV 549  
Db 454 SWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDILRRISPGQISTLRV 513  
QY 550 NINPFFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDYKTRTVGFTT 609  
Db 514 NITAPLSQRYVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFTT 573  
QY 610 PFSFLDVQSTFTIGAMFNSSGNEVYIDRIEFVPEVVEYEAEDFEKAQEKVTALFTSTNP 669  
Db 574 PFNPSNGSVFTLSAHVFNSSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQ 633  
QY 670 RGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
Db 634 IGLKTDVTDYHIDQVSNLVECLSDDEFCLDEKSELSEKVKHAKRLSDERNL 683

RESULT 13  
I39838  
parasporal crystal protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C>Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: I39838  
R/Heford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.  
J. Biotechnol. 6, 307-322, 1987  
A>Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki  
A/Reference number: I39838  
A/Accession: I39838  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1155 <RES>  
A/Cross-references: UNIPROT:P06578; GB:M37263; NID:G142885; PIDN:AAA2420.1; PID:G142886  
C/Superfamily: parasporal crystal protein  
C/Keywords: delta-endotoxin

Query Match 38.1%; Score 1434; DB 2; Length 1155;  
Best Local Similarity 44.1%; Pred. No. 1.3e-92;  
Matches 313; Conservative 109; Mismatches 232; Indels 56; Gaps 13;

QY 36 NINHEDECLMSEYENVE-PFVSASTIQG-----IGIAGKILGTGVFPAGQVSLYS 87  
Db 4 NPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62  
QY 88 FILGELWPCKGNQWELFMHVEEINQKISTYARNKALTDKLGDLALAVYHDSLESWVG 147  
Db 63 IIWGI--GPSQWDAFLVQIEQLINQRIEFPARNQAIISRLGSLNLYQIYAESFREWEA 119  
QY 148 NRNNTPARSVRSQYIALMLFMVQKLPFAVSGEEVPLLPYQAANLHLLLRDASIFG 207  
Db 120 DPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAANLHLSVLDRDVSFG 179  
QY 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWVRYNQFRDMLTLM 267

Db 180 QRWGFDAAATINSRYNDLTRIGNYTDHVRWYNTGLSERVGMGDSRDWRVYNQFRELTLT 239  
 Qy 268 VLDLVALFPDYDTOMYPIKTTAQLTREYVYDAIGTVHPHPSFTSTTWYNNAPSFSAIEA 327  
 Db 240 VLDIVSLFPNDYDRTYPIRTVSQLTREIYTNPV-----LENPDGSGRGSQA 285  
 Qy 324 AIEAAVVRNPHLLDFLEQVITYSLLSR-----WSNTQYNNM---WGHKLEPRTIGTLLNI 376  
 Db 286 GIEGS-IRSHMLDLNLSITYIDAHREGYWGSCHQMASPVGFSGPEFTPLPYMTMGNA 344  
 Qy 377 STQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTOPVNGVPRVDFHMKFVTHPIASDN 436  
 Db 345 AQQRIVAGQGGVYRTLSLTYRRPFNIGIN---NOQLSVLDGTEFAYG-----TSSN 395  
 Qy 437 FYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI-----SASHVKALVY 489  
 Db 396 LPSAVYRKSGT--VDSLDBIPQNNVPPRQGFSHRLSHVSMFRSGFSNVSIIAPMF 453  
 Qy 490 SWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTWTFGDIRV 549  
 Db 454 SWIHSANFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGTGGDILRRTPSGQISTLRV 513  
 Qy 550 NINPPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKYTFRTVGF 609  
 Db 514 NITAPLSQRYVRIRYASTNLQFHTSHGRPINQGNFSATMSSGNLQSGSFHGLGFTT 573  
 Qy 610 PFSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEFAKQKVTALFTSTNP 669  
 Db 574 PNFNSNGSVFTLSAHVNSGNEVYIDRIEFVPAETFEAEYDLERAQKAVNELFTSSNQ 633  
 Qy 670 RGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 634 IGLKTDVTDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 682

RESULT 14  
 A22798  
 parasporal crystal protein - Bacillus thuringiensis  
 C;Species: Bacillus thuringiensis  
 C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 09-Jul-2004  
 C;Accession: A22798  
 R;Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takanami, M.  
 Gene 34, 243-251, 1985  
 A;Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuringiensis  
 A;Reference number: A22798; MUID:85232070; PMID:2989108  
 A;Accession: A22798  
 A;Molecule type: DNA  
 A;Residues: 1-934 <SHI>  
 A;Cross-references: UNIPROT:Q9SV8; GB:M10917; NID:G143100; PIDN:AA22552.1; PID:G551713  
 C;Comment: The authors translated the codon ACA for residue 264 as Ser.  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1430.5; DB 2; Length 934;  
 Best Local Similarity 43.3%; Pred. No. 1.7e-92;  
 Matches 308; Conservative 116; Mismatches 227; Indels 61; Gaps 12;

Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLVFPFAGQVASIYS 87  
 Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62

Qy 88 FILGELWPKGNQWEILFMEHVEEINQKISTYARNKALTDLKGDLALAVYHDSLESWVG 147  
 Db 63 IIWGIF---GPSQWDAFLVQIEQLNQRIEFAFNQAIISLEGLSNLYQIYAESFREWEA 119

Qy 148 NRNTRASVVRSQYIALELMFVQKLPSPAVSGEVEPLPIYQAANLHLLLRDASIFG 207  
 Db 120 DPTNPALREEMRIQFNDMNSALTTPLEFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179

Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRDMLTLM 267  
 Db 180 QRWGFDAAATINSRYNDLTRIGNYTDHVRWYNTGLSERVGMGDSRDWRVYNQFRELTLT 239

Qy 268 VLDLVALFPDYDTOMYPIKTTAQLTREYVYDAIGTVHPHPSFTSTTWYNNAPSFSAIEA 327  
 Db 240 VLDIVSLFPNDYDRTYPIRTVSQLTREIYTNPV-----LENPDGSGRGSQA 285  
 Qy 328 AV---VRNPHLLDFLEQVITYSLLSRWNTQYNNMGHKLERTTIGGT---LNISTQGS 381  
 Db 286 RIEQNIRQPHLMDILNRIITYTDVHRG-----FNYWSHQITASPVGFSGPEFAFLFGN 340  
 Qy 382 TNSINPVTLPFTSRDVRTESL-----AGNLFLTOPVNGVPRVDFHMKFVTHPI 432  
 Db 341 AGNAAPVLVSLTGLGIFRTLSPLRYRILGSGPN---NQELFVLDGTEFSASLTNNL 397  
 Qy 433 ASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISAS-----HVKAL 487  
 Db 398 PSTIYRQGV-----DSLVDIPPQNSVPPRAGFSHRLSHVMTLSQAAGAVYTLRAP 450  
 Qy 488 VSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRNTWTFGDI 547  
 Db 451 TFSWQHSRABFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGTGGDILRRTPSGQISTL 510  
 Qy 548 RWINPPFAQRYVRIRYASTDLOFHTSINGKAINQGNFSATMNRGDLKYTFRTVGF 607  
 Db 511 RVNITAPLSQRYVRIRYASTNLQFHTSIDGRPINQGNFSATMSSGNLQSGSFRTVGF 570  
 Qy 608 TTPSFLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEFAKQKVTALFTST 667  
 Db 571 TTPFNFSNGSVFTLSAHVNSGNEVYIDRIEFVPAETFEAEYDLERAQKAVNELFTSS 630  
 Qy 668 NPRGLKTDVKDHYDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 631 NQIGLKTVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 682

RESULT 15  
 JT0241  
 parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)  
 N;Alternate names: 135K insecticidal protein  
 C;Species: Bacillus thuringiensis  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C;Accession: JT0241  
 R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.  
 Agric. Biol. Chem. 52, 1565-1573, 1988  
 A;Title: Cloning and expression in Escherichia coli of the 135-kDa insecticidal protein  
 A;Reference number: JT0241  
 A;Accession: JT0241  
 A;Molecule type: DNA  
 A;Residues: 1-1176 <SHI>  
 A;Cross-references: UNIPROT:P02965  
 A;Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein  
 C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae.  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 38.0%; Score 1429.5; DB 2; Length 1176;  
 Best Local Similarity 43.3%; Pred. No. 2.8e-92;  
 Matches 308; Conservative 115; Mismatches 228; Indels 61; Gaps 12;

Qy 36 NINHEDCLKMSEYENVE-PFVSASTIQTG-----IGIAGKILGTGLVFPFAGQVASIYS 87  
 Db 4 NPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF-VPGAGFVLGLVD 62

Qy 88 FILGELWPKGNQWEILFMEHVEEINQKISTYARNKALTDLKGDLALAVYHDSLESWVG 147  
 Db 63 IIWGIF---GPSQWDAFLVQIEQLNQRIEFAFNQAIISLEGLSNLYQIYAESFREWEA 119

Qy 148 NRNTRASVVRSQYIALELMFVQKLPSPAVSGEVEPLPIYQAANLHLLLRDASIFG 207  
 Db 120 DPTNPALREEMRIQFNDMNSALTTPLEFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 179

Qy 208 KEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRDMLTLM 267  
 Db 180 QRWGFDAAATINSRYNDLTRIGNYTDHVRWYNTGLSERVGMGDSRDWRVYNQFRELTLT 239





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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MKLKNQDKHQSPSSNAKVDK.....KRELPIVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3720	98.9	719	3	US-08-286-870A-8
2	3442.5	91.5	710	4	US-09-661-322A-42
3	3370	89.6	648	3	US-08-286-870A-4
4	3341	88.8	719	2	US-09-003-217-2
5	3336	88.7	719	3	US-09-218-942-2
6	2776	73.8	535	3	US-08-286-870A-6
7	2417.5	64.3	1229	1	US-08-100-709-4
8	2417.5	64.3	1229	1	US-08-176-865-4
9	2417.5	64.3	1229	1	US-08-474-038-4
10	2417.5	64.3	1229	2	US-08-779-046-4
11	2417.5	64.3	1229	2	US-08-881-340-4
12	2318.5	61.6	488	1	US-08-448-170-10
13	2318.5	61.6	488	3	US-08-961-803-10
14	2236.5	59.5	1207	1	US-07-951-715A-7
15	2236.5	59.5	1207	2	US-08-459-488A-7
16	2236.5	59.5	1207	3	US-08-459-595A-7
17	2236.5	59.5	1207	3	US-08-459-504B-7
18	2236.5	59.5	1207	3	US-08-459-444-7
19	2236.5	59.5	1207	3	US-09-053-549-8
20	2236.5	59.5	1207	3	US-09-547-422-7
21	2236.5	59.5	1207	4	US-09-988-462-7
22	2235.5	59.4	1227	3	US-09-053-549-2
23	2166.5	57.6	1227	1	US-08-448-170-8
24	2166.5	57.6	1227	3	US-08-961-803-9
25	2157.5	57.4	1227	4	US-09-661-322A-63
26	2142.5	57.0	1186	3	US-09-178-252-23
27	2142.5	57.0	1186	4	US-09-826-660-23

Sequence 38, Appl  
Sequence 25, Appl  
Sequence 25, Appl  
Sequence 4, Appl  
Sequence 6, Appl  
Sequence 30, Appl  
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Sequence 5, Appl  
Sequence 5, Appl  
Sequence 4, Appl  
Sequence 4, Appl

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US-09-178-252-25  
US-09-826-660-25  
PCT-US91-02560-4  
US-09-661-322A-6  
US-07-876-280-30  
US-07-812-180A-2  
US-08-315-468-2  
US-07-941-650A-2  
US-08-257-999-2  
US-08-532-547-5  
US-08-379-656B-5  
US-08-455-838-5  
US-09-019-809-5  
US-09-471-177-5  
US-09-220-806-5  
US-08-291-368-4  
US-08-962-190-4

ALIGNMENTS

RESULT 1  
US-08-286-870A-8  
; Sequence 8, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S.....  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-286-870A-8

Query Match 98.9%; Score 3720; DB 3; Length 719;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 714; Conservative- 3; Mismatches 1; Indels 2; Gaps 2;  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60  
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWELFMEHVER-INOKISTY 119  
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWELFMEHVER-INOKISTY 119  
QY 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVRSQYIALELMFVKLPSPFVS 179  
Db 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVRSQYIALELMFVKLPSPFVS 179  
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSSEISTFYNQVERAGDYSCHCVKWY 239  
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSSEISTFYNQVERAGDYSCHCVKWY 239  
QY 240 STGLNLRGTNAESWVRVYNOFRDMDTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVTD 299  
Db 240 STGLNLRGTNAESWVRVYNOFRDMDTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVTD 299  
QY 300 IGTVPHPSPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYMMN 359  
Db 300 IGTVPHPSPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYMMN 359  
QY 360 WGGHKLFRITIGTILNISTQGSNTSINPVTLPFTSRDVRYSAGLNLFLTPVNGVP 419  
Db 360 WGGHKLFRITIGTILNISTQGSNTSINPVTLPFTSRDVRYSAGLNLFLTPVNGVP 419  
QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLI 479  
Db 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLI 479  
QY 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDL 599  
Db 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDL 599  
QY 600 KTFRTVGTTPFSPFLDVQSTFTTCAMNPFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
Db 600 KTFRTVGTTPFSPFLDVQSTFTTCAMNPFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDKFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDKFYLDKRELFEIVKYAKQLHIERNM 719  
RESULT 2  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rel  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661.322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT

ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (200)..  
OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42  
Query Match 91.5%; Score 3442.5; DB 4; Length 710;  
Best Local Similarity 91.9%; Pred. No. 3.3e-304;  
Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;  
QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60  
Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWELFMEHVER-INOKISTY 119  
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELMPKGNQWELFMEHVER-INOKISTY 119  
QY 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVRSQYIALELMFVKLPSPFVS 179  
Db 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVRSQYIALELMFVKLPSPFVS 179  
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSSEISTFYNQVERAGDYSCHCVKWY 239  
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSSEISTFYNQVERAGDYSCHCVKWY 239  
QY 240 STGLNLRGTNAESWVRVYNOFRDMDTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVTD 299  
Db 240 STGLNLRGTNAESWVRVYNOFRDMDTLMVLDLVALPSPYDTQMPYIKTTAQLTREYVTD 299  
QY 300 IGTVPHPSPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYMMN 359  
Db 300 IGTVPHPSPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLRSWNTQYMMN 359  
QY 360 WGGHKLFRITIGTILNISTQGSNTSINPVTLPFTSRDVRYSAGLNLFLTPVNGVP 419  
Db 360 WGGHKLFRITIGTILNISTQGSNTSINPVTLPFTSRDVRYSAGLNLFLTPVNGVP 419  
QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLI 479  
Db 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLI 479  
QY 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDL 599  
Db 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDL 599  
QY 600 KTFRTVGTTPFSPFLDVQSTFTTCAMNPFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
Db 600 KTFRTVGTTPFSPFLDVQSTFTTCAMNPFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDKFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVQDYHIDQVSNLVESLSDKFYLDKRELFEIVKYAKQLHIERNM 719  
RESULT 3  
US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of  
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/286,870A  
FILING DATE: 05-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/520228  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 8910624.9  
FILING DATE: 09-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-4

Query Match 89.6%; Score 3370; DB 3; Length 648;  
Best Local Similarity 99.5%; Pred. No. 1.1e-297;  
Matches 646; Conservative 1; Mismatches 0; Indels 2; Gaps 2;  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPFSASTI 60  
Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPFSASTI 60  
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
Db 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
QY 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVRSQYIALELMFVKLPSPFVS 179  
Db 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVRSQYIALELMFVKLPSPFVS 179  
QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
Db 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
QY 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVYTD 299  
Db 240 STGLNNLRGTNAESWVRYNQFRDMLVLDLVALPSPYDTQMPYIKTTAQLTREVYTD 299  
QY 300 IGTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVITYSLRSWSNTQYMM 359  
Db 300 IGTVHPHPSFTSTWYNNAPSFSAEAAVVRNPHLLDFLEQVITYSLRSWSNTQYMM 359  
QY 360 WGGHKLERTIGTGLNISTQSTNTSINPVTLPFTSRDVYRTESLAGNLFLOPVNGVP 419  
Db 360 WGGHKLERTIGTGLNISTQSTNTSINPVTLPFTSRDVYRTESLAGNLFLOPVNGVP 419  
QY 420 RVDHFWKFTVHTPIASDNFYPYAGICTQLQDSNELPPEATGQPNYESYSHRISHIGLI 479  
Db 420 RVDHFWKFTVHTPIASDNFYPYAGICTQLQDSNELPPEATGQPNYESYSHRISHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRT 539  
Db 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGTGGDILRRT 539  
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
Db 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
QY 600 KTFRTVGFTTFFSFLDVQSTFTIGAMNFFSSGNEVYIDRIEFVPEVITYE 648  
Db 600 KTFRTVGFTTFFSFLDVQSTFTIGAMNFFSSGNEVYIDRIEFVPEVITYE 648  
RESULT 4  
US-09-003-217-2  
Sequence 2, Application US/09003217  
Patent No. 5986177  
GENERAL INFORMATION:  
APPLICANT: Osman, Yehia A.  
APPLICANT: Madkour, Magdy A.  
APPLICANT: Bulla, Lee A.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh  
STATE: NC  
COUNTRY: US  
ZIP: 27622  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/003,217  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Spruill, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919 420 2202  
TELEFAX: 919 881 3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 88.8%; Score 3341; DB 2; Length 719;  
Best Local Similarity 89.2%; Pred. No. 5.8e-295;  
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;  
QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPFSASTI 60  
Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPFSASTI 60  
QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
Db 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
QY 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVRSQYIALELMFVKLPSPFVS 179  
Db 120 ARNKALTDLKGDLALAVYHDSLESVGNRNNTARSVRSQYIALELMFVKLPSPFVS 179  
QY 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
Db 180 GEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239

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Db 180 GEEVPLPIYAQAANLHLLLRDASIFKXNGGLSASEISTFYNRQVTRTRDYSYHCVKWN 239
QY 240 STGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299
Db 240 NTGLNLRATNGQSWVRYNQFRKDIELMVLVLRVFPSTYDILVPIKTTSQLTREVTDA 299
QY 300 IGTVPHPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYMMN 359
Db 300 IGTVDPNQALRSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYMMN 359
QY 360 WGGHLEFRPTIGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVP 419
Db 360 WGGHLEFRPTIGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVP 419
QY 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLI 479
Db 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
QY 600 KTFRTVGFTTFFSFDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEK 659
Db 600 KTFRTVGFTTFFSFDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVIVKYANELHIERNM 719

RESULT 5
US-09-218-942-2
; Sequence 2, Application US/09218942
; Patent No. 6232439
; GENERAL INFORMATION:
; APPLICANT: Osman, Yehia
; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum
; FILE REFERENCE: CryII
; CURRENT APPLICATION NUMBER: US/09/218,942
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/035,361
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 09/003,217
; EARLIER FILING DATE: 1998-01-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-218-942-2

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Query Match 88.7%; Score 3336; DB 3; Length 719;
Best Local Similarity 89.2%; Pred. No. 1.7e-294;
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDLKNETDIELONINHEDECLKMSYEVENPEPVASSTI 60
Db 1 MCLKNPDKHQTLSSNAKVDKISTDLKNETDIELKMNNEDEYLRMSHEHSDIDPEVASTI 60
QY 61 QTGGIAGKILGTLPVGPAGVASLYSIFILGELWPKGKNQWEILFMEHVEE-INQIKSTY 119
Db 61 QTGGIAGKILGTLPVGPAGQASLYSIFILGELWPKGKSQWEI-FMEHVEAIINRKISTY 119
QY 120 ARNKALTDLKGIDALAVYHDSLESWGNRNNTNRASVVRVSOYIALELNFVQKLPSPAVS 179
Db 120 ARNKALTDLKGIDALAVYHDSLESWGNRNNTNRASVVRVSOYIALELNFVQKLPSPAVS 179

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QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVTRAGDYSYHCVKWKY 239
Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSASEISTFYNRQVTRTRDYSYHCVKWN 239
QY 240 STGLNLRGTNAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTTAQLTREVTDA 299
Db 240 NTGLNLRATNGQSWVRYNQFRKDIELMVLVLRVFPSTYDILVPIKTTSQLTREVTDA 299
QY 300 IGTVPHPSTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYMMN 359
Db 300 IGTVDPNQALRSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYMMN 359
QY 360 WGGHLEFRPTIGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVP 419
Db 360 WGGHLEFRPTIGTILNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFLTPQVNGVP 419
QY 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLI 479
Db 420 RVDHFKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
Db 540 KSGTFGHIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDY 599
QY 600 KTFRTVGFTTFFSFDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEK 659
Db 600 KTFRTVGFTTFFSFDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVVEYEAEDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFVIVKYANELHIERNM 719

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RESULT 6
US-08-286-870A-6
; Sequence 6, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989

```

ATTORNEY/AGENT INFORMATION:  
NAME: PAUL N. KOKULIS  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 70608/220720  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-286-870A-6

Query Match 73.8%; Score 2776; DB 3; Length 535;  
Best Local Similarity 99.4%; Pred. No. 9.5e-244;  
Matches 533; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVFSASTI 60  
DB 1 MKLKNQDKHQSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPVFSASTI 60

QY 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
DB 61 QTGIGIAGKILGTGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTY 119

QY 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSQVYIALELMFVKLPSPAVS 179  
DB 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSQVYIALELMFVKLPSPAVS 179

QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKMY 239  
DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKMY 239

QY 240 STGLNLRGNTAESWRYNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREVTDA 299  
DB 240 STGLNLRGNTAESWRYNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREVTDA 299

QY 300 IGVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYNNM 359  
DB 300 IGVHPHPSFTSTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYNNM 359

QY 360 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPVGVP 419  
DB 360 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVRESLAGNLFLOPVGVP 419

QY 420 RVDPHKFEVTHPIASDNFYPGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLI 479  
DB 420 RVDPHKFEVTHPIASDNFYPGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDI 535  
DB 480 SASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7  
US-08-100-709-4  
Sequence 4, Application US/08100709  
Patent No. 5322687  
GENERAL INFORMATION:  
APPLICANT: Donovan, William P.  
APPLICANT: Tan, Yiping  
APPLICANT: Jany, Christine S.  
APPLICANT: Gonzalez Jr., Jose M.  
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
ADDRESSEE: Nadel  
STREET: 1601 Market Street, 36th Floor  
CITY: Philadelphia

STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/100,709  
FILING DATE: 19930729  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Egoif, Christopher  
REGISTRATION NUMBER: 27633  
REFERENCE/DOCKET NUMBER: 7205-49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-757-1590  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1229 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-100-709-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
Best Local Similarity 65.3%; Pred. No. 1.6e-210;  
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLKN-ETDIELQ-NINHEDCMKSEYENVEPVFSASTIQTGIGIAGKI 70  
DB 7 NENEINALSIPVSNPSTQMNLSPPDARIEDSLCAEVNIDPPFVSASTVQTGINIAGRI 66

QY 71 LGTLGVFPAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129  
DB 67 LGVLGVFPAGQLASFSYFLVGLWLPSPGRDPWEI-FLEHVEQLIRQOVNTENTARTAIARLE 125

QY 130 GLGDALAVYHDSLESVGNRNTRARSQVYIALELMFVKLPSPAVSGEEVPLPIY 189  
DB 126 GLGRGYSVQQALETWLDNDRDARSRIILERYVALELDITAIPLFRIRNEEVPLLMVY 185

QY 190 AQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKMYSTGLNLRGT 249  
DB 186 AQAANLHLLLRDASIFGSEWGWASSDVNYQEQIRYTEEYSNHCQVWYNTGLNLRGT 245

QY 250 NAEVRYNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSF 309  
DB 246 NAEVRYNQFRDMLVLDLVALPSPSYDTQMPYIKTTAQLTREVTDAIGTVHPHPSF 305

QY 310 TSTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYNNMGGHKLERT 369  
DB 306 ASTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYNNMGGHKLERT 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRVRESLAGNLFLOPVGVPVDFHKKFV 428  
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRVRESLAGNLFLOPVGVPVDFHKKFV 422

QY 429 THPIASDNFYPG-----YAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLIISA 481  
DB 423 ---INPQNIYERGATTYSQYQGVIGIQLFDSETELPETTERPNEYESYSHRLSHIGLIIG 479

QY 482 SHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541  
DB 480 NTLRAPVYSWTHRSADRTNTEPNSTQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 539

QY 542 GTFGDIRVNINPPFAQRVYRIRYASTTDLQFHTSINGKAINCQGNFSAATMRGEDLDYKT 601  
DB 540 GTFGDIRVNINPPFAQRVYRIRYASTTDLQFHTSINGKAINCQGNFSAATMRGEDLDYKT 599

QY 602 FRTVGTTPPSFLDQVQSTTIGAWNFSSGNEVYIDRIFVPEVVEYAEYFEKAEKVT 661  
DB 600 FRTAGFSTPFNLAQSTFTLGAQSFN-QEVYIDRVEFVPAEVTFFAEYDILERAQKAVN 658

QY 662 ALFTSTNPRGLKTDVYHIDQVSNLVSLSDFYLDKRELFEIVKYANLHIERNM 719  
 DB 659 ALFTSTNPRGLKTDVYHIDQVSNLVSLSDFYLDKRELFEIVKYANLHIERNM 716

RESULT 8  
 US-08-176-865-4  
 ; Sequence 4, Application US/08176865  
 ; Patent No. 5616319  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yuping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 23-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-176-865-4

Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
 Best Local Similarity 65.3%; Pred. No. 1.6e-210;  
 Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSLN-ETDIELQ-NINHECLKMEYENVEPVFVASTIQTGTGIAGKI 70  
 DB 7 NENSIINALSIPTVSNPSTQNLSPDARIEDSLCVAEAVNIDPFVFASTVQTGINIAGRI 66

QY 71 LGTGVPPAGQVSLYSILGELWPKQKQWELFMEHVEE-INQKISTYARNKALTDLK 129  
 DB 67 LGVLGVPPAGQVSLYSILGELWPKQKQWELFMEHVEE-INQKISTYARNKALTDLK 125

QY 130 GLGALAVYHDSLESVGNRNTRVRSQYIALELMFVQKLPSPFVSGVEVPLLPY 189  
 DB 126 GLGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIFLFRIRNEEVPFLMUY 185

QY 190 AQANLHLLLRDASIFGKESWGLSSSISTFYNRQVAGDYSDHCWKYSTGLNNLRGT 249  
 DB 186 AQANLHLLLRDASIFGSEWGMASDVNQYQEQRYTTEYSNHCQVWNTGLNNLRGT 245

QY 250 NAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTKAQLTREVYTDAGTGVHPHPSF 309

DB 246 NAESWVRYNQFRDMLVLDLVALFPSYDTQMPYIKTKAQLTREVYTDAGTGVHPHPSF 305  
 QY 310 TSTTWNANNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMWGGHGLEFRT 369  
 DB 306 ASTNWNANNAPSFSAIEAAVVRNPHLLDFLEQVTIYLLSRWSNTQYMMWGGHGLEFRT 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRYSGLAGNLFLTPQVNGVPRVDFHFKV 428  
 DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRYSGLAGNLFLTPQVNGVPRVDFHFKV 422

QY 429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQFNPYSYSHLSHIGLISA 481  
 DB 423 ---INPQNIYERGATTYSQYQGVGIQDFDSETELPETTERPNYESYSHLSHIGLIIG 479

QY 482 SHVKALVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRRNT 541  
 DB 480 NTLRAPVSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGGDIILRRNT 539

QY 542 GTFGDIRVINPPEAQRVVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLIDYKT 601  
 DB 540 GTFGDIRVINPPEAQRVVRIRYASTTDLQPHTSINGKAINQGNFSATMNRGDLIDYKT 599

QY 602 FRTVGTTPSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVTEAEYDFEKAQEKVT 661  
 DB 600 FRTVGTTPSPFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTVTEAEYDFEKAQEKVT 658

QY 662 ALFTSTNPRGLKTDVYHIDQVSNLVSLSDFYLDKRELFEIVKYANLHIERNM 719  
 DB 659 ALFTSTNPRGLKTDVYHIDQVSNLVSLSDFYLDKRELFEIVKYANLHIERNM 716

RESULT 9  
 US-08-474-038-4  
 ; Sequence 4, Application US/08474038  
 ; Patent No. 5679343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yuping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESS: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,038  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 23-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-038-4

Query Match      64.3%; Score 2417.5; DB 1; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.6e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLKSEYENVEPFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEANNIDFFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSEFELGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
Db 67 LGVLGVPPAGQLASFYSLFVGLWPSGRDPWEI-FLEHVEQLIRQVQVTRNTAIAELE 125

QY 130 GLGDALAVYHDSLESWVGNNRNTARSVRSQYIALFELMFVQKLPFSFVSGEEVPLPIY 189
Db 126 GLGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVY 185

QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKQWYSTGLNNLRGT 249
Db 186 AQANLHLLLRDASLFGSEWGMASDVNQYIQEIRYTEEYSNHCYQWYNTGLNNLRGT 245

QY 250 NAESWVRYNQFERDMTLMVLDLVALPESYDTQMPYIKTTAQLTREVTDAIGTVHPHPSF 309
Db 246 NAESWLRYNQFRDLTLGVLDLVALPESYDTRTYPINTSAQLTREIYTDPIGRTNAPSGF 305

QY 310 TSTWYNNAPSAIEAAVVRNPRLDLEQVTIYSLLSWSNTQYMMWGGHKLERT 369
Db 306 ASTWNNAPSAIEAAIFRPPHLLDPEQVTIYSSASSRWSSTQHMVWVGHRLNFRP 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFV 428
Db 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFV 422

QY 429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA 481
Db 423 ---INPQNIYERGATTYSQYQGVIGLFDSETELPPTTERPNYESYSHRLSHIGLIIG 479

QY 482 SHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541
Db 480 NTLRAPVYSWTHRSADRTNTEIPNRIITQIPLVKALNLHSGVTVVGPGFTGGDILRRNT 539
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## RESULT 10

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US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yaping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-779-046-4
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Query Match      64.3%; Score 2417.5; DB 2; Length 1229;
Best Local Similarity 65.3%; Pred. No. 1.6e-210;
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLKSEYENVEPFSASTIQTGIGIAGKI 70
Db 7 NENEIINALSIPTVSNPSTQMNLSPDARIEDSLCVAEANNIDFFVSASTVQTGINIAGRI 66

QY 71 LGTLGVPPAGQVASYLSEFELGELWPKGNQWEILFMEHVEE-INQKISTYARNKALTDLK 129
Db 67 LGVLGVPPAGQLASFYSLFVGLWPSGRDPWEI-FLEHVEQLIRQVQVTRNTAIAELE 125

QY 130 GLGDALAVYHDSLESWVGNNRNTARSVRSQYIALFELMFVQKLPFSFVSGEEVPLPIY 189
Db 126 GLGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVY 185

QY 190 AQANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKQWYSTGLNNLRGT 249
Db 186 AQANLHLLLRDASLFGSEWGMASDVNQYIQEIRYTEEYSNHCYQWYNTGLNNLRGT 245

QY 250 NAESWVRYNQFERDMTLMVLDLVALPESYDTQMPYIKTTAQLTREVTDAIGTVHPHPSF 309
Db 246 NAESWLRYNQFRDLTLGVLDLVALPESYDTRTYPINTSAQLTREIYTDPIGRTNAPSGF 305

QY 310 TSTWYNNAPSAIEAAVVRNPRLDLEQVTIYSLLSWSNTQYMMWGGHKLERT 369
Db 306 ASTWNNAPSAIEAAIFRPPHLLDPEQVTIYSSASSRWSSTQHMVWVGHRLNFRP 365

QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFV 428
Db 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDFHWKFV 422

QY 429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA 481
Db 423 ---INPQNIYERGATTYSQYQGVIGLFDSETELPPTTERPNYESYSHRLSHIGLIIG 479

QY 482 SHVKALVSWTHRSADRTNTEIPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541
Db 480 NTLRAPVYSWTHRSADRTNTEIPNRIITQIPLVKALNLHSGVTVVGPGFTGGDILRRNT 539
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QY 542 GTFGDIRVINPPFAQRYEVRIYASTTDLQFHTSINGKAINQGNESATMNRGDLDTKT 601  
 DB 540 GTFGDIRLININPLSRQYRVIRYASTTDLQFTRINGTTNIGNFSRTMNRGDNLEYS 599  
 QY 602 FRTVGTTPSFDFLDVQSTTIGAWNFSSGNEVVIDRIEFVFPVEVYAEYDFEKAQKVT 661  
 DB 600 FRTAGFSTPFLNAQSTFTLGAQSFNS-QEVYIDRVFVPAEVTFAEYDLERAQKAVN 658  
 QY 662 ALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEIVKYAKRLSDERNL 716

RESULT 11  
 US-08-881-340-4  
 ; Sequence 4, Application US/08881340  
 ; Patent No. 5942658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/881,340  
 ; FILING DATE: 24-JUN-1997  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egolf, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-881-340-4

Query Match 64.3%; Score 2417.5; DB 2; Length 1229;  
 Best Local Similarity 65.3%; Pred. No. 1.6e-210;  
 Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;

QY 13 SSNAKVDKISTDSIKN-ETDIELQ-NINHECLKMEYENVEPFSASTIQTGIGIAGKI 70  
 DB 7 NENEIINALSIPTVSNSTQMLSPDARIEDSLCAEVNIDPFSASTVQTGINIAGRI 66  
 QY 71 LGTLGVFPAGVASLYSIFLGLWPKGNQWELFWEHVEE-INQKISTYARNKALTDLK 129  
 DB 67 LGVLGVFPAGQLASFYSLVGLWPSGRDPWEI-FLEHVEQLIRQVTEENTRTAIARLE 125  
 QY 130 GLGDALAVYHDSLESVGNRRNTRARSVVRVRSQYIALELMFVQKLPSPFAVSGEEVPLPIY 189

DB 126 GLGRGYSYQQALETWLDNENDARSRSILERYVALELDITTAIPLERIRNEEVPLLMVY 185  
 QY 190 AQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYSTGLANLRGT 249  
 DB 186 AQAANLHLLLRDASLFGSEWGMASDDVNOYQOEIRYTEESNHCQVWYNTGLANLRGT 245  
 QY 250 NAEWSVRYNOFRDMDTLMVLDLVALFSPYDTQWYPIKTTAQLTREVVYDTAIGTVHPHPSF 309  
 DB 246 NAEWSLRYNOFRDMDTLMVLDLVALFSPYDTQWYPIKTTAQLTREVVYDTAIGTVHPHPSF 305  
 QY 310 TSTTWNNAAPSFAIEAAVVRNPHLLDLEQVITYLSLRSKSNTOVMNMWGGHLEERT 369  
 DB 306 ASTNMFNNAPSFAIEAAIFRPPHLLDPEQLTIYSASSRWSSTQHMVYVWGHRLNFRP 365  
 QY 370 IGGTLNISTOGST-NTSINPVTLPFTSRDVRVRESLAGLNLFLOTPVNGVPRVDHFKFV 428  
 DB 366 IGGTLNISTOGLTNNTSINPVTLPFTSRDVRVRESLAGLNLFLOTPVNGVPRVDHFKFV 422  
 QY 429 THPIASDNFYYPG-----YAGIGTQLQDSNELPEATGQPNYESYSHLSHIGLISA 481  
 DB 423 ---INPQNIYERGATTYSQPYQGVGIQDFSETELPETTERPNYESYSHLSHIGLIIG 479  
 QY 482 SHVKALVSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGDIERTNT 541  
 DB 480 NTLAPVYSWTHRSADRNTNIEPNSITQIPLVKAFNLSGAAVVRGPGFTGDIERTNT 539  
 QY 542 GTFGDIRVINPPFAQRYEVRIYASTTDLQFHTSINGKAINQGNESATMNRGDLDTKT 601  
 DB 540 GTFGDIRLININPLSRQYRVIRYASTTDLQFTRINGTTNIGNFSRTMNRGDNLEYS 599  
 QY 602 FRTVGTTPSFDFLDVQSTTIGAWNFSSGNEVVIDRIEFVFPVEVYAEYDFEKAQKVT 661  
 DB 600 FRTAGFSTPFLNAQSTFTLGAQSFNS-QEVYIDRVFVPAEVTFAEYDLERAQKAVN 658  
 QY 662 ALFTSTNPRGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 659 ALFTSTNPRRLKTDVTDYHIDQVSNMVACLSDEFCLDEKRELFEIVKYAKRLSDERNL 716

RESULT 12  
 US-08-448-170-10  
 ; Sequence 10, Application US/08448170  
 ; Patent No. 5723758  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Payne, Jewel  
 ; APPLICANT: Cummings, David A.  
 ; APPLICANT: Cannon, Raymond J.C.  
 ; APPLICANT: Narva, Kenneth E.  
 ; APPLICANT: Steelman, Steve  
 ; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
 ; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
 ; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/448,170  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/069,902  
 ; FILING DATE: 01-JUNE-1993  
 ; CLASSIFICATION: 424

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/S 102D.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-170-10

Query Match 61.6%; Score 2318.5; DB 1; Length 488;
Best Local Similarity 89.4%; Pred. No. 3.6e-202;
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVVPPVSASTI 60
Db 1 MKSKQNMQHQSLSNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51
QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWELLFMEHVVEE-INQKISTY 119
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGKSQWEI-FMEHVVEELINQKISTY 110
QY 120 ARNKALTDLKLGDALAVYHDSLESVGNRNNTARSVRSQYIALELMFVQKLPSPFAVS 179
Db 111 ARNKALADLKLGDALAVYHESLESWIENRNTTRSVVKSQYITLELMFVQSLPSPFAVS 170
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKQWGLSSSEISTFYNRQVERAGDYSDDHCVKWY 239
Db 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKYSDDHCVKWY 230
QY 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKYSDDHCVKWY 230
Db 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKYSDDHCVKWY 230
QY 240 STGLNLRGNTAESWRYNQFRDWTMLVLDLVALFPSYDTQMYPIKTTAQLTREVTDA 299
Db 231 NTGLNRLMGNAESWRYNQFRDWTMLVLDLVALFPSYDTQMYPIKTTAQLTREVTDA 290
QY 300 IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMN 359
Db 291 IGTVHPHPSFTSTTWYNNAPSFSTIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMN 350
QY 360 WGGHKLPRFTIGTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVP 419
Db 351 WGGHKLPRFTIGTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVP 410
QY 420 RVDPHWKFTVHTPIASDNFYYPGYAGIGTQLOQDSNELPPEATQGPNYESYSHRLSHIGLI 479
Db 411 RVDPHWKFTVHTPIASDNFYYPGYAGIGTQLOQDSNELPPEATQGPNYESYSHRLSHIGLI 470
QY 480 SASHVKALVYSWTHRSAD 497
Db 471 SASHVKALVYSWTHRSAD 488

RESULT 13
US-08-961-803-10
; Sequence 10, Application US/08961803
; Patent No. 6150589
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Cummings, David A.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stelman, Steve
; TITLE OF INVENTION: No. 6150589el Bacillus thuringiensis Isolate Denoted
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes
```

```

; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jay M. Sanders
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,803
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,902
; FILING DATE: 01-JUNE-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,247
; FILING DATE: 13-SEPT-1991
; CLASSIFICATION: 800
; APPLICATION NUMBER: US 08/448,170
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: M/S 102DCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-961-803-10

Query Match 61.6%; Score 2318.5; DB 3; Length 488;
Best Local Similarity 89.4%; Pred. No. 3.6e-202;
Matches 445; Conservative 13; Mismatches 29; Indels 11; Gaps 3;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSYENVVPPVSASTI 60
Db 1 MKSKQNMQHQSLSNNATVDKNFTGSLNNTNTELQNFH-----EGIEPFSVSTI 51
QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSFILGELWPKGNQWELLFMEHVVEE-INQKISTY 119
Db 52 QTGIGIVGKILGNLGVPPAGQVASYLSFILGELWPKGKSQWEI-FMEHVVEELINQKISTY 110
QY 120 ARNKALTDLKLGDALAVYHDSLESVGNRNNTARSVRSQYIALELMFVQKLPSPFAVS 179
Db 111 ARNKALADLKLGDALAVYHESLESWIENRNTTRSVVKSQYITLELMFVQSLPSPFAVS 170
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKQWGLSSSEISTFYNRQVERAGDYSDDHCVKWY 239
Db 171 GEEVPLLPPIYAQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKYSDDHCVKWY 230
QY 240 STGLNLRGNTAESWRYNQFRDWTMLVLDLVALFPSYDTQMYPIKTTAQLTREVTDA 299
Db 231 NTGLNRLMGNAESWRYNQFRDWTMLVLDLVALFPSYDTQMYPIKTTAQLTREVTDA 290
QY 300 IGTVHPHPSFTSTTWYNNAPSFSAIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMN 359
Db 291 IGTVHPHPSFTSTTWYNNAPSFSTIEAAVVRNPHLLDLEQVTIYSLLSRWSNTQYMMN 350
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QY 360 WGGHKLFRFTIGTNTSTQSTNTSINPVTLPFTSRDVTSTSLAGLNLFLTQPVNGVP 419  
 Db 351 WGGHKLFRFTIGTNTSTQSTNTSINPVTLPFTSRDVTSTSLAGLNLFLTQPVNGVP 410  
 QY 420 RVDFHFWKFTVTHPIASDNFYPGYAGIGTQLODSSENLPPPEATGQPNYESYSHRLSHIGLI 479  
 Db 411 RVDFHFWKFTVTHPIASDNFYPGYAGIGTQLODSSENLPPPEATGQPNYESYSHRLSHIGLI 470  
 QY 480 SASHVKALVYSWTHRSAD 497  
 Db 471 SASHVKALVYSWTHRSAD 488

RESULT 14

US-07-951-715A-7

; Sequence 7, Application US/07951715A

; Patent No. 5625136

GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation  
 ; STREET: 7 Skyline Drive  
 ; CITY: Hawthorne  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.308

; CURRENT APPLICATION DATA:

; FILING DATE: 25-SEP-1992

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruill, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

; TELEPHONE: (919)541-8615

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1207 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-951-715A-7

Query Match 59.5%; Score 2236.5; DB 1; Length 1207;

Best Local Similarity 64.1%; Pred. No. 4.7e-194;  
 Matches 441; Conservative 76; Mismatches 156; Indels 15; Gaps 7;  
 QY 40 EDCLKMSEYENVEPVSASTIQTGIGIAGKILGTGVFPAGVASLYSFIIGELWPKGN 99  
 Db 10 EDLSLCAEGNNIDPVSASTVQTGINIAGRIAGLGTGVFPAGQLASFYSFLVGLWPRGRD 69  
 QY 100 QWEILFMHEVEE-INQKISTYARNKALTDKGLGDALAVYHDSLESVWGNRNTRRSVV 158  
 Db 70 QWEI-FLHVEQLINQOITENARNTALRQLGSDSPAYQQSLEDLENRDDARTSVL 128  
 QY 159 RSQYIALELMFVQKLPSPFAVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSEIS 218  
 Db 129 YTOYIALELDFLNAMPLFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEGLTSQEIQ 188  
 QY 219 TPNROVERAGDYSCHVKWYSTGLNNLRGTNAESWRYNQFRRDWTLMVLDLVALFPSSY 278  
 Db 189 RYERQVTRDYSYCVWYNTGLNLRGTNAASWRYNQFRRDWTLMVLDLVALFPSSY 248  
 QY 279 DTQMPYIKTTAQLTREVTDAIGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDF 338  
 Db 249 DTRTYPINTSAQLTREVTDAIGAT--GYNMAMNWNNNAPSFAIEAAAIRSPHLLDF 306  
 QY 339 LEQVTYISLLSRWSNTQYMMWGHKLEFRTIGGTALISTQGSTNTSINPVTLPFTSRDV 398  
 Db 307 LEQLTIFSASSRWSNTRHMTYRGHTIQSRPIGGGLNTSTHGATNTSINPVTLPFTSRDV 366  
 QY 399 YRTESLAGLNF--LTQPVNGVPRVDFHKKFVTHP-----IASDNFYPGYAGIGTQLOD 451  
 Db 367 YRTESYAGVLLWGIYLEPIHGVPVTFNF--TNPNISDRGTANYSQP-YESPGIQLKD 422  
 QY 452 SENELPPEATQPNYESYSHRLSHIGLSASHVKALVYSWTHRSADRTNTIEPNSITQIP 511  
 Db 423 SETELPPETTERPNYESYSHRLSHIGLILOSRVNVVYVSWTHRSADRTNTIEPNSITQIP 482  
 QY 512 LVKAFNLSSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPPFAQSYRVRIRYASTTDL 571  
 Db 483 MVKASELPQGTTVVRGPGFTGGDILRRNTGTGDIRVNNINPPFAQSYRVRIRYASTVDF 542  
 QY 572 QPHTSINGKAINQGNFSATMNRGDDLDYKTFRTVGFPTTPEFLDVOSTFTTIGAMNFSGN 631  
 Db 543 DFFVSRGGTTVNNFRFLRTMNSGDELKYNFVRRAFPTTFTTQIQDIIRTSIQGLSGNG 602  
 QY 632 EVIDRIEFVPEVTYEAEDFEKAEKVATLTSTPRGLKTDVXDYHIDQVSNLVESL 691  
 Db 603 EVIDKIEIIPVTATFEASYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVAQL 662  
 QY 692 SDEFYLDKRELFELVKYANELHIERNM 719  
 Db 663 SDEFCLDEKRELEKVKYAKRLSDERNL 690

RESULT 15

US-08-459-448A-7

; Sequence 7, Application US/08459448A

; Patent No. 5859336

GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lyle D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFVVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5  
Searched: 1825181 seqs, 575374646 residues  
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3733	99.3	719	2	CAC85964
2	3724	99.0	719	1	C1JA_BACTK
3	3724	99.0	719	2	Q6X181
4	3724	99.0	719	2	AAP86782
5	3719	98.9	719	2	Q93NJ5
6	3718	98.9	719	2	O85796
7	3589	95.4	719	2	Q8KY61
8	3517	93.5	719	2	Q9F0P8
9	3484	92.6	719	1	C1IB_BACTE
10	3363	89.4	719	1	C1ID_BACTU
11	3341	88.8	719	1	C1IC_BACTU
12	2417.5	64.3	1229	1	C1BB_BACTU
13	2417.5	64.3	1233	1	C1BC_BACTM
14	2250.5	59.8	1228	2	Q93T75
15	2248.5	59.8	1228	1	C1BA_BACTK
16	2240.5	59.6	1228	2	Q93NM5
17	2166.5	57.6	849	2	Q6PYW8
18	2166.5	57.6	849	2	AAS93797
19	2166.5	57.6	1227	1	C1BE_BACTU
20	2078.5	55.4	1231	2	Q8KNY2
21	2078.5	55.3	1231	1	C1BD_BACT2
22	1971.5	52.4	1215	1	C1KA_BACTM
23	1876	49.9	381	2	Q45740
24	1643.5	43.7	1157	1	C8AA_BACUK
25	1630	43.3	1144	2	O8KZL7
26	1466	39.0	1157	1	C9CA_BACTO
27	1460.5	38.8	1169	1	C8BA_BACTU
28	1458.5	38.8	1166	1	C1GA_BACTU
29	1455	38.7	1169	1	C1FE_BACTM
30	1451	38.6	1167	1	C1JA_BACTU
31	1449	38.5	1174	2	Q45749

RESULT 1  
CAC85964  
ID CAC85964 PRELIMINARY; PRT; 719 AA.  
AC CAC85964;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DE Delta-endotoxin.  
GN CRY11A.  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;  
OC Bacillus cereus group; Bacillus thuringiensis.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BNS3;  
RA Tounsi S., Zouari N., Jaoua S.;  
RT "Cloning and study of the expression of a novel cryIIa-type gene from  
RL J. Appl. Microbiol. 95:23-28 (2003).  
DR EMBL; AJ315121; CAC85964.1; -.  
SQ SEQUENCE 719 AA; 81203 MW; 8676E5A6C25DAPE8 CRC64;

ALIGNMENTS

32	1443	38.4	1155	1	C1AB_BACTK	P06578	Bacillus	th
33	1443	38.4	1155	2	Q7BE98	Q7be98	Bacillus	th
34	1443	38.4	1155	2	Q9F296	Q9f296	Bacillus	th
35	1443	38.4	1155	2	AA76494	Aa76494	Bacillus	th
36	1443	38.4	1155	2	AA013302	Aa013302	Bacillus	th
37	1441	38.3	1118	2	Q9AMB3	Q9am83	Bacillus	th
38	1438	38.2	1156	2	Q6GUA7	Q6gua7	Bacillus	th
39	1433	38.1	1177	2	Q6EIX3	Q6eix3	Bacillus	th
40	1431	38.0	1155	2	Q93T21	Q93t21	Bacillus	th
41	1430.5	38.0	793	2	Q6PYW7	Q6pyw7	Bacillus	th
42	1430.5	38.0	793	2	AAS93798	Aa93798	Bacillus	th
43	1430.5	38.0	1180	2	Q9S5V8	Q9s5v8	Bacillus	th
44	1429.5	38.0	1176	2	Q7WZT9	Q7wzt9	Bacillus	th
45	1425.5	37.9	1181	1	C1AE_BACTL	Q03748	Bacillus	th

Qy	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEFPVSA	60
Db	1	MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINNHEDCLKMSYENVEFPVSA	60
Qy	61	QTGIGTAGKILGTLGVPPAGQVSLYSFTLGELWPKGNQWELFMEHVEEINQKISTY	119
Db	61	QTGIGTAGKILGTLGVPPAGQVSLYSFTLGELWPKGNQWELFMEHVEEINQKISTY	119
Qy	120	ARNKALTDLKGLDALAVYHDSLESWVGNNNTRRSVVRSQVIAELMFVQKLPFAVS	179
Db	120	ARNKALTDLKGLDALAVYHDSLESWVGNNNTRRSVVRSQVIAELMFVQKLPFAVS	179
Qy	180	GEEVPLPIVAQAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYS	239
Db	180	GEEVPLPIVAQAANLHLLLRDASIFGKEWGLSSSEISFTFYNRQVERAGDYS	239
Qy	240	STGLNLRGNTNAESWVRVYQFRDMLVLDLVALFSPSYDTQWYPIKTTAQ	299
Db	240	STGLNLRGNTNAESWVRVYQFRDMLVLDLVALFSPSYDTQWYPIKTTAQ	299
Qy	300	IGTVHPSPSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYILLSRWSNTQ	359
Db	300	IGTVHPSPSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYILLSRWSNTQ	359
Qy	360	WGGHKLFRIGGTINISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNFLT	419
Db	360	WGGHKLFRIGGTINISTQGSTNTSINPVTLPFTSRDVRVYRTESLAGLNFLT	419

QY 420 RVDHFKFVTHPIASDNFYYPGAGICTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDHFKFVTHPIASDNFYYPGAGICTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 Db 480 SASHKALVYSWTHRSADRTNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLOQFHTSINGKAINQCNFSATMNRGEDLDY 599  
 Db 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLOQFHTSINGKAINQCNFSATMNRGEDLDY 599  
 QY 600 KTRFRTVGFTTFFSFLDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAQEK 659  
 Db 600 KTRFRTVGFTTFFSFLDVQSTFTTGAMNFSNGNEVYIDRIEFVPEVTEAEYDEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFVIVKANLHIERNM 719  
 Db 660 VTALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFVIVKANLHIERNM 719

RESULT 2  
 CIIA\_BACTK STANDARD; PRT; 719 AA.  
 AC Q45752; P71092; Q45750; Q45751; Q45756;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pestidical crystal protein cryIIa (insecticidal delta-endotoxin  
 CryII(a)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Names-cryIIa; Synonyms-cryII(a), cryV, cryVI, CGCryV;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 CX NCBI\_TaxID=29339;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSIR732;  
 RX MEDLINE=93298009; PubMed=8517758;  
 RA Gleave A.P., Williams R., Hedges R.J.;  
 RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
 RT serotypes for the presence of cryV-like insecticidal protein genes and  
 RT characterization of a cryV gene cloned from B. thuringiensis subsp.  
 RT kurstaki.";  
 RL Appl. Environ. Microbiol. 59:1683-1687 (1993).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=JHCC4835;  
 RX MEDLINE=92269582; PubMed=1588820;  
 RA Tailor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
 RT "Identification and characterization of a novel Bacillus thuringiensis  
 RT delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";  
 RL Mol. Microbiol. 6:1211-1217 (1992).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=HD-1;  
 RX MEDLINE=95314293; PubMed=7793960;  
 RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
 RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
 RT thuringiensis and cloning of cryV-type genes from Bacillus  
 RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
 RT entomocidus.";  
 RL Appl. Environ. Microbiol. 61:2402-2407 (1995).  
 RN [4]

RP SEQUENCE FROM N.A.  
 RC STRAIN=AB88;  
 RX MEDLINE=96178985; PubMed=8606196;  
 RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
 RA Craig J.A., Koziel M.G., Estruch J.J.;  
 RT "Cloning of a cryV-type insecticidal protein gene from Bacillus  
 RT thuringiensis: the cryV-encoded protein is expressed early in  
 RT stationary phase.";  
 RL J. Bacteriol. 178:2141-2144 (1996).

[5]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=61;  
 RC "Isolation, cloning and expression of cryV gene.";  
 RT Selvapandian A., Bhatnagar R.K.;  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 CC FUNCTION: Promotes colloidotomic lysis by binding to the midgut  
 CC epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella and Bombyx mori.  
 CC DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of  
 CC the spore coat.  
 CC MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 CC terminus.  
 CC SIMILARITY: Belongs to the delta endotoxin family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; M98544; AAA22354.1; -  
 DR EMBL; X62821; CAA44633.1; -  
 DR EMBL; L36338; AAC36999.1; -  
 DR EMBL; L49391; AAB00958.1; -  
 DR EMBL; Y08920; CAA70124.1; -  
 DR FIR; I39815; I39815.  
 DR FIR; S2383; S2383.  
 DR HSSP; P02965; ICIV.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 FT VARIANT 159 159 K -> R (in strain 61).  
 FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 FT VARIANT 443 443 A -> V (in strain AB88).  
 FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
 SQ SEQUENCE 719 AA; 81216 MW; 3627ESA6C25DAFF5 CRC64;  
 Query Match 99.0%; Score 3724; DB 1; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-252;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;  
 QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDCCLKMSEYENVEPFFVSASTI 60  
 Db 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDCCLKMSEYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKITGLTGVPPAGQVAVSLYSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
 Db 61 QTGIGIAGKITGLTGVPPAGQVAVSLYSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
 QY 120 ARNKALTDKGLGDALAVYHDSLESWGNRNTRARSVVRSQYIALELMFVQKLPFAVS 179  
 Db 120 ARNKALTDKGLGDALAVYHDSLESWGNRNTRARSVVRSQYIALELMFVQKLPFAVS 179  
 QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKWLSSSBEISTYNNRQVERAGDYSCHVKWY 239  
 Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKWLSSSBEISTYNNRQVERAGDYSCHVKWY 239  
 QY 240 STGLNNLRGTNAESWVRVYQNFQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVYTD 299  
 Db 240 STGLNNLRGTNAESWVRVYQNFQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVYTD 299  
 QY 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359

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Db 300 IGVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
QY 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFUTQPVNGVP 419
Db 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFUTQPVNGVP 419
QY 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLI 479
Db 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTEPNSTIQLPVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEPNSTIQLPVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599
QY 600 KTFRTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
Db 600 KTFRTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 3
Q6X181
ID Q6X181 PRELIMINARY; PRT; 719 AA.
AC Q6X181;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CryII.
GN Name=cryII;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;

Query Match 99.0%; Score 3724; DB 2; Length 719;
Best Local Similarity 99.3%; Pred. No. 1.9e-252;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPFSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTLGVPPAGQVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119
QY 120 ARNKALTDLKGDLALAVYHDSLESWGVRNTRARSVVRYSQYIALELMFVKLPSPAVS 179
Db 120 ARNKALTDLKGDLALAVYHDSLESWGVRNTRARSVVRYSQYIALELMFVKLPSPAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNNRQVERAGDYSCHVKWY 239
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNNRQVERAGDYSCHVKWY 239
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QY 240 STGLNNLRGTNAESWRYNQFRDRDWTMLVLDLVALFPYSYDTQMYPIKTTAQTLREVYTD 299
Db 240 STGLNNLRGTNAESWRYNQFRDRDWTMLVLDLVALFPYSYDTQMYPIKTTAQTLREVYTD 299
QY 300 IGVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
Db 300 IGVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359
QY 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFUTQPVNGVP 419
Db 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVYRTESLAGLNLFUTQPVNGVP 419
QY 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLI 479
Db 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQDSENELPPEATGQPNYESYSHRSLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTEPNSTIQLPVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEPNSTIQLPVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599
QY 600 KTFRTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
Db 600 KTFRTVGFTTTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 4
AAP86782
ID AAP86782 PRELIMINARY; PRT; 719 AA.
AC AAP86782;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CryII.
GN CryII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T01 328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RL "Complete sequence of cryII gene of isolate T01 328 from Bacillus thuringiensis from Cubatao (SP - Brazil) soil.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1; -.
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

Query Match 99.0%; Score 3724; DB 2; Length 719;
Best Local Similarity 99.3%; Pred. No. 1.9e-252;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPFSASTI 60
Db 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDCMKSEYENVEPFSASTI 60
QY 61 QTGIGIAGKILGTLGVPPAGQVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTLGVPPAGQVASYLSPILGELWPKGNQWEILFMEHVEE-INQKISTY 119
QY 120 ARNKALTDLKGDLALAVYHDSLESWGVRNTRARSVVRYSQYIALELMFVKLPSPAVS 179
Db 120 ARNKALTDLKGDLALAVYHDSLESWGVRNTRARSVVRYSQYIALELMFVKLPSPAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSISTFYNNRQVERAGDYSCHVKWY 239
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Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKWLSSSISTFYNRQVERAGDSDHCVKWY 239
Qy 240 STGLNLRGTNAESWVRYNQFRDMLMVLVALPFSYDTQMPYIKTTAQLTREYVYDA 299
Db 240 STGLNLRGTNAESWVRYNQFRDMLMVLVALPFSYDTQMPYIKTTAQLTREYVYDA 299
Qy 300 IGTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMMN 359
Db 300 IGTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMMN 359
Qy 360 WGGHKLFEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFLLTQPVNGVP 419
Db 360 WGGHKLFEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFLLTQPVNGVP 419
Qy 420 RVDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRNTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRNTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNINPFPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDY 599
Db 540 NTGTFGDIRVNINPFPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDY 599
Qy 600 KTFRTVGFTTFFSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Db 600 KTFRTVGFTTFFSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVYHIDQVSNLVSDEFLYDEKRELFEIVKYAKQLHIERNM 719
Db 660 VTALFTSTNPRGLKTDVYHIDQVSNLVSDEFLYDEKRELFEIVKYAKQLHIERNM 719

RESULT 5
Q93NJ5 PRELIMINARY; PRT; 719 AA.
ID Q93NJ5
AC Q93NJ5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Crylia.
GN Name=crylia;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK6742.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

Query Match 98.9%; Score 3719; DB 2; Length 719;
Best Local Similarity 99.2%; Pred. NO. 4.3e-252;
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;
Qy 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60
Db 1 MKLKNQDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLKMEYENVEPFSASTI 60

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Qy 61 QTGIGIAGKILGTGLVFPAGQVASYLSFILGELWPKGNQWELFMEHVER-INQKISTY 119
Db 61 QTGIGIAGKILGTGLVFPAGQVASYLSFILGELWPKGNQWEL-FMEHVERIINQKISTY 119
Qy 120 ARNKALTDLXGLGDALAVYHDSLESWGNRNTRARSVVRQVIALELMFVQKLPFAVS 179
Db 120 ARNKALTDLXGLGDALAVYHDSLESWGNRNTRARSVVRQVIALELMFVQKLPFAVS 179
Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKWLSSSISTFYNRQVERAGDSDHCVKWY 239
Db 180 GEEVPLPIYAQAANLHLLLRDASIFGKWLSSSISTFYNRQVERAGDSDHCVKWY 239
Qy 240 STGLNLRGTNAESWVRYNQFRDMLMVLVALPFSYDTQMPYIKTTAQLTREYVYDA 299
Db 240 STGLNLRGTNAESWVRYNQFRDMLMVLVALPFSYDTQMPYIKTTAQLTREYVYDA 299
Qy 300 IGTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMMN 359
Db 300 IGTVHPHPSSTTTWYNNAPSAIEAAVVRNPHLLDLEQVTIYSLLSRWSTQYMMN 359
Qy 360 WGGHKLFEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFLLTQPVNGVP 419
Db 360 WGGHKLFEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFLLTQPVNGVP 419
Qy 420 RVDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDFHKKFVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479
Qy 480 SASHVKALVYSWTHRSADRNTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRNTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539
Qy 540 NTGTFGDIRVNINPFPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDY 599
Db 540 NTGTFGDIRVNINPFPFAQRYVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDLDY 599
Qy 600 KTFRTVGFTTFFSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Db 600 KTFRTVGFTTFFSFLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659
Qy 660 VTALFTSTNPRGLKTDVYHIDQVSNLVSDEFLYDEKRELFEIVKYAKQLHIERNM 719
Db 660 VTALFTSTNPRGLKTDVYHIDQVSNLVSDEFLYDEKRELFEIVKYAKQLHIERNM 719

RESULT 6
O85796 PRELIMINARY; PRT; 719 AA.
ID O85796
AC O85796;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Insecticidal protein.
GN Name=cryI01;
OS Bacillus thuringiensis (subsp. kurstaki).
OG Plasmid large plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S101;
RA Zhong Q., Deng R., Yuan M., Pang Y., Wang X.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076953; AAC26910.1; -
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.

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Db 1 MKLNKPDKHQSSNAKVDKIATDLSLKNVETDIELKNVNNEDYLRMSEHESIDPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPAGQVAVSLYFGLGELWPKGNQWELFMEHVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTGVPAGQVAVSLYFGLGELWPKGNQWELFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDKGLDALAVYHDSLESWGNRNTRARVRSQYIALELMEFVKQLPSFAVS 179  
 Db 120 ARNKALSDRLGDLALAVYHDSLESWGNRNTRARVRSQYIALELMEFVKQLPSFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 QY 240 STGLNNLRGTNAESWVRVYQFRDMTLMVLDLVALPSPSYDTPQYPIKTTAQLTREVYTDA 299  
 Db 240 STGLNNLRGTNAESWVRVYQFRDMTLMVLDLVALPSPSYDTPQYPIKTTAQLTREVYTDA 299  
 QY 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN 359  
 Db 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN 359  
 QY 360 WGGHKLFPRTIGTFLNISTQGSTNTSINPVTLPFTSRDVARTESLAGLNLFLTQPVNGVP 419  
 Db 360 WGGHKLFPRTIGTFLNISTQGSTNTSINPVTLPFTSRDVARTESLAGLNLFLTQPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENLPPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENLPPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSTITQPLVKAFNLSSGAAVVRGPGFTGGDILART 539  
 Db 480 SASHVKALVYSWTHRSADRTNTEPNSTITQPLVKAFNLSSGAAVVRGPGFTGGDILART 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
 Db 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
 QY 600 KTFRTVGTTPFPFLDVQSTFTTICAWNPSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
 Db 600 KTFRTVGTTPFPFLDVQSTFTTICAWNPSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659

RESULT 10  
 CLID\_BACTU STANDARD; PRT; 719 AA.  
 AC Q9XDL1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin  
 DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
 GN Name=cryIId; Synonyms=cryII(d), NRcryV;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR30;  
 RX MEDLINE=20374042; PubMed=10919402;  
 RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.-M., Park S.-H.;  
 RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein  
 RT gene.";  
 RL Curr. Microbiol. 41:65-69(2000).  
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
 CC epithelial cells of many lepidopteran larvae. Active on Plutella  
 CC xylostella and on Bombyx mori.  
 CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 CC sporulation and is accumulated both as an inclusion and as part of

CC the spore coat.  
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; AF047579; AAD44366.1; -;  
 CC HSSP; P02965; 1CIY.  
 CC InterPro; IPR001178; Endotoxin.  
 CC InterPro; IPR005638; endotoxin\_C.  
 CC InterPro; IPR005639; endotoxin\_N.  
 CC InterPro; IPR008979; Gal bind like.  
 CC Pfam; PF03944; Endotoxin\_C; 1.  
 CC Pfam; PF00555; Endotoxin\_M; 1.  
 CC Pfam; PF03945; Endotoxin\_N; 1.  
 CC Sporulation; Toxin.  
 CC KW SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;  
 CC -----  
 CC Query Match 89.4%; Score 3363; DB 1; Length 719;  
 CC Best Local Similarity 89.3%; Pred. No. 4.2e-227;  
 CC Matches 643; Conservative 36; Mismatches 39; Indels 2; Gaps 2;  
 QY 1 MKLNKPDKHQSSNAKVDKIATDLSLKNVETDIELKNVNNEDYLRMSEHESIDPVSASTI 60  
 Db 1 MKLNKPDKHQSSNAKVDKIATDLSLKNVETDIELKNVNNEDYLRMSEHESIDPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPAGQVAVSLYFGLGELWPKGNQWELFMEHVEE-INQKISTY 119  
 Db 61 QTGIGIAGKILGTGVPAGQVAVSLYFGLGELWPKGNQWELFMEHVEE-INQKISTY 119  
 QY 120 ARNKALTDKGLDALAVYHDSLESWGNRNTRARVRSQYIALELMEFVKQLPSFAVS 179  
 Db 120 ARNKALADLKGDLALAVYHDSLESWGNRNTRARVRSQYIALELMEFVKQLPSFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 QY 240 STGLNNLRGTNAESWVRVYQFRDMTLMVLDLVALPSPSYDTPQYPIKTTAQLTREVYTDA 299  
 Db 240 STGLNNLRGTNAESWVRVYQFRDMTLMVLDLVALPSPSYDTPQYPIKTTAQLTREVYTDA 299  
 QY 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN 359  
 Db 300 IGTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN 359  
 QY 360 WGGHKLFPRTIGTFLNISTQGSTNTSINPVTLPFTSRDVARTESLAGLNLFLTQPVNGVP 419  
 Db 360 WGGHKLFPRTIGTFLNISTQGSTNTSINPVTLPFTSRDVARTESLAGLNLFLTQPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENLPPPEATGQPNYESYSHRLSHIGLI 479  
 Db 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENLPPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSTITQPLVKAFNLSSGAAVVRGPGFTGGDILART 539  
 Db 480 SASHVKALVYSWTHRSADRTNTEPNSTITQPLVKAFNLSSGAAVVRGPGFTGGDILART 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
 Db 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
 QY 600 KTFRTVGTTPFPFLDVQSTFTTICAWNPSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659  
 Db 600 KAFRTVGTTPFPFSNAQSTFTTICAWNPSGNEVYIDRIEFVPEVTEAEYDFEKAQEK 659

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QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFELVYKYNELHIERNM 719
Db 660 ITAMPTSTNLRRLKTNVTDCHIDQVSNLVESLSDEFYLDKRELFELVYKYNELHIERNM 719

RESULT 11
CLIC_BACTU
ID CLIC_BACTU STANDARD; PRT; 719 AA.
AC O87404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Pesticidal crystal protein cryIc (insecticidal delta-endotoxin
DE CryII(c)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).
GN Name=cryIc; Synonyms=cryII(c);
OS Bacillus thuringiensis.
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C18 / Egypt;
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC
CC EMBL; AF056933; AAC62933.1; -
CC HSSP; P02965; 1CIY..
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal bind like.
CC Pfam; PF03944; Endotoxin_C; 1.
CC Pfam; PF00555; Endotoxin_M; 1.
CC Pfam; PF03945; Endotoxin_N; 1.
CC Plasmid; Sporulation; Toxin.
KW SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;

Query Match 88.8%; Score 3341; DB 1; Length 719;
Best Local Similarity 89.2%; Pred. No. 1.5e-225;
Matches 642; Conservative 35; Mismatches 41; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60
Db 1 MKLKNPKDHQTLSSNAKVDKIATDSLKNETDIELKNMNEDEYLRWSEHESIDPVSASTI 60

QY 61 QTGIGIAGKILGTGVPPAGQVASLYSIFILGELWPKQKQWELFMEHVEE-INQKISTY 119
Db 61 QTGIGIAGKILGTGVPPGQIASLYSIFILGELWPKGKSQWEI-FMEHVEAIINRKISY 119

QY 120 ARNKALTDLKLGLDALAVYHDSLESWGNNRNNTRASVRSQYIALELMFVQKLPSFAVS 179
Db 120 ARNKALTDLKLGLDALAVYHDSLESWGNNRNNTRASVRSQYIALELMFVQKLPSFAVS 179

QY 180 GEEVPLPIYAQAANHLHLLLRDASIFGKEWGLSSSEISTFYNNQVERAGDYSCHVKWY 239
Db 180 GEEVPLPIYAQAANHLHLLLRDASIFGKGLSASEISTFYNNQVERIRDYSYHCVKNW 239

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QY 240 STGLANLRGTNAESWVRYNQFRDWTMLVLDLVALFSDYDTQMYPIKTTAOLTRVYTDA 299
Db 240 NTGLANLRATNGQSWVRYNQFRKDIELMVLDRVFPSTLTVPIKTTSQLTRVYTDA 299

QY 300 IGTVEHPSPSTSTTWNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYSLLSWSNTOYMMN 359
Db 300 IGTVDENQALRSTTWNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLLSWSNTOYMMN 359

QY 360 WGGHKLLEFRITIGTTLNISTQGSTNTSINPVTLPFTSRDVRVTSGLAGNLFLTPQVNGVP 419
Db 360 WGGHRLLESPIGGALNTSQGSTNTSINPVTLPFTSRDVRVTSGLAGNLFLTPQVNGVP 419

QY 420 RVDFHMKFVTHPIASDNFYYPGAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLI 479
Db 420 RVDFHMKFPLPIASDNFYLYGAGVGTLQDSENELPPEATGQPNYESYSHRLSHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAENLSSGAAVVRGPGFTGGHILRRT 539

QY 540 NTGTGDIRVYNINPFAQRYRVRIRYASTDLQFHTSINGKAINQGNFSATMNRGSDLDY 599
Db 540 KSGTFGHIRVYNINPFAQRYRVRIRYASTDLQFHTSINGKAINQGNFSATMNRGSDLDY 599

QY 600 KTFRTVGTFTPFPSLDVQSTFTICAWNFSNGNEVYIDRIEFVPEVTEYAEVDFEKAQEK 659
Db 600 KTFRTVGTFTPFPSLDVQSTFTICAWNFSNGNEVYIGRIEFVPEVTEYAEVDFEKAQEK 659

QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFELVYKYNELHIERNM 719
Db 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFELVYKYNELHIERNM 719

RESULT 12
CLIBB_BACTU
ID CLIBB_BACTU STANDARD; PRT; 1229 AA.
AC Q45739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIbB (insecticidal delta-endotoxin
DE CryIb(b)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=cryIb; Synonyms=cryIb(b), cryET5;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NREL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects.";
RL Patent number US5322687, 21-JUN-1994.
CC -!- FUNCTION: Promotes colloidotomic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L32020; AAA23344.1; -
CC HSSP; P02965; 1CIY.
CC InterPro; IPR001178; Endotoxin.

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OC InterPro; IPR005638; endotoxin\_C.  
OX InterPro; IPR005639; endotoxin\_N.  
RN InterPro; IPR008979; Gal bind like.  
RP Pfam; PF03944; Endotoxin\_C; 1.  
RA Pfam; PF00555; Endotoxin\_M; 1.  
RT Pfam; PF03945; Endotoxin\_N; 1.  
CC Sporulation; Toxin.  
CC SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;  
Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
Best Local Similarity 65.3%; Pred. No. 2e-160;  
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;  
QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLKSEYENVEPVSASTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVNNDPFSASTVQTGINIAGRI 66  
QY 71 LGTLGVPPAGQVASYLSPILGELWPKGNQWELFMEHVEE-INQKISTYARNKALTDLK 129  
DB 67 LGVLGVPPAGQLASFYSLVGLWPSGRDPWEI-FLEHVEQLIRQQVTENTRTAARLE 125  
QY 130 GLGDALAVYHDSLESWVGNNRTRARVRSQYIALELMFVQKLPFAVSGEEVPLLPY 189  
DB 126 GLGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVY 185  
QY 190 AQANLHLLLRDASIFGKESGLSSSEISTFYNNRQVRAGDYSDHCVKWKYSTGLNNLRGT 249  
DB 186 AQANLHLLLRDASLFGSEWGMASDVNQYQEIRYTEYSNHCYQWYNTGLNNLRGT 245  
QY 250 NAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTTAQLTRVYTDALGTVHPHPSF 309  
DB 246 NAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTTAQLTRVYTDALGTVHPHPSF 305  
QY 310 TSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHKLFRFT 369  
DB 306 ASTNWFNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHKLFRFT 365  
QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLOPVGNGVPRVDFHWKFV 428  
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLOPVGNGVPRVDFHWKFV 422  
QY 429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA 481  
DB 423 ---INPQNIYERGATTSYQYQGVIGLFDSETELPPETTERPNYESYSHRLSHIGLIG 479  
QY 482 SHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541

DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Sporulation; Toxin.  
SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;  
Query Match 64.3%; Score 2417.5; DB 1; Length 1229;  
Best Local Similarity 65.3%; Pred. No. 2e-160;  
Matches 469; Conservative 90; Mismatches 140; Indels 19; Gaps 8;  
QY 13 SSNAKVDKISTSLKN-ETDIELQ-NINHEDECLKSEYENVEPVSASTIQTGIGIAGKI 70  
DB 7 NENEIINALSIPTVSNPSTQNLSPDARIEDSLCAEVNNDPFSASTVQTGINIAGRI 66  
QY 71 LGTLGVPPAGQVASYLSPILGELWPKGNQWELFMEHVEE-INQKISTYARNKALTDLK 129  
DB 67 LGVLGVPPAGQLASFYSLVGLWPSGRDPWEI-FLEHVEQLIRQQVTENTRTAARLE 125  
QY 130 GLGDALAVYHDSLESWVGNNRTRARVRSQYIALELMFVQKLPFAVSGEEVPLLPY 189  
DB 126 GLGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLMVY 185  
QY 190 AQANLHLLLRDASIFGKESGLSSSEISTFYNNRQVRAGDYSDHCVKWKYSTGLNNLRGT 249  
DB 186 AQANLHLLLRDASLFGSEWGMASDVNQYQEIRYTEYSNHCYQWYNTGLNNLRGT 245  
QY 250 NAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTTAQLTRVYTDALGTVHPHPSF 309  
DB 246 NAESWVRYNQFRDMLVLDLVALFSPYDTQMPYIKTTAQLTRVYTDALGTVHPHPSF 305  
QY 310 TSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHKLFRFT 369  
DB 306 ASTNWFNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHKLFRFT 365  
QY 370 IGGTLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLOPVGNGVPRVDFHWKFV 428  
DB 366 IGGTLNISTQGST-NTSINPVTLPFTSRDVRVYTESLAGNLFLOPVGNGVPRVDFHWKFV 422  
QY 429 THPIASDNFYYPG-----YAGIGTQLQDSENELPPEATGQPNYESYSHRLSHIGLISA 481  
DB 423 ---INPQNIYERGATTSYQYQGVIGLFDSETELPPETTERPNYESYSHRLSHIGLIG 479  
QY 482 SHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 541  
DB 480 NTLRAPVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNT 539  
QY 542 GTFGDIRNINPFAQVRVIRYASTTDLOPHTSINGKALNQGNFSAATMNRGSDLDYKT 601  
DB 540 GTFGDIRNINPFAQVRVIRYASTTDLOPHTSINGKALNQGNFSAATMNRGSDLDYKT 599  
QY 602 FRTVGFSTPFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQKVT 661  
DB 600 FRTAGFSTPFLDVQSTFTIGAWNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQKVT 658  
QY 662 ALFTSTNPRGLTKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 719  
DB 659 ALFTSTNPRGLTKTDVYHIDQVSNLVESLSEDFYLDKRELFEIVKYANLHIERNM 716  
RESULT 13  
CIBC BACTM STANDARD; PRT; 1233 AA.  
ID C1BC BACTM  
AC Q45774;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryIbC (Insecticidal delta-endotoxin  
DE CryIb(c) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
GN Name=cryIbC; Synonyms=cryIb(c), cryIbC;  
OS Bacillus thuringiensis (subsp. morrisoni).

D6	299	ASMNWYNNAPSFSAIEAAAIIRSPHLLDFLEQLTIFPSASSWSNTRHMTYVRGHTTIQSRP	358
QY	370	IGGTLNISTQGSTNTSINPVLTPTTSRSDVYRTESLAGLNLF--LTOPVNGVPRVDPHKF	427
D6	359	IGGGLNSTHGATNTSINPVLTFRFASRDVYRTESYAGVLLWGVIYLPPIHGVTYRFNF--	416
QY	428	VTHP-----IASDNFYPGYAGIGTQLODSNELPEATGCPNYEYSYSHRLSHIGHISAS	482
D6	417	-TNPNQISDRGTANYSQP-YESPGLQKDSLETPLPETTERPNYESYSHRLSHIGHILOS	474
QY	483	HVKALIVSWTHRSADRTNIIPNSITQIPLVKAFNLSSGAAVRWGPFTGGDILRRNTG	542
D6	475	RVMVPVSWTHRSADRTNITGNRIITQIPMVKASELPQGTTVRVGPFTGGDILRRNTG	534
QY	543	TFGDIRVINPPFAQRVRYRYASTTDLQFHTSINGKAINGCNFSATMNRGEDLDYKTF	602
D6	535	GFGPIRVTVNGPLTQRYRIGFPYASTVDFDFVSRGTTVNFRFLRTMNSGDELKYGNF	594
QY	603	RTVGFTTPFSFDVQSTFTIGAWNFSGNEVIYIDRIEFVPEVETVYBAEDYPEKAQEKVTA	662
D6	595	VRAFTPTFTTQIQDIIRTISQIGLSGGEVYIDKTEIIPVATFEAEYDLERAQEAUNA	654
QY	663	LFTSTNPRGLTKDVKDHYHDIOVSNLVESLSDEFYLDEKRELFEIVKYANELHIERNM	719
D6	655	LFTNTNPRRLKTDTVTDYHDIOVSNLVACLSDEFCLDEKRELLKVKYAKRLSDERNL	711

RESULT 15

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C1BA_BACTK          STANDARD;             PRT;   1228 AA.
AC    P05517; Q45731;
DT    01-NOV-1988 (Rel. 09, Created)
DT    01-FEB-1996 (Rel. 33, Last sequence update)
DT    05-JUL-2004 (Rel. 44, Last annotation update)
DE    Pesticidial crystal protein crylBa (Insecticidal delta-endotoxin
DE    CryIB(a)) (Crystalline entomocidical protoxin) (140 kDa crystal protein).
GN    Names=crylBa; Synonyms=cryIB(a), cryA4;
OS    Bacillus thuringiensis (subsp. kurstaki), and
OS    Bacillus thuringiensis (subsp. entomocidus).
OC    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX    NCBI_TaxID=29339, 1436;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    SPECIES=B.t.kurstaki; STRAIN=HD-2;
RX    MEDLINE=88203216; PubMed=3362680;
RA    Brizzard B.L., Whiteley H.R.;
RT    "Nucleotide sequence of an additional crystal protein gene cloned from
RT    Bacillus thuringiensis subsp. thuringiensis.",
RL    Nucleic Acids Res. 16:2723-2723(1988).
RN    [2]
RP    SEQUENCE FROM N.A.
RC    SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA    Soetaert P.;
RL    Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC    -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut
CC    epithelial cells of insects.
CC    -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC    sporulation and is accumulated both as an inclusion and as part of
CC    the spore coat.
CC    -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC    terminus.
CC    -!- SIMILARITY: Belongs to the delta endotoxin family.
CC    -----
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC    or send an email to license@isb-sib.ch).
CC    -----
DR    EMBL; X06711; CAA29898.1; -.
DR    EMBL; X95704; CAA65003.1; -.

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Search completed: October 28, 2004, 18:30:09  
Job time : 105.579 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-58

Perfect score: 3761  
Sequence: 1 MKLKNQDKHQSFSSNAKVDK.....KRELFVIVKANELHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3724	99.0	719	17	US-10-782-020-10
2	3724	99.0	719	17	US-10-782-141-8
3	3724	99.0	719	17	US-10-782-096-10
4	3724	99.0	719	17	US-10-782-570-7
5	3442.5	91.5	710	14	US-10-428-961-42
6	2250.5	59.8	1228	16	US-10-809-953-10
7	2236.5	59.5	1207	10	US-09-988-462-7
8	2157.5	57.4	1227	14	US-10-428-961-63
9	2142.5	57.0	1186	9	US-09-826-660-23
10	2087	55.5	1228	14	US-10-428-961-38
11	2087	55.5	1228	15	US-10-614-524-2
12	1909.5	50.8	643	9	US-09-826-660-25
13	1694.5	45.1	1167	14	US-10-089-678-1

14	1658.5	44.1	653	14	US-10-428-961-6	Sequence 6, Appli
15	1643.5	43.7	1157	17	US-10-782-141-16	Sequence 16, Appl
16	1643.5	43.7	1157	17	US-10-782-096-17	Sequence 17, Appl
17	1643.5	43.7	1157	17	US-10-782-570-13	Sequence 13, Appl
18	1485	39.5	1206	13	US-10-032-717-2	Sequence 2, Appli
19	1485	39.5	1206	14	US-10-414-637-2	Sequence 2, Appli
20	1485	39.5	1206	15	US-10-606-320-2	Sequence 2, Appli
21	1485	39.5	1206	17	US-10-746-914-2	Sequence 2, Appli
22	1469	39.1	1210	13	US-10-032-717-4	Sequence 4, Appli
23	1469	39.1	1210	14	US-10-414-637-4	Sequence 4, Appli
24	1469	39.1	1210	15	US-10-606-320-4	Sequence 4, Appli
25	1469	39.1	1210	17	US-10-746-914-4	Sequence 4, Appli
26	1459.5	38.8	1156	14	US-10-099-285-72	Sequence 28, Appl
27	1459.5	38.8	1156	14	US-10-428-961-28	Sequence 72, Appl
28	1443	38.4	1155	9	US-09-756-643-2	Sequence 2, Appli
29	1443	38.4	1155	10	US-09-988-462-9	Sequence 9, Appli
30	1443	38.4	1155	14	US-10-136-998A-2	Sequence 2, Appli
31	1443	38.4	1177	14	US-10-035-060-6	Sequence 6, Appli
32	1443	38.4	1181	10	US-09-988-462-11	Sequence 11, Appl
33	1443	38.4	1181	10	US-09-988-462-13	Sequence 13, Appl
34	1443	38.4	1181	10	US-09-988-462-15	Sequence 15, Appl
35	1443	38.4	1181	10	US-09-988-462-17	Sequence 17, Appl
36	1443	38.4	1181	10	US-09-988-462-28	Sequence 28, Appl
37	1443	38.4	1181	14	US-10-136-998A-4	Sequence 4, Appli
38	1443	38.4	1181	14	US-10-136-998A-8	Sequence 8, Appli
39	1443	38.4	1181	14	US-10-136-998A-10	Sequence 10, Appl
40	1443	38.4	1181	14	US-10-136-998A-12	Sequence 12, Appl
41	1438	38.2	1177	14	US-10-035-060-2	Sequence 2, Appli
42	1436	38.2	1177	14	US-10-035-060-8	Sequence 8, Appli
43	1435	38.2	1177	14	US-10-102-469-24	Sequence 24, Appl
44	1419.5	37.7	1176	17	US-10-782-141-6	Sequence 6, Appli
45	1419.5	37.7	1176	17	US-10-782-096-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and Methods for Its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 99.0%; Score 3724; DB 17; Length 719;  
Best Local Similarity 99.3%; Pred. No. 1e-305;  
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

Qy	1	MKLKNQDKHQSFSSNAKVDKISTDSLSKNETDIELQINHEDCLKMSEYENVPFVSASTI	60
Db	1	MKLKNQDKHQSFSSNAKVDKISTDSLSKNETDIELQINHEDCLKMSEYENVPFVSASTI	60
Qy	61	QTGIGIAGKILGTLGVPPFAGQVASYLSFTLGLWPKGNQWEILFMEHVEE-INQKISTY	119
Db	61	QTGIGIAGKILGTLGVPPFAGQVASYLSFTLGLWPKGNQWEILFMEHVEE-INQKISTY	119

QY 120 ARNKALTDLGLDALAVYHDSLESWGNNRNNTRARSVVRQYIALELMFVQKLPSPFAVS 179  
 DB 120 ARNKALTDLGLDALAVYHDSLESWGNNRNNTRARSVVRQYIALELMFVQKLPSPFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSISSTFYNNRQVERAGDYSDHCVKWY 239  
 DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSISSTFYNNRQVERAGDYSDHCVKWY 239  
 QY 240 STGLNLRGTNAESWVRVYNNQFRDMLMVLVDFVPSYDTQMPYIKTTAQLTREYVYTD 299  
 DB 240 STGLNLRGTNAESWVRVYNNQFRDMLMVLVDFVPSYDTQMPYIKTTAQLTREYVYTD 299  
 QY 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN 359  
 DB 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN 359  
 QY 360 WGGHKLFEFTIGTINISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTOPVNGVP 419  
 DB 360 WGGHKLFEFTIGTINISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTOPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 DB 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDL 599  
 DB 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDL 599  
 QY 600 KTFRTVGTFTPFSLDVOSTFTIGAMNFSNGNEVYIDRIEVPVETYEAEYDPEKAQEK 659  
 DB 600 KTFRTVGTFTPFSLDVOSTFTIGAMNFSNGNEVYIDRIEVPVETYEAEYDPEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 2

US-10-782-141-8  
 ; Sequence 8, Application US/10782141  
 ; Publication No. US20040197917A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Kozziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
 ; FILE REFERENCE: 045600/274143  
 ; CURRENT APPLICATION NUMBER: US/10782,141  
 ; CURRENT FILING DATE: 2004-02-20  
 ; PRIOR APPLICATION NUMBER: 60/448,632  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-141-8

Query Match 99.0%; Score 3724; DB 17; Length 719;  
 Best Local Similarity 99.3%; Pred. No. 1e-305;  
 Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINNHEDCLKXSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKIIGTLGVFPAGQVAVSLYSFILGELWPKGNQWEIFLMEHVEE-INOXISTY 119  
 DB 61 QTGIGIAGKIIGTLGVFPAGQVAVSLYSFILGELWPKGNQWEIFLMEHVEEINOXISTY 119  
 QY 120 ARNKALTDLGLDALAVYHDSLESWGNNRNNTRARSVVRQYIALELMFVQKLPSPFAVS 179  
 DB 120 ARNKALTDLGLDALAVYHDSLESWGNNRNNTRARSVVRQYIALELMFVQKLPSPFAVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSISSTFYNNRQVERAGDYSDHCVKWY 239  
 DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSISSTFYNNRQVERAGDYSDHCVKWY 239  
 QY 240 STGLNLRGTNAESWVRVYNNQFRDMLMVLVDFVPSYDTQMPYIKTTAQLTREYVYTD 299  
 DB 240 STGLNLRGTNAESWVRVYNNQFRDMLMVLVDFVPSYDTQMPYIKTTAQLTREYVYTD 299  
 QY 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN 359  
 DB 300 IGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLSRWSNTQYMMN 359  
 QY 360 WGGHKLFEFTIGTINISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTOPVNGVP 419  
 DB 360 WGGHKLFEFTIGTINISTQGSTNTSINPVTLPFTSRDVRATESLAGLNFLTOPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 DB 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDL 599  
 DB 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGDL 599  
 QY 600 KTFRTVGTFTPFSLDVOSTFTIGAMNFSNGNEVYIDRIEVPVETYEAEYDPEKAQEK 659  
 DB 600 KTFRTVGTFTPFSLDVOSTFTIGAMNFSNGNEVYIDRIEVPVETYEAEYDPEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 3

US-10-782-096-10  
 ; Sequence 10, Application US/10782096  
 ; Publication No. US20040210964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Kozziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-009, A Delta-Endotoxin Gene and  
 ; FILE REFERENCE: 045600/274148  
 ; CURRENT APPLICATION NUMBER: US/10782,096  
 ; CURRENT FILING DATE: 2004-02-19  
 ; PRIOR APPLICATION NUMBER: 60/448,633  
 ; PRIOR FILING DATE: 2003-02-20  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-782-096-10

Query Match 99.0%; Score 3724; DB 17; Length 719;

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Best Local Similarity 99.3%; Pred. No. 1e-305;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSEYENVEPFVSASTI 60
Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEILFMEHVTEE-INQKISTY 119
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEILFMEHVTEE-INQKISTY 119
QY 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPFAVS 179
Db 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239
QY 240 STGLNNLRGTNAESWVRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299
Db 240 STGLNNLRGTNAESWVRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299
QY 300 IGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYMMN 359
Db 300 IGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYMMN 359
QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVP 419
Db 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVP 419
QY 420 RVDPHWKVTHPIASDNFYYPGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLI 479
Db 420 RVDPHWKVTHPIASDNFYYPGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDY 599
QY 600 KTRFTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEK 659
Db 600 KTRFTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

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RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; Methods for Its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719

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TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 99.0%; Score 3724; DB 17; Length 719;
Best Local Similarity 99.3%; Pred. No. 1e-305;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSEYENVEPFVSASTI 60
Db 1 MCLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQINHHEDCLKMSEYENVEPFVSASTI 60
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEILFMEHVTEE-INQKISTY 119
Db 61 QTGIGIAGKILGTGVPFAGQVASYLSPILGELWPKGNQWEILFMEHVTEE-INQKISTY 119
QY 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPFAVS 179
Db 120 ARNKALTDLKGGLDALAVYHDSLESVGNRNTRARSVRSQYIALELMFVQKLPFAVS 179
QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239
QY 240 STGLNNLRGTNAESWVRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299
Db 240 STGLNNLRGTNAESWVRYNQFRDMLMVLDLVALPSPYDTQMPYIKTTAQLTREYVYDA 299
QY 300 IGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYMMN 359
Db 300 IGVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSTQYMMN 359
QY 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVP 419
Db 360 WGGHKLFPRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTQPVNGVP 419
QY 420 RVDPHWKVTHPIASDNFYYPGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLI 479
Db 420 RVDPHWKVTHPIASDNFYYPGYAGIGTQDSENELPPEATGPQNYESYSHRLSHIGLI 479
QY 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
Db 480 SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDY 599
Db 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDY 599
QY 600 KTRFTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEK 659
Db 600 KTRFTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEK 659
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

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RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupa, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

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; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 42

; LENGTH: 710  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis

; FEATURE:  
 ; NAME/KEY: misc feature

; LOCATION: (200)..(200)

; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid

US-10-428-961-42

Query Match 91.5%; Score 3442.5; DB 14; Length 710;  
 Best Local Similarity 91.9%; Pred. No. 6.7e-282;  
 Matches 662; Conservative 16; Mismatches 31; Indels 11; Gaps 3;

Qy 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLMSEYENVEPFFVSASTI 60  
 Db 1 MKSKNQVTHQSLSNNAATVDKFTGSLNNTNTELQNFH-----EGIEPFFVSASTI 51

Qy 61 QTGIGIAGKILGTLPVFPAGQVASYLSPILGELWPKGNOWEILFMEHVEE-INOKISTY 119  
 Db 52 QTGIGIAGKILGNLGVFPAGQVASYLSPILGELWPKGQWEI-FMEHVEELINQKISTY 110

Qy 120 ARNKALTDLKLGLDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPSPAVS 179  
 Db 111 ARNKALADLKLGLDALAVYHDSLESWGNRNTRARSVRSQYITLELMFVQKLPSPAVS 170

Qy 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 Db 171 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 230

Qy 240 STGLNLRGTAESWVRNQFRDMLTMVLVALPSPYDTQMYPIKTTAQLTREVTDA 299  
 Db 231 NTGLNRLMGNAESWVRNQFRDMLTMVLVALPSPYDTQMYPIKTTAQLTREVTDA 290

Qy 300 IGVHPHPGFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMM 359  
 Db 291 IGVHPHPGFTSTTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMM 350

Qy 360 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVP 419  
 Db 351 WGGHKLERTIGTGLNISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVP 410

Qy 420 RVDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 479  
 Db 411 RVDFHWKFTVTHPIASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLI 470

Qy 480 SASHVKALVYSWTHRSADRTNTEPNSTIQTPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
 Db 471 SASHVKALVYSWTHRSADRTNTEPNSTIQTPLVKAFNLSSGAAVVRGPGFTGGDILRRT 530

Qy 540 NTGTFGDIRVNIPLPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDY 599  
 Db 531 NTGTFGDIRVNIPLPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDY 590

Qy 600 KTRFTVGFTTFFSDFDQSTFTIGAMNFSNGEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
 Db 591 KTRFTVGFTTFFSDFDQSTFTIGAMNFSNGEVYIDRIEFVPEVTEAEYDPEKAQEK 650

Qy 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 651 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 710

RESULT 6  
 US-10-809-953-10  
 ; Sequence 10, Application US/10809953  
 ; Publication No. US2004018125A1  
 ; GENERAL INFORMATION:

; APPLICANT: Van Mellaert, Herman  
 ; APPLICANT: Botterman, Johan  
 ; APPLICANT: Van Rie, Jeroen  
 ; APPLICANT: Joos, Henk  
 ; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bc INSECTIC  
 ; TITLE OF INVENTION: CRYSTAL PROTEINS  
 ; FILE REFERENCE: 021565-078  
 ; CURRENT APPLICATION NUMBER: US/10/809,953  
 ; CURRENT FILING DATE: 2004-03-26  
 ; PRIOR APPLICATION NUMBER: US/09/661,016  
 ; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/EP90/00905  
 ; PRIOR FILING DATE: 1990-05-30  
 ; PRIOR APPLICATION NUMBER: GB 89401499.2  
 ; PRIOR FILING DATE: 1989-05-31  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-809-953-10

Query Match 59.8%; Score 2250.5; DB 16; Length 1228;  
 Best Local Similarity 62.5%; Pred. No. 1.1e-180;  
 Matches 448; Conservative 78; Mismatches 164; Indels 27; Gaps 8;

Qy 23 TDSLKNETDIELQNH-----EDCLKMSEYENVEPFFVSASTIQTGIGIAGKI 70  
 Db 2 TSNKRNENEINAVSNHSAQMOLLDPADIEDSLCIAEGNIDPFFVSASTVQTGINIAGRI 61

Qy 71 LGTLGVFPAGQVASYLSPILGELWPKGNOWEILFMEHVEE-INOKISTYARNKALTDLK 129  
 Db 62 LGVLGVFPAGQVASYLSPILGELWPKGRDQWEI-FLEHVEQLINQOITENARNTALRLQ 120

Qy 130 GLGDALAVYHDSLESWGNRNTRARSVRSQYIALELMFVQKLPSPAVSGEEVPLPIY 189  
 Db 121 GLGDSFRAVQOSLEDWLENRDDRARSVLHTQYIALELDLFLNAMPPLFAIRNQEVLLMVY 180

Qy 190 AQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWYSTGLNLRGT 249  
 Db 181 AQAANLHLLLRDASIFGSEFGLTSQIORYYERQVETRTDYSDYCVIEWNTGLNLRGT 240

Qy 250 NAESWVRYNQFRDMLTMVLVALPSPYDTQMYPIKTTAQLTREVTDAIGTVHPHPSF 309  
 Db 241 NAESWVRYNQFRDMLTMVLVALPSPYDTQMYPIKTTAQLTREVTDAIGAT--GVNM 298

Qy 310 TSTTWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMMWGGHKLERT 369  
 Db 299 ASMWYNNAPSAIEAAVVRNPHLLDFLEQVITYSLSRWSNTQYMMWGGHKLERT 358

Qy 370 IGGTINISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVPDFHWK 427  
 Db 359 IGGTINISTQGSTNTSINPVTLPFTSRDVRATESLAGLNLFLTOPVNGVPDFHWK 416

Qy 428 VTHP-----IASDNFYPGYAGIGTQLODSENELPPEATQPNYESYSHRLSHIGLISAS 482  
 Db 417 -TNPQNISDRGTANYSQP-YESPGLQKDSLETLPPTETTERPNYESYSHRLSHIGLISAS 474

Qy 483 HVKALVYSWTHRSADRTNTEPNSTIQTPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 542  
 Db 475 RVNVPVYSWTHRSADRTNTEPNSTIQTPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTG 534

Qy 543 TFGDIRVNIPLPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTF 602  
 Db 535 GFGDIRVNIPLPPFAQRYVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTF 594

Qy 603 RTVGFTTFFSDFDQSTFTIGAMNFSNGEVYIDRIEFVPEVTEAEYDPEKAQEKVTA 662  
 Db 595 VRRFTTFFSDFDQSTFTIGAMNFSNGEVYIDRIEFVPEVTEAEYDPEKAQEKVTA 654

Qy 663 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 Db 651 LFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 710

Db 655 LFTNTPRLKTDVTDYHIDQVSNLVACLSDFFCLDEKRELLKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7

Sequence 7, Application US/09988462

Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Weigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1207 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 59.5%; Score 2236.5; DB 10; Length 1207;

Best Local Similarity 64.1%; Pred. No. 1.6e-179;

Matches 44; Conservative 76; Mismatches 156; Indels 15; Gaps 7;

Qy 40 EDCLKMSEYNEVPFVASTIQTGIGIAGKILGTGLGVFFAGOVASLYSFIILGELWPKGN 99

Db 10 EDLSLCAEGNNIDPFVASTVQTGINAGRIILGVLFVFFAGQLASYSFLVGLWPRGRD 69

Qy 100 QWEILFMEHVEE-INQKISTYARNKALTDLKLGDALAVYHDSLESWVGNNRNTFRASV 158

Db 70 QWEI-FLEHVEQLINQQTENARNTALRQLGLGDSFRAYQOQSLEDWLENRDARTSVL 128

Qy 159 RSQYIALELMFVQKLPSFAVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEIS 218

Db 129 YTYIALELDFLNLAMPLFAIRNQEVPLLMVYIAQAANLHLLLRDASLFGSFGLTQEIQ 188

Qy 219 TFYNRQVERAGDYSCHVKWYSTGLNLRGTTNAESWRYNQRRDMLMVLDLVALFPYS 278

Db 189 RYERQVERTRDYSYCVWEYNTGLNSURGTNAASWRYNQRRDMLTGLVLDLVALFPYS 248

Qy 279 DTQYPIKTTAQLTREVYTDAGITVHPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLDF 338

Db 249 DTRTYPINTSAQLTREVYTDAGIT--GVNMAWMNNAPSFSAIEAAIRSPHLLDF 306

Qy 339 LEQVTIYLSRWSTQYNNMGGHKLBFRTTGGTLNISTQSTNTSINPVTLPTFSRDV 398

Db 307 LEQLTIFSASSRWSTNTRHMTYWRGHTIOSRPIGGGLNTSTHGATNTSINPVTLRFASRDV 366

Qy 399 YRTESLAGLNLF--LTQPVNGVPRVDFHMKFVTHP-----IASDNFYYPGYAGIGTQLQD 451

Db 367 YRTESYAGVLLMGYILEPIHGVPVRFNF---TNPNISDRGTANYSQP-YESPGQLQKD 422

Qy 452 SENELPPEATGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTEPNSITQIP 511

Db 423 SETELFPETTERPNYESYSHRLSHIGIILQSRVNVVYSWTHRSADRTNIGPNRITQIP 482

Qy 512 LVKAFNLSSGAAYVRGPGTGGDILRRNTGTGDIIRVNINPPFAQRYVRIRYASTDL 571

Db 483 MVKASELPQGTTVVRGPGTGGDILRRNTGTGFGPIRVTVNGFLTQYRIGRPRYASTVDF 542

Qy 572 QFHTSINGKAINQGNFSATWNGEDLDYKTRFVGTTPFPFLDVQSTFTTICAWNFSNGN 631

Db 543 DFFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRATFTTFTQIQDIIRTSIQGLSGNG 602

Qy 632 EYIDRIEFVPEVETYEAEYDFEKAQEKVYALTSTNPRGLKTDVXDYHIDQVSNLVESL 691

Db 603 EYIDKIEIIPVTATFEAEYDLERAQEAVALTNTNPRRLKTDVTDYHIDQVSNLVACL 662

Qy 692 SDEFYLDKRELFELVKYANELHIERNM 719

Db 663 SDEFCLDEKRELLKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63

Sequence 63, Application US/10428961

Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Chu, Chih-Rei

APPLICANT: Donovan, William P.

APPLICANT: Gilmer, Amy J.

APPLICANT: Rupal, Mark J.

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECO201--1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT FILING DATE: 2003-05-02

PRIOR APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patent in version 3.2

SEQ ID NO 63

LENGTH: 1227

TYPE: PRT

ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 57.4%; Score 2157.5; DB 14; Length 1227;

Best Local Similarity 59.0%; Pred. No. 7.8e-173;

Matches 422; Conservative 103; Mismatches 175; Indels 15; Gaps 5;

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QY 13 SSNAKVDKISTDSLKN-----ETDIELQNIHEDCLKMSVENVEPFVSASTIQTIG 65
Db 7 NENEIINALSIPAVSNHSAQNLSTDAI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61

QY 66 IAGKILGTLGVPPFAGQVASYIFLIGELWPKGNQWELFMEHVEE-INQKISTYARNKA 124
Db 62 IAGRILGVLGVPPFAGQIASFYSLVGLWPRGRDPWEI-FLEHVEQLRQQVTENTRDTA 120

QY 125 LTDLKGDLALAVYHDSLSWVGNRNTRARSVRSQYIALELMFVQKLPFAVSGEEVP 184
Db 121 LARLOGLGNSFRAYQOQSLDWLENRDARTSVLYTQYIALELDFLNAMPLFAIRNQEV 180

QY 185 LLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKWTSTGLN 244
Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQETQRYVERQVETREYSDYCARWNTGLN 240

QY 245 NLRGTNAESWVRYNQFRRLDMLVLDLVALFPSTYDQVPIKTTAQLTREYVTDIGTVH 304
Db 241 NLRGTNAESWVRYNQFRRLDMLVLDLVALFPSTYDQVPIKTTAQLTREYVTDIGTVH 300

QY 305 PHPSFTTWNNAAPSFAIEAAVVRPHLLDFLEQVITYLSLLSRWSNTQYMMNMGCHK 364
Db 301 APSGFASNTWNNAPSFSAIEAAVVRPHLLDFLEQVITYLSLLSRWSNTQYMMNMGCHK 360

QY 365 LEFRITGTLNISTOGSTNTSINPVTLPSTSDVRYTESLAGNLFLTPVNGVPRVDFH 424
Db 361 LESRTIRGSLSTWTHGNTNTSINPVTLPSTSDVRYTESLAGNLFLTPVNGVPRVDFH 420

QY 425 WKFTVTHPIASDNFYYPGYAGIGTQLODSENEPPEATQPNYESYSHRLSHIGLISASHV 484
Db 421 WRNPLNSLRGSLLYTIGYTGVTGQVLTQPLVKSFNLSNSTSVSGPGTGGDIIRTNVGSV 480

QY 545 GDIRVNINPPFAQRYRIRYASTDLQFHTSINGKAINQGNFSAATMNRGDLDTYKTFRT 604
Db 541 LSMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTDOGFPTMSANESLTSQSFRF 600

QY 605 VGFTTFFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTLF 664
Db 601 AEFPGVIGSAGSQ-TAGISISNNAAGRTQFTHFDKIEFTPTATFEAYDLERAQAVNALF 659

QY 665 TSTNPRGLKTDVKDHYDIDOVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 TSTNPRGLKTDVKDHYDIDOVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 714

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RESULT 9

```

US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

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Query Match 57.0%; Score 2142.5; DB 9; Length 1186;
Best Local Similarity 58.7%; Pred. No. 1.4e-171;
Matches 420; Conservative 106; Mismatches 174; Indels 15; Gaps 5;

QY 13 SSNAKVDKISTDSLKN-----ETDIELQNIHEDCLKMSVENVEPFVSASTIQTIG 65
Db 7 NENEIINALSIPAVSNHSAQNLSTDAI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61

QY 66 IAGKILGTLGVPPFAGQVASYIFLIGELWPKGNQWELFMEHVEE-INQKISTYARNKA 124
Db 62 IAGRILGVLGVPPFAGQIASFYSLVGLWPRGRDPWEI-FLEHVEQLRQQVTENTRDTA 120

QY 125 LTDLKGDLALAVYHDSLSWVGNRNTRARSVRSQYIALELMFVQKLPFAVSGEEVP 184
Db 121 LARLOGLGNSFRAYQOQSLDWLENRDARTSVLYTQYIALELDFLNAMPLFAIRNQEV 180

QY 185 LLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKWTSTGLN 244
Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQETQRYVERQVETREYSDYCARWNTGLN 240

QY 245 NLRGTNAESWVRYNQFRRLDMLVLDLVALFPSTYDQVPIKTTAQLTREYVTDIGTVH 304
Db 241 NLRGTNAESWVRYNQFRRLDMLVLDLVALFPSTYDQVPIKTTAQLTREYVTDIGTVH 300

QY 305 PHPSFTTWNNAAPSFAIEAAVVRPHLLDFLEQVITYLSLLSRWSNTQYMMNMGCHK 364
Db 301 APSGFASNTWNNAPSFSAIEAAVVRPHLLDFLEQVITYLSLLSRWSNTQYMMNMGCHK 360

QY 365 LEFRITGTLNISTOGSTNTSINPVTLPSTSDVRYTESLAGNLFLTPVNGVPRVDFH 424
Db 361 LESRTIRGSLSTWTHGNTNTSINPVTLPSTSDVRYTESLAGNLFLTPVNGVPRVDFH 420

QY 425 WKFTVTHPIASDNFYYPGYAGIGTQLODSENEPPEATQPNYESYSHRLSHIGLISASHV 484
Db 421 WRNPLNSLRGSLLYTIGYTGVTGQVLTQPLVKSFNLSNSTSVSGPGTGGDIIRTNVGSV 480

QY 545 GDIRVNINPPFAQRYRIRYASTDLQFHTSINGKAINQGNFSAATMNRGDLDTYKTFRT 604
Db 541 LSMGLNFNTSLQRYRVRVRYAASQTMVLRTVVGSTTDOGFPTMSANESLTSQSFRF 600

QY 605 VGFTTFFSLDVQSTFTTICAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTLF 664
Db 601 AEFPGVIGSAGSQ-TAGISISNNAAGRTQFTHFDKIEFTPTATFEAYDLERAQAVNALF 659

QY 665 TSTNPRGLKTDVKDHYDIDOVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719
Db 660 TSTNPRGLKTDVKDHYDIDOVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 714

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RESULT 10

```

US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MEC0201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

```



; Sequence 25, Application US/09826660  
 ; Patent No. US20010026940A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cardineau, Guy A.  
 ; APPLICANT: Stelman, Steven J.  
 ; APPLICANT: Narva, Kenneth E.  
 ; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
 ; FILE REFERENCE: MA-714XC2D1  
 ; CURRENT APPLICATION NUMBER: US/09/826,660  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 09/178,252  
 ; PRIOR FILING DATE: 1998-10-23  
 ; PRIOR APPLICATION NUMBER: 60/065,215  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/076,445  
 ; PRIOR FILING DATE: 1998-03-02  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 25  
 ; LENGTH: 643  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
 US-09-826-660-25

Query Match 50.8%; Score 1909.5; DB 9; Length 643;  
 Best Local Similarity 57.6%; Pred. No. 2.7e-152;  
 Matches 371; Conservative 99; Mismatches 159; Indels 15; Gaps 5;  
 QY 13 SSNAKVDKSTDSLN-----ETDIQLQINHNHEDCLKMSYENVPFVSASTIQTG 65  
 Db 7 NENEIINALSIPVSNHSAQNLSTDARI-----EDSLCIAEGNNIDPFVSASTVQTGIN 61  
 QY 66 IAGKILGTIGVPPAGQVASYLSFILGELMPKGNQWEILFNEHVEB-INQKISTYARNKA 124  
 Db 62 IAGRILGLVLPVPPAGQIASFYSPFLVGLWPRGRDPWEI-FLEHVEQLIRQVTTNTRDTA 120  
 QY 125 LTDLXGLDALAVYHDSLESWGNRNNTARSVVRQYIALELMFVKLPSPFVSGEVP 184  
 Db 121 LARLOGLGNSFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDFNAMFLFAIRNQEV 180  
 QY 185 LLPIYAQAANLHLLLRDASIFGKESWGLSSSEISTPYNQVERAGDYSDHCVKMYSTGLN 244  
 Db 181 LLMVYAQAANLHLLLRDASLFGSEFGLTSQIRYQYERQVEKREYSYDCARWNTGLN 240  
 QY 245 NLRGTAESWVRNQFRDMLMVLVLPSPSYDTQMPYIKTTAQLTREVTDAIGTVH 304  
 Db 241 NLRGTAESWVRNQFRDMLMVLVLPSPSYDTQMPYIKTTAQLTREVTDAIGTVH 300  
 QY 305 PHPSFTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHK 364  
 Db 301 APSGFSTWNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMNWGGHK 360  
 QY 365 LEFRIGGLTINISQGSNTSINPVLPTSDVYTESLAGNLFLTPQVNGVPRVDPH 424  
 Db 361 LESRTIRGLSTSGHNTSINPVLPTSDVYTESLAGNLFLTPQVNGVPRVDPH 420  
 QY 425 WKFTVTHPIASDNFYPGVAGIGTQLODSENELPPEATGPQNYESYSHRLSHIGLISASHV 484  
 Db 421 WRNPLNSRGLLYTIGYGVGTQLODSENELPPEATGPQNYESYSHRLSHIGLISASHV 480  
 QY 485 KALVYSWTHRSADTNTIEPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDILRNTGTTF 544  
 Db 481 RAPVYSWTHRSADTNTIEPNSITQIPLVKAFNLSSGAADVVRGPGFTGGDILRNTGTTF 540  
 QY 545 GDIRVNINPPFAQRVRYRISTTDIQFHTSINGKAINQGNFSAATMRGEDLDYKTRT 604  
 Db 541 LSMGLNFNTSLQYRVRYRISTTDIQFHTSINGKAINQGNFSAATMRGEDLDYKTRT 600  
 QY 605 VGFTTFFSLDVOSTFTTCANWFFSGNEVYIDRIEFVPEVITYE 648  
 Db 601 AEFVPGISAGSQ--TAGISISNAGROTTFHDKIEFIPITATLE 643

RESULT 13  
 US-10-089-678-1  
 ; Sequence 1, Application US/10089678  
 ; Publication No. US20030017967A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ASANO, Shinichiro  
 ; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN  
 ; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD  
 ; FILE REFERENCE: Q6821  
 ; CURRENT APPLICATION NUMBER: US/10/089,678  
 ; CURRENT FILING DATE: 2002-05-02  
 ; PRIOR APPLICATION NUMBER: JP 2000-236140  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06660  
 ; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1167  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-089-678-1

Query Match 45.1%; Score 1594.5; DB 14; Length 1167;  
 Best Local Similarity 47.7%; Pred. No. 1.1e-133;  
 Matches 360; Conservative 125; Mismatches 219; Indels 51; Gaps 14;  
 QY 1 MKLKNQDKHQ---SFSSNAKVDKISTDSLNKNETDIQLQINHNHEDCLKMSYE-----NV 51  
 Db 1 MSPNNQNEYILDDASSSTVSVDNSVRYPFLANDOTTITQNNMYKDYLRMSEGENPELFGNP 60  
 QY 52 EPFVSASTIQTIGIGIAGKILGTIGVPPAGQVASYLSFILGELMPKGNQWEILFNEHVE 110  
 Db 61 ETFISSSTVGTIGIGVQVGLGALGVPPAGQIASFYSPFLVGLWPSSTVSVWEMI-MKQVE 119  
 QY 111 E-INOKISTYARNKALTDLKGLGDALAYYHDSLESWGNRNNTARSVVRQYIALELMF 169  
 Db 120 DLIDQKITSVRKTALAGLQGLGDLVYQSKLNWLENRNDTRARSVVVTQYIALELDF 179  
 QY 170 VQKLPFAVSGEVEPLPIYAQAANLHLLLRDASIFGKESWGLSSSEISTPYNQVERAG 229  
 Db 180 VAKIPSAISGQVEPLLSVYAQAANLHLLLRDASIFGAEWGTGPEISTFYDQVTRTA 239  
 QY 230 DYSCHCVKYSTGLNLRGTAESWVRNQFRDMLMVLVLPSPSYDTQMPYIKTTA 289  
 Db 240 QYSDYCVKYNLTGLDKGTNAASWLYKHQFRREMTLLVLDLVALFPNYDTRTYPIETTA 299  
 QY 290 QLTREYVTDAGTVHPHPSFTSTTWNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLS 349  
 Db 300 QLTREYVTDPIVFNRETSGFCRRWSLNSDISFSEVESAVIRSPHFLDILSEIEFVTRA 359  
 QY 350 --RWSNTQYMNWGGHKLEFRITIGTGLINISQGSNTSINPVLPTSDVYTESLAGNLFLTP 406  
 Db 360 GLPLNNTVELEYWVCHSIKYKNTNASSALERNYGTITSNKIKYYDLANKDIFQVSLGAD 419  
 QY 407 LNLFLTPQVNGVPRVDFHMKFVTHPIASDNFYPGVAGIG-----TQLQDS 452  
 Db 420 LANYAQ-VYGVPIYASF-----TLIDKN-----TGSGVGGFTYSXPHHTMQVCTQNYNT 468  
 QY 453 ENELPPEATGPQNYESYSHRLSHIGLIS-----ASHVKALVYSWTHRSADTNTIEP 504  
 Db 469 IDEIPEE--NEPLSRGYSRSLSHITSYFSKNASSPARYGNLPVFAWTHRSADVTNTVVS 526  
 QY 505 NSITQIPLVKAFNLSSGAADVVRGPGFTGGDILRNTGTGDIRVNINPPFAQRVRYR 564  
 Db 527 DKITQIPVKAHTLVSGTIVKPGFTGCGNLIKRTSSGGLAYTSVSKVSPLSQRYRARIR 586  
 QY 565 YASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYKTRTGTFTTFFSFLDVOSTFTTIGA 624  
 Db 587 YASTTNLRFLVFTISGTRIYSINWKNKMGDDLTFTNTFDLATIGTAFTFSGNSYSDSLTVA 646

```

QY 625 WNFSSGNEVYIDRIEFVPVEVTYAEVDFEKAQEKVTALTFTSTNPRGLKTDVKDYHIDQV 684
Db   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 647 DFPASGGEVVYDKFELIPVNATFEABEDLDVAKKAVNGLFTTSKKD-ALQTSVTDPVQNQA 705
Db   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 695 SNLVESISDEFYLDDEKRELFETVKYANELHIERNM 719
Db   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 706 ANLVECLSDLEYPNEKERMLWDVAKEAKRLVQARNL 740
Db   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 14
US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRP
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match      44.1%; Score 1658.5; DB 14; Length 653;
Best Local Similarity 51.4%; Pred. No. 4.7e-131;
Matches 346; Conservative 105; Mismatches 173; Indels 49; Gaps 16;

QY 13 SSNAKVDKISTDSLKN---ETDIQLQNINHEDCMKSEYENVEPFVSASTIQTIGIAGK 69
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 2 NENEIINALSIPAVNSHAQMDLSL-DARIEDSLCIAEGNNINPLVSASTVQICINIAGR 60
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 70 ILGTGVFFAGOVASLYSFILGELWPKGNQWEILFMHVTEE-INQISTYARKNALIDL 128
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 61 ILGVLGVFFAGOLASYSFLGELWPSGRDFWEI-FLEYEQLIRQQVTENTRTAIARL 119
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 129 KGLGDALAVYHDSLESVGWGNNRNTRRASVVRSQYTIALELMFVQKLPSFAVSGEEVPLLP 188
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 120 EGLGRGYRSYQOALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEEVPLLV 179
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 189 YAAANLHLILLRDASFGEKWGLSSEISTFYNQVERAGDYSCHCVKWSYTCGLNNLRG 248
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 180 YAAANLHLILLRDASLFGSEGMASSDVNQYQEQIRYTEEYNHCVMQYNTGLNNLRG 239
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 249 TNAESVRYNOFRDRMTLWLDLVALFPSYDTQMYPKTTAQLTREVVYDAIGTVHPHS 308
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 240 TNAESWLRYNOFRDRDLTLGVLDLVALFPSYDTRTPINTSAQLTREIYTDPIGRNAPSG 299
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 309 FTSTTYNNNAPSFSIAEAAYRNPHLLDFLEQVTIYSLSRWNTQYMMWGGHKLEFR 368
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 300 FASTNWFNNAAPSFSIAEAAIFRPPhLLDPPEQLTIYSASSRWSSSTOHMYNVGHRLNFR 359
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 369 TIGGTLNISTQGST-NTSINPVTLFF-TSRDYYRTESLAGLNFLTQPONGVPRVDFHWK 426
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 360 PIGGTLNTSTQGLTNNTSINEVTLHYVSSRDVYRTESNAGTNILFTTPONGVPPWARFN-- 417
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 427 FVTHPTASDNFYYP-----GYACIGTGLOQDSNELPPEATQPNYESYSHRLSHIG- 477
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 418 FITLRFIMKEAPLPTVNRIRELGENVLIQKLNHYOK-----QONDOIMNHIVIDISY 469
Db   : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 478 -LISASHVKALVYSWTHRSDRNTTEPNSITQIPLVKAFNLSSCAAVVRGPGETGGDIL 536

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Db      470  RLIIGNTLRAVPYVSWTHRSADRTNTIGPNRITQIPAVKGRFLFNG-SVISGPGFTGDDV 522
QY      537  R-RTNTGTF--GDIVRNIN-PPPAQRYRVIRYASTTDLQFHTSINGKAINQGNFSATM 591
Db      529  RLNRNNGNIQNRGVIETPIQFTSTSTRYRVRYASVTSELNVNLGNSSIFTNTLPATA 588
QY      592  NRGEDLDYKTRTGVGTFPTFSFLDVQSTFT-----IGAWNFSSGNEVYIDRIEFVPEV 645
Db      599  ASLDNLQ-----SGDFGYVEINNAFTSATGNIVGARNFNSANAEEVIIDRFEPVTA 639
QY      646  TYEAEYDFEKAQE 658
Db      640  TFEVEYDLERAQK 652

RESULT 15
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match      43.7%; Score 1643.5; DB 17; Length 1157;
Best Local Similarity 49.1%; Pred. No. 2.1e-129;
Matches 372; Conservative 96; Mismatches 229; Indels 61; Gaps 21

QY      1  MKLKNODKHQSPSSNAKYDKISTDS---LKNETDIELQNIHEDCLKMSEYE-----N 50
Db      1  MSPNNQNEYIIDATPST-SVSSDSNRYPPFANEPTDALQNNYKYDLYLKNXSGGENPELFGN 59
QY      51  VEPVSASTIQIGIGIAGKIILGTGVPAGOVASLYSFTILGELWP-KGKNQW-EILFMEH 108
Db      60  PETFISSTIQTGIGIVGRILGALGVPPASQIASFYSPFVIGQLWPSPKSVDIWGEI--MER 117
QY      109  VEE-INQISTYARNKALTDLKGLGDALAVYHDSLESWSVGNRNNTTRARSVRSQVIALEL 167
Db      118  VEEVDQKIEKYVKDKALAEKLGIGNALDVYQCSLEDWLENRNDARTRSVVSNQFIADL 177
QY      168  MFVQKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSIISTFYNRQVER 227
Db      178  NFVSSIPIFAVSGHEVJLLAVTAQAANLHLLLRDASIFGEEWGFTPGEISRFYNRQVOL 237
QY      228  AGDYSCHCVKMYSTGLNRLRGTAENASWVRYNQFRRDMTLMVLDLVALFPSTYDTOMYPIKT 287
Db      238  TAEYSDYCVKWKYIGLKLKGTTSKSWLNHQFREMTEMLLVLDLVALFPNYDTHMYPIET 297
QY      288  TAQLTREYVYTDAGTVHHPSPSTST---TWYNNNAPSFAIEAAVVRNPHLLDFLEQVT 343
Db      298  TAQLTRDVTDPDIA----FNIVTSTGFCNPWSTHSGIILFYEVENNVIRPPLHFLPILSSVE 353
QY      344  IYSLLSR----WSNTQYMMWGGHKLFR-----TIGGTNLNISTQGSTNTSINPVTLPFT 394
Db      354  INT--SRGGITLNNDAINYWSGHTLKYRRTADSTVTVTANYGRITSEKNS-----FALE 406

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-58  
Perfect score: 3761  
Sequence: 1 MKLKNQDKHQSFSNAKVDK.....KRELFEIVKYANELHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3736	99.3	719	4 AAB66911	Aab66911 Insectici
2	3736	99.3	719	6 AAB36275	Aae36275 B. thurin
3	3724	99.0	719	4 AAB66908	Aab66908 Insectici
4	3724	99.0	719	4 AAB66909	Aab66909 Insectici
5	3724	99.0	719	6 AAB36273	Aae36273 B. thurin
6	3724	99.0	719	6 AAB36272	Aae36272 B. thurin
7	3720	98.9	719	4 AAB66910	Aab66910 Insectici
8	3720	98.9	719	6 AAB36274	Aae36274 B. thurin
9	3715	98.8	719	4 AAU02095	Aau02095 Bacillus
10	3703	98.5	719	2 AAR08041	Aar08041 81 kD end
11	3692.5	98.2	718	6 AAB36271	Aae36271 B. thurin
12	3686.5	98.0	718	4 AAB66907	Aab66907 Insectici
13	3517	93.5	719	7 ADM74717	Adm74717 B. thurin
14	3484	92.6	719	4 AAB66912	Aab66912 Insectici
15	3484	92.6	719	6 AAB36276	Aae36276 B. thurin
16	3442.5	91.5	710	4 AAU02041	Aau02041 B. thurin
17	3363	89.4	719	3 ABB07073	Abb07073 Bacillus
18	3341	88.8	719	2 AAW49089	Aaw49089 Bacillus
19	3257	86.6	1217	4 AAU02092	Aau02092 Bacillus
20	2705	71.9	1208	4 AAU02093	Aau02093 Bacillus
21	2419	64.3	1230	8 ADK98484	Adk98484 B thuring
22	2419	64.3	1230	8 ADK98489	Adk98489 B thuring
23	2419	64.3	1230	8 ADK98481	Adk98481 B thuring
24	2419	64.3	1230	8 ADK98491	Adk98491 B thuring
25	2419	64.3	1230	8 ADK98487	Adk98487 B thuring

26	2417.5	64.3	1229	2 AAR54074	Aar54074 CryET5. 2
27	2417.5	64.3	1229	2 AAW35259	Aaw35259 Bacillus
28	2417.5	64.3	1229	2 AAW17699	Aaw17699 CryET5. 3
29	2417.5	64.3	1229	2 AAW87633	Aaw87633 CryET5 pr
30	2417.5	64.3	1229	2 AAY30923	Aay30923 B. thurin
31	2417.5	64.3	1229	8 ADK98479	Adk98479 B thuring
32	2318.5	61.6	488	2 AAW44322	Aaw44322 Bacillus
33	2318.5	61.6	488	2 AAB19947	Aab19947 Bacillus
34	2250.5	59.8	1228	2 AAR50955	Aar50955 Bacillus
35	2244.5	59.7	1209	4 AAU02094	Aau02094 Bacillus
36	2235.5	59.4	1227	2 AAY31990	Aay31990 Chimeric
37	2166.5	57.6	1227	2 AAW44321	Aaw44321 Bacillus
38	2166.5	57.6	1227	4 AAB19950	Aab19950 Bacillus
39	2157.5	57.4	1227	4 AAU02046	Aau02046 B. thurin
40	2142.5	57.0	1186	2 AAY16796	Aay16796 Amino aci
41	2127.5	56.6	1221	4 AAU00421	Aau00421 B. thurin
42	2113.5	56.2	1221	4 AAU00420	Aau00420 B. thurin
43	2087	55.5	1228	4 AAB84628	Aab84628 Amino aci
44	2087	55.5	1228	4 AAU02039	Aau02039 B. thurin
45	1909.5	50.8	643	2 AAY16797	Aay16797 Amino aci

ALIGNMENTS

RESULT 1  
ID AAB66911 standard; protein; 719 AA.  
XX AAB66911;  
AC AAB66911;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa5.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
FN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
production.  
XX  
PS Claim 14; Page 62-64; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66911 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;

Query Match 99.3%; Score 3736; DB 4; Length 719;  
Best Local Similarity 99.7%; Pred. No. 1.1e-291;  
Matches 718; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P P V S A S T I 60  
D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P P V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I N Q K I S T Y 119  
D b 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I N Q K I S T Y 119  
QY 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q Y I A L E L M F V Q K L P S F A V S 179  
D b 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q Y I A L E L M F V Q K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R O V E R A G D Y S D H C V K W Y 239  
D b 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R O V E R A G D Y S D H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
D b 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
QY 300 I G T V H P H P S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359  
D b 300 I G T V H P H P S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359  
QY 360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
D b 360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
QY 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I 479  
D b 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I 479  
QY 480 S A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539  
D b 480 S A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539  
QY 540 N T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599  
D b 540 N T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599  
QY 600 K T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
D b 600 K T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
QY 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
D b 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

RESULT 2  
AAE36275  
ID AAE36275 standard; protein; 719 AA.  
XX AC AAE36275;  
XX DT 26-JUN-2003 (first entry)  
XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX OS Bacillus thuringiensis.  
XX PN WO200298911-A2.  
XX PD 12-DEC-2002.  
XX PF 30-MAY-2002; 2002WO-GB002666.  
XX PR 07-JUN-2001; 2001GB-00013900.  
XX PA (SYGN ) SYNGENTA LTD.  
XX

Pi Vincent JL, Viner R;  
XX WPI; 2003-175137/17.  
XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX Claim 12; Page 53-56; 67pp; English.  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX Sequence 719 AA;  
SQ  
Query Match 99.3%; Score 3736; DB 6; Length 719;  
Best Local Similarity 99.7%; Pred. No. 1.1e-291;  
Matches 718; Conservative 0; Mismatches 0; Indels 2; Gaps 2;  
QY 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P P V S A S T I 60  
D b 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y N E V P P V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I N Q K I S T Y 119  
D b 61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I N Q K I S T Y 119  
QY 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q Y I A L E L M F V Q K L P S F A V S 179  
D b 120 A R N K A L T D L K G L G D A L A V Y H D S L E S W G N R N N T R A S V R S Q Y I A L E L M F V Q K L P S F A V S 179  
QY 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R O V E R A G D Y S D H C V K W Y 239  
D b 180 G E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R O V E R A G D Y S D H C V K W Y 239  
QY 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
D b 240 S T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A 299  
QY 300 I G T V H P H P S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359  
D b 300 I G T V H P H P S T T W Y N N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M 359  
QY 360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
D b 360 W G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N L F L T Q P V N G V P 419  
QY 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I 479  
D b 420 R V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I 479  
QY 480 S A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539  
D b 480 S A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T 539  
QY 540 N T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599  
D b 540 N T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y 599  
QY 600 K T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
D b 600 K T F R T V G F T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K 659  
QY 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719  
D b 660 V T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A N E L H I E R N M 719

```

RESULT 3
ID AAB66908 standard; protein; 719 AA.
XX
AC AAB66908;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa2.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX
PS Claim 14; Page 55-57; 72pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 719 AA;

Query Match 99.0%; Score 3724; DB 4; Length 719;
Best Local Similarity 99.3%; Pred. No. 1e-290;
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFVSASTI 60
DB 1 MKLKQDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTGVPAGQVASYLFGELWPKGNQWELLFMEHVEE-INQKISTY 119
DB 61 QTGIGIAGKILGTGVPAGQVASYLFGELWPKGNQWELLFMEHVEE-INQKISTY 119

QY 120 ARNKALTDKGLDALAVYHDSLESWGNRNTRNSVRSQYIALELMFVQKLPSPAYS 179
DB 120 ARNKALTDKGLDALAVYHDSLESWGNRNTRNSVRSQYIALELMFVQKLPSPAYS 179

QY 180 GEEVPLLPYAAQANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSDHCVKWY 239
DB 180 GEEVPLLPYAAQANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSDHCVKWY 239

QY 240 STGLNNLRGTNAESWVRNQFRDMLMVLVDLVALFPSPYDTQMPYPIKTTAQLTRVYIDA 299
DB 240 STGLNNLRGTNAESWVRNQFRDMLMVLVDLVALFPSPYDTQMPYPIKTTAQLTRVYIDA 299

QY 300 IGTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359
DB 300 IGTVHPHPSFTSTTWNNAAPSFSAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359

RESULT 4
ID AAB66909 standard; protein; 719 AA.
XX
AC AAB66909;
XX
DT 12-APR-2001 (first entry)
XX
DE Insecticidal protein cryIIa3.
XX
KW Insecticide; transgenic plant; insect-resistance.
XX
OS Paecilomyces sp.
XX
PN WO200100841-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-GB002457.
XX
PR 29-JUN-1999; 99GB-00015215.
PR 23-DEC-1999; 99GB-00030536.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;
PI Vincent JL, Lee MD;
XX
DR WPI; 2001-123015/13.
XX
PT Novel insecticidal protein obtained from species of Paecilomyces for
PT controlling insects, and for insect-resistant transgenic plant
PT production.
XX
PS Claim 14; Page 57-59; 73pp; English.
XX
CC The present invention relates to novel insecticidal proteins obtained
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
CC insecticidal proteins can be used to produce transgenic plants, which are
CC insect-resistant. Also, the insecticidal proteins are useful for
CC controlling insects by providing them at a locus where insects feed
XX
SQ Sequence 719 AA;

Query Match 99.0%; Score 3724; DB 4; Length 719;
Best Local Similarity 99.4%; Pred. No. 1e-290;
Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

```

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSYILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSYILGELWPKGNQWEI-FMEHVEEIIINQKISTY 119  
 QY 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVVRQYIALELMFVQKLPSPFVS 179  
 DB 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVVRQYIALELMFVQKLPSPFVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239  
 DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239  
 QY 240 STGLNNLRGTNAESWVRVYNNQFRDMLMVLVLPFSDYDQMPYIKTTAQLTREYVYTD 299  
 DB 240 STGLNNLRGTNAESWVRVYNNQFRDMLMVLVLPFSDYDQMPYIKTTAQLTREYVYTD 299  
 QY 300 IGTVPHPSTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMN 359  
 DB 300 IGTVPHPSTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMN 359  
 QY 360 WGGHKLFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVP 419  
 DB 360 WGGHKLFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRSLHIGLI 479  
 DB 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRSLHIGLI 479  
 QY 480 SASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTGDIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDY 599  
 DB 540 NTGTGDIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDY 599  
 QY 600 KTFRTVGTFTTFFSFLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
 DB 600 KTFRTVGTFTTFFSFLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 5  
 AAE36273  
 ID AAE36273 standard; protein; 719 AA.  
 XX AAE36273;  
 AC  
 XX 26-JUN-2003 (first entry)  
 DT  
 XX  
 DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.  
 XX  
 KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX Bacillus thuringiensis.  
 OS  
 XX WO200298911-A2.  
 FN  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 DR  
 XX  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT  
 XX  
 PS Claim 12; Page 47-50; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is  
 CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC  
 XX SQ Sequence 719 AA;  
 Query Match 99.0%; Score 3724; DB 6; Length 719;  
 Best Local Similarity 99.4%; Pred. No. 1e-290;  
 Matches 716; Conservative 1; Mismatches 1; Indels 2; Gaps 2;  
 QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVASYLSYILGELWPKGNQWEILFMEHVEE-INQKISTY 119  
 DB 61 QTGIGIAGKILGTGVPFAGQVASYLSYILGELWPKGNQWEI-FMEHVEEIIINQKISTY 119  
 QY 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVVRQYIALELMFVQKLPSPFVS 179  
 DB 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNNTRARSVVRQYIALELMFVQKLPSPFVS 179  
 QY 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239  
 DB 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNNRQVERAGDYSDHCVKWY 239  
 QY 240 STGLNNLRGTNAESWVRVYNNQFRDMLMVLVLPFSDYDQMPYIKTTAQLTREYVYTD 299  
 DB 240 STGLNNLRGTNAESWVRVYNNQFRDMLMVLVLPFSDYDQMPYIKTTAQLTREYVYTD 299  
 QY 300 IGTVPHPSTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMN 359  
 DB 300 IGTVPHPSTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVITYSLLSRWSNTQYMMN 359  
 QY 360 WGGHKLFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVP 419  
 DB 360 WGGHKLFRITGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTQPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRSLHIGLI 479  
 DB 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENEPPEATGQPNYESYSHRSLHIGLI 479  
 QY 480 SASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTGDIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDY 599  
 DB 540 NTGTGDIRVNNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLDY 599  
 QY 600 KTFRTVGTFTTFFSFLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
 DB 600 KTFRTVGTFTTFFSFLDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 6  
AAE36272 standard; protein; 719 AA.  
XX  
AC AAE36272;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
XX  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-GB002666.  
XX  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX  
PI Vincent JL, Viner R;  
XX  
DR WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
PS Claim 12; Page 44-47; 67pp; English.  
XX  
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
XX  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 719 AA;  
  
Query Match 99.0%; Score 3724; DB 6; Length 719;  
Best Local Similarity 99.3%; Pred. No. 1e-290;  
Matches 715; Conservative 2; Mismatches 1; Indels 2; Gaps 2;  
  
QY 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
Db 1 MKLNQDKHQSFSSNAKVDKISTSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
  
QY 61 QTGIGIAGKILGTGVPAGQVASYLSFGLWPKGKNOWEILFMEHVEE-INQKISTY 119  
Db 61 QTGIGIAGKILGTGVPAGQVASYLSFGLWPKGKNOWEILFMEHVEEINQKISTY 119  
  
QY 120 ARNKALTDLKGIDALAVYHDSLESWYGNRNTRARSVRSQYIALELMFVQKLPSEAVS 179  
Db 120 ARNKALTDLKGIDALAVYHDSLESWYGNRNTRARSVRSQYIALELMFVQKLPSEAVS 179  
  
QY 180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISFYNQVERAGDYSCHVKWY 239  
Db 180 GEEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISFYNQVERAGDYSCHVKWY 239  
  
QY 240 STGLNNLRCTNAESWVRNQFRDMTLMVLVLPSPDYDTQMYPIKTTAQLTREVYTD 299  
Db 240 STGLNNLRCTNAESWVRNQFRDMTLMVLVLPSPDYDTQMYPIKTTAQLTREVYTD 299  
  
QY 300 IGVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359  
Db 300 IGVHPHPSFTSTWYNNAPSFSAIEAAVVRNPHLLDFLEQVTIYSLSRWSNTQYMMN 359

QY 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGINLFLTQPVNGVP 419  
Db 360 WGGHKLFRFTIGTGLNISTQGSTNTSINPVTLPFTSRDVTYTESLAGINLFLTQPVNGVP 419  
QY 420 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENEPEATQOPNYESYSHRLSHIGLI 479  
Db 420 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENEPEATQOPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVTSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAADVPGPGFTGGDIILRT 539  
Db 480 SASHVKALVTSWTHRSADRNTNIEPNSITQIPLVKAFNLSSGAADVPGPGFTGGDIILRT 539  
QY 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDDLDY 599  
Db 540 NTGTFGDIRVNINPPFAQRYRIRYASTTDLOFHTSINGKAINQGNFSATMNRGDDLDY 599  
QY 600 KTFRTVGTTPPFFSLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
Db 600 KTFRTVGTTPPFFSLDVQSTFTTIGAWNFSNGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDYHIDOVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKDYHIDOVSNLVESLSDEFYLDKRELFEIVKYAKQLHIERNM 719

RESULT 7  
AAB66910 standard; protein; 719 AA.  
XX  
AC AAB66910;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa4.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
XX  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
XX  
PT controlling insects, and for insect-resistant transgenic plant  
XX  
PT production.  
XX  
PS Claim 14; Page 60-62; 72pp; English.  
XX  
CC The present invention relates to novel insecticidal proteins obtained  
XX  
CC from Paecilomyces sp. (see AAB66910 to AAB66901 and AAB66913). The  
XX  
CC insecticidal proteins can be used to produce transgenic plants, which are  
XX  
CC insect-resistant. Also, the insecticidal proteins are useful for  
XX  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 719 AA;

Query Match 98.9%; Score 3720; DB 4; Length 719;  
Best Local Similarity 99.2%; Pred. No. 2.2e-290;  
Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEILFMEHVEE-INOXISTY 119  
 DB 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEI - FMEHVEEIIINOXISTY 119  
 QY 120 ARNKALTDLKGDLAVYHDSLESWGNNRNRARSVRSQVIALELMFVKQLPSFAVS 179  
 DB 120 ARNKALTDLKGDLAVYHDSLESWGNNRNRARSVRSQVIALELMFVKQLPSFAVS 179  
 QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 QY 240 STGLNNLRGTNAESWVRNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVYTD 299  
 DB 240 STGLNNLRGTNAESWVRNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVYTD 299  
 QY 300 IGTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMM 359  
 DB 300 IGTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMM 359  
 QY 360 WGGHKLFEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP 419  
 DB 360 WGGHKLFEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYYPGVYIGTQLQDSNELPPEATGQPNYESYSHRSLHIGLI 479  
 DB 420 RVDHFWKFTVTHPIASDNFYYPGVYIGTQLQDSNELPPEATGQPNYESYSHRSLHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
 DB 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
 QY 600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 DB 600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719

RESULT 8  
 AAE36274

ID AAE36274 standard; protein; 719 AA.

AC AAE36274;

XX 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

OS WO20029811-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-GB002666.

XX 07-JUN-2001; 2001GB-00013900.

XX (SYGN ) SYNGENTA LTD.

XX Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX Claim 12; Page 50-53; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 XX Sequence 719 AA;

Query Match 98.9%; Score 3720; DB 6; Length 719;  
 Best Local Similarity 99.2%; Pred. No. 2.2e-290;

Matches 714; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQINHEDECLKMSYENVEPFFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEILFMEHVEE-INOXISTY 119  
 DB 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEI - FMEHVEEIIINOXISTY 119  
 QY 120 ARNKALTDLKGDLAVYHDSLESWGNNRNRARSVRSQVIALELMFVKQLPSFAVS 179  
 DB 120 ARNKALTDLKGDLAVYHDSLESWGNNRNRARSVRSQVIALELMFVKQLPSFAVS 179  
 QY 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 DB 180 GEEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSCHVKWY 239  
 QY 240 STGLNNLRGTNAESWVRNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVYTD 299  
 DB 240 STGLNNLRGTNAESWVRNQFRDMTLMVLDLVALPFSYDTQMPYIKTTAQLTREYVYTD 299  
 QY 300 IGTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMM 359  
 DB 300 IGTVHPHPSSTTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSTQYMM 359  
 QY 360 WGGHKLFEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP 419  
 DB 360 WGGHKLFEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRRTESLAGLNLFLTQPVNGVP 419  
 QY 420 RVDHFWKFTVTHPIASDNFYYPGVYIGTQLQDSNELPPEATGQPNYESYSHRSLHIGLI 479  
 DB 420 RVDHFWKFTVTHPIASDNFYYPGVYIGTQLQDSNELPPEATGQPNYESYSHRSLHIGLI 479  
 QY 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 DB 480 SASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRT 539  
 QY 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
 DB 540 NTGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
 QY 600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 DB 600 KTFRTVGFTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEK 659  
 QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719  
 DB 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHIERNM 719



CC be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278,  
CC or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11  
CC (NCIB 40275). The delta-endo- toxin produced by the transformants can be  
CC used in formulations for combatting Lepidoptera and Coleoptera pests.  
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 719 AA;

Query Match 98.5%; Score 3703; DB 2; Length 719;  
Best Local Similarity 98.9%; Pred. No. 5e-289;  
Matches 712; Conservative 2; Mismatches 4; Indels 2; Gaps 2;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPFSASTI 60  
DB 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPFSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
QY 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVRSGYIALLELMFVQKLPFAVS 179  
DB 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVRSGYIALLELMFVQKLPFAVS 179  
QY 180 GEEVPLLPYQAANLHLLLRDASIFGKESGLSSSEISTFYNNRQVERAGDYSHCVKWY 239  
DB 180 GEEVPLLPYQAANLHLLLRDASIFGKESGLSSSEISTFYNNRQVERAGDYSHCVKWY 239  
QY 240 STGLNNLRGTNAESWVRYNQFRDMLMVLVLDLVALPSPYDTQMPYIKTTAQLTREVYTD 299  
DB 240 STGLNNLRGTNAESWVRYNQFRDMLMVLVLDLVALPSPYDTQMPYIKTTAQLTREVYTD 299  
QY 300 IGVHPPHPSFTTWNNAEVSFAIAAARNVPHLLDLEQVTTIYSLLSRWSTQYMMN 359  
DB 300 IGVHPPHPSFTTWNNAEVSFAIAAARNVPHLLDLEQVTTIYSLLSRWSTQYMMN 359  
QY 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTESLAGNLFLTQPVNGVP 419  
DB 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTESLAGNLFLTQPVNGVP 419  
QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRUSHIGLI 479  
DB 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRUSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
DB 480 SASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
QY 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATMRGEDLDY 599  
DB 540 NTGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSGATMRGEDLDY 599  
QY 600 KTFRTVGTFTPSFLDVOSTFTIGAMNFSNGNEVYDRIEFPVPEVTEAEYDEKAQEK 659  
DB 600 KTFRTVGTFTPSFLDVOSTFTIGAMNFSNGNEVYDRIEFPVPEVTEAEYDEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDPEYLDKRELFEIVKYANLHIERNM 719  
DB 660 VTALFTSTNPRGLKTDVYHIDQVSNLVESLSDPEYLDKRELFEIVKYANLHIERNM 719

RESULT 11  
AAE36271  
ID AAE36271 standard; protein; 718 AA.  
XX  
AC AAE36271;  
XX AC  
XX AC  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa1.  
XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
KW

XX  
OS Bacillus thuringiensis.  
XX  
PN WO200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-GB002666.  
XX  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX  
PI Vincent JL, Viner R;  
XX  
DR WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
PS Claim 12; Page 42-44; 67pp; English.  
XX  
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 718 AA;

Query Match 98.2%; Score 3692.5; DB 6; Length 718;  
Best Local Similarity 98.9%; Pred. No. 3.5e-288;  
Matches 712; Conservative 2; Mismatches 3; Indels 3; Gaps 3;

QY 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPFSASTI 60  
DB 1 MKLNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPFSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWEILFMEHVEE-INOKISTY 119  
QY 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVRSGYIALLELMFVQKLPFAVS 179  
DB 120 ARNKALTDLKGGLDALAVYHDSLESWGNNRNRARSVVRSGYIALLELMFVQKLPFAVS 179  
QY 180 GEEVPLLPYQAANLHLLLRDASIFGKESGLSSSEISTFYNNRQVERAGDYSHCVKWY 239  
DB 180 GEEVPLLPYQAANLHLLLRDASIFGKESGLSSSEISTFYNNRQVERAGDYSHCVKWY 239  
QY 240 STGLNNLRGTNAESWVRYNQFRDMLMVLVLDLVALPSPYDTQMPYIKTTAQLTREVYTD 299  
DB 240 STGLNNLRGTNAESWVRYNQFRDMLMVLVLDLVALPSPYDTQMPYIKTTAQLTREVYTD 299  
QY 300 IGVHPPHPSFTTWNNAEVSFAIAAARNVPHLLDLEQVTTIYSLLSRWSTQYMMN 359  
DB 300 IGVHPPHPSFTTWNNAEVSFAIAAARNVPHLLDLEQVTTIYSLLSRWSTQYMMN 359  
QY 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTESLAGNLFLTQPVNGVP 419  
DB 360 WGGHKLFEFTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTESLAGNLFLTQPVNGVP 419  
QY 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRUSHIGLI 479  
DB 420 RVDHFWKFTVTHPIASDNFYYPGAGIGTQLODSENELPPEATQPNYESYSHRUSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
DB 479 SASHVKALVYSWTHRSADRTNTEPNSTIQPLVKAFNLSSGAAVVRGPGFTGGDILRT 538

QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
DB 539 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 598  
QY 600 KTRFTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVTYEAAYDFEKAQEK 659  
DB 599 KTRFTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVTYEAAYDFEKAQEK 658  
QY 660 VTALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDPYLDEKRELFEIVKYANELHIERNM 719  
DB 659 VTALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDPYLDEKRELFEIVKYAKQLHIERNM 718

RESULT 12  
AAB66907  
ID AAB66907 standard; protein; 718 AA.  
XX AAB66907;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cryIIa1.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces, sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;  
XX  
DR WPI; 2001-123015/13.  
XX  
PT Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.  
XX  
PS Claim 14; Page 53-55; 72pp; English.  
XX  
XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed  
XX  
SQ Sequence 718 AA;

Query Match 98.0%; Score 3686.5; DB 4; Length 718;  
Best Local Similarity 98.8%; Pred. No. 1.1e-287;  
Matches 711; Conservative 2; Mismatches 4; Indels 3; Gaps 3;

QY 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60  
DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNIHEDCLKMSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWELLFMEHVEB-INOKISTY 119  
DB 61 QTGIGIAGKILGTGVPFAGQVASYLSFILGELWPKGNQWELLFMEHVEB-INOKISTY 119  
QY 120 ARNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVRVRSQYIALELMFVQKLSFAVS 179  
DB 120 ARNKALTDLKGGLDALAVYHDSLESWGNRNNTARSVVRVRSQYIALELMFVQKLSFAVS 179

QY 180 GEEVPLLPPIYAANLHLLLRDASIFGKEWGLSSSSBISTFYNRQVERAGDYSCHCVKWY 239  
DB 180 GEEVPLLPPIYAANLHLLLRDASIFGKEWGLSSSSBISTFYNRQVERAGDYSYHCVKWY 239  
QY 240 STGLNLRGNAESWVRNQFRDMLMVLDLVALFSDYDTOMYPKTKTAQLTREVYTDA 299  
DB 240 STGLNLRGNAESWVRNQFRDMLMVLDLVALFSDYDTOMYPKTKTAQLTREVYTDA 299  
QY 300 IGTVHPSPSTTTWYNNNAPSFAIEAAVVRNPHLDFLEQVTIYSLLSRWSNTQYMMN 359  
DB 300 IGTVHPSPSTTTWYNNNAPSFAIEAAVVRNPHLDFLEQVTIYSLLSRWSNTQYMMN 359  
QY 360 WGGHKLFEFTIGGTNLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVP 419  
DB 360 WGGHKLFEFTIGGTNLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVN-VP 418  
QY 420 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELEPPEATGQPNYESYSHRLSHIGLI 479  
DB 419 RVDFHWKFVTHPIASDNFYYPGYAGIGTQLODSENELEPPEATGQPNYESYSHRLSHIGLI 478  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 539  
DB 479 SASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRT 538  
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 599  
DB 539 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDY 598  
QY 600 KTRFTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVTYEAAYDFEKAQEK 659  
DB 599 KTRFTVGTTPPSFLDVQSTFTTIGAMNFSNGNEVYIDRIEFVPEVVTYEAAYDFEKAQEK 658  
QY 660 VTALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDPYLDEKRELFEIVKYANELHIERNM 719  
DB 659 VTALFTSTNPRGLTKDVKDYHIDQVSNLVESLSDPYLDEKRELFEIVKYAKQLHIERNM 718

RESULT 13  
ADM74717  
ID ADM74717 standard; protein; 719 AA.  
XX  
AC ADM74717;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE B. thuringiensis cryIIel SEQ ID NO:2.  
XX  
KW cryII; toxicity; lepidoptera; cryIIab; cryIIba; coleoptera; diptera;  
KW cryIIel.  
XX  
OS Bacillus thuringiensis.  
XX  
PN CN1401772-A.  
XX  
PD 12-MAR-2003.  
XX  
PF 20-AUG-2001; 2001CN-00124163.  
XX  
PR 20-AUG-2001; 2001CN-00124163.  
XX  
PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
XX  
PI Song F, Zhang J, Huang D;  
XX  
DR WPI; 2003-442339/42.  
DR N-PSDB; ADM74716.  
XX  
PT Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
PT with high-toxicity to lepidoptera pests, encoded protein, primer  
PT sequences and the shuttle vector pSXY422b, useful as a pesticide.  
XX  
PS Example 3; SEQ ID NO 2; 29pp; Chinese.

XX The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
CC combination, expression vector, nucleotide sequence of the B  
CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
CC amino acid sequence of the protein encoded by it, cooperative use of the  
CC cryI gene with the expression product of cryIaB or cryIaC, primer  
CC sequences for expressing the genes, and the constructed shuttle vector  
CC pSXY422b. The gene in combination with the cryIaB or cryIaC genes  
CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
CC The present sequence represents the cryIIa1 protein.

XX SQ Sequence 719 AA;

Query Match 93.5%; Score 3517; DB 7; Length 719;  
Best Local Similarity 93.1%; Pred. No. 4.8e-274;  
Matches 670; Conservative 27; Mismatches 21; Indels 2; Gaps 2;

Qy 1 MKLKNDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDECLRMSEYENVEPFSASTI 60  
Db 1 MKLKNDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDECLRMSEYENVEPFSASTI 60

Qy 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVES-INOKISTY 119  
Db 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVES-INOKISTY 119

Qy 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRARSVVRQYIALELMFVQKLPFAVS 179  
Db 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRARSVVRQYIALELMFVQKLPFAVS 179

Qy 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSISITFNNRQVERAGDYSDHCVKY 239  
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSISITFNNRQVERAGDYSDHCVKY 239

Qy 240 STGLNLRGNAESWVRNQFRDMLVLDLVALPFSYDQMPYIKTTAQLTREYVTD 299  
Db 240 STGLNLRGNAESWVRNQFRDMLVLDLVALPFSYDQMPYIKTTAQLTREYVTD 299

Qy 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359  
Db 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359

Qy 360 WGGHLEFRITIGTINISQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVP 419  
Db 360 WGGHLEFRITIGTINISQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVP 419

Qy 420 RVDHFWKFTPTPIASDNFYLYGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDHFWKFTPTPIASDNFYLYGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479

Qy 480 SASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAPNLSSGAAVVRGPGFTGGDILRRT 539  
Db 480 SASHVKALVYSWTHRSADRNTNIEPNSITQIPLVKAPNLSSGAAVVRGPGFTGGDILRRT 539

Qy 540 NTGIFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLDY 599  
Db 540 NTGIFGDIRVNIWPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMRGDLDY 599

Qy 600 KTRFTVGFTTFFSDVOSTFTIGAMNFSNGNEVYIDRIEVPVVEYEAEDFEKAQEK 659  
Db 600 KTRFTVGFTTFFSDVOSTFTIGAMNFSNGNEVYIDRIEVPVVEYEAEDFEKAQEK 659

Qy 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDYFLDEKRELFEIVKYANELHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDYFLDEKRELFEIVKYANELHIERNM 719

RESULT 14  
AAB66912  
ID AAB66912 standard; protein; 719 AA.  
XX AAB66912;  
AC AAB66912;  
XX AAB66912;  
DT 12-APR-2001 (first entry)

XX Insecticidal protein cryIIb1.  
XX Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
XX WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
XX (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
XX Vincent JL, Lee MD;  
XX WPI; 2001-123015/13.  
XX Novel insecticidal protein obtained from species of Paecilomyces for  
XX controlling insects, and for insect-resistant transgenic plant  
XX production.  
XX Claim 14; Page 64-66; 72pp; English.  
XX The present invention relates to novel insecticidal proteins obtained  
XX from Paecilomyces sp. (see AAB6699 to AAB6901 and AAB6913). The  
XX insecticidal proteins can be used to produce transgenic plants, which are  
XX insect-resistant. Also, the insecticidal proteins are useful for  
XX controlling insects by providing them at a locus where insects feed  
XX Sequence 719 AA;

Query Match 92.6%; Score 3484; DB 4; Length 719;  
Best Local Similarity 92.2%; Pred. No. 2.2e-271;  
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;

Qy 1 MKLKNDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDECLRMSEYENVEPFSASTI 60  
Db 1 MKLKNDKHQSFSSNAKVDKISTDSLNKNETDIELQINHEDECLRMSEYENVEPFSASTI 60

Qy 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVES-INOKISTY 119  
Db 61 QTGIGIAGKILGTGVPFAGQVSLYSFILGELWPKGNQWEIFMEHVES-INOKISTY 119

Qy 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRARSVVRQYIALELMFVQKLPFAVS 179  
Db 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRARSVVRQYIALELMFVQKLPFAVS 179

Qy 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSISITFNNRQVERAGDYSDHCVKY 239  
Db 180 GEEVPLLPPIYAQAANLHLLLRDASIFGKWLSSSISITFNNRQVERAGDYSDHCVKY 239

Qy 240 STGLNLRGNAESWVRNQFRDMLVLDLVALPFSYDQMPYIKTTAQLTREYVTD 299  
Db 240 STGLNLRGNAESWVRNQFRDMLVLDLVALPFSYDQMPYIKTTAQLTREYVTD 299

Qy 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359  
Db 300 IGTVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMMN 359

Qy 360 WGGHLEFRITIGTINISQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVP 419  
Db 360 WGGHLEFRITIGTINISQGSTNTSINPVTLPFTSRDVRTESLAGNLFLTPQVNGVP 419

Qy 420 RVDHFWKFTPTPIASDNFYLYGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDHFWKFTPTPIASDNFYLYGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLI 479

QY 480 SASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
Db 480 SASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDY 599  
Db 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDY 599  
QY 600 KTRFTVGTTPRSGFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
Db 600 KTRFTIGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 15  
AAE36276  
ID AAE36276 standard; protein; 719 AA.  
XX  
AC AAE36276;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIb1.  
XX  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
OS Bacillus thuringiensis.  
XX  
PN WO200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-GB002666.  
XX  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX  
PI Vincent JL, Viner R;  
XX  
DR WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
PS Claim 12; Page 56-58; 67pp; English.  
XX  
CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
XX  
SQ Sequence 719 AA;

Query Match 92.6%; Score 3484; DB 6; Length 719;  
Best Local Similarity 92.2%; Pred. No. 2.2e-271;  
Matches 664; Conservative 33; Mismatches 21; Indels 2; Gaps 2;

QY 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKXSEYENVEPVSASTI 60  
Db 1 MKLKNPDKHQSLSSNAKVDKXATDSLKNETDIELKXNWNEDYLRMSEHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTGVPPAGQVASYLGFILGELWPKGKNQWELFMEHVEE-INQKISTY 119  
Db 61 QTGIGIAGKILGTGVPPAGQIASLYSILGELWPKGKSQWEI-FMEHVEEIIQKILTY 119

Search completed: October 28, 2004, 18:20:05  
Job time : 89.6903 secs

QY 120 ARNKALTDLKGDLAVYHDSLESWGNRNTRARSVVRQYIALELMFVKLPFAVS 179  
Db 120 ARNKALSDLRGLDALAVYHESLESWENRNTRARSVVKQYIALELMFVKLPFAVS 179  
QY 180 GEEVPLLPYQAANLHLLLRDASI FQKEWGLSSSSISTFYNRQVERAGDYSDHCVKWY 239  
Db 180 GEEVPLLPYQAANLHLLLRDASI FQKEWGLSASISITFYNRQVERTRDYSDHCWKY 239  
QY 240 STGLNLRGNAESWVRVNOFRDMDTLMVLDLVALPFSYDTQMPKTTAOLTRVYVTA 299  
Db 240 NTGLNLRGNAESWVRVNOFRDMDTLMVLDLVALPFSYDTQMPKTTAOLTRVYVTA 299  
QY 300 IGTVPHPSTSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYMM 359  
Db 300 IGTVPHPQAFSTTWYNNAPSPSAIEAAVVRNPHLLDFLEQVTTIYSLLSWSNTQYMM 359  
QY 360 WGGHKLFRFTIGTILNISTQGSTNTSINPVTLPFTSRDVRATESLAGNLFLTPVNGVP 419  
Db 360 WGGHLESRPFGALNTSTQGSTNTSINPVTLPFTSRDVRATESLAGNLFLTPVNGVP 419  
QY 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENELEPPEATGQPNYESYSHRLSHIGLI 479  
Db 420 RVDHFWKFTVTHPIASDNFYYPGYAGIGTQLODSENELEPPEATGQPNYESYSHRLSHIGLI 479  
QY 480 SASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
Db 480 SASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRT 539  
QY 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDY 599  
Db 540 NTGTFGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFATMNRGEDLDY 599  
QY 600 KTRFTVGTTPRSGFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
Db 600 KTRFTIGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEK 659  
QY 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHIERNM 719  
Db 660 VTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSEDEFYLDKRELFEIVKYAKQIHIERNM 719



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:05:43 ; Search time 19,191 Seconds  
(without alignments)  
3604.811 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPDKHQSLSNAKVDK.....KRELFEIVKAKQIHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3742	100.0	719	2 I40590	cryV465 protein -
2	3520	94.1	719	2 I39815	insecticidal prote
3	3511	93.8	719	2 S25383	parasporal crystal
4	3503	93.6	719	2 I39814	insecticidal prote
5	2321.5	62.0	1228	2 S00873	parasporal crystal
6	1813	48.5	380	2 B42459	hypothetical prote
7	1507	40.3	1157	1 S49247	parasporal crystal
8	1503.5	40.2	1166	2 S32645	parasporal crystal
9	1491.5	39.9	1174	2 S32649	parasporal crystal
10	1487.5	39.8	1155	2 A26513	parasporal crystal
11	1480.5	39.6	1155	2 JD0002	parasporal crystal
12	1480.5	39.6	1156	2 A29125	parasporal crystal
13	1463.5	39.1	1155	2 S02134	parasporal crystal
14	1463.5	39.1	1181	2 A41052	parasporal crystal
15	1461.5	39.1	1155	2 I39838	parasporal crystal
16	1459	39.0	934	2 A22798	parasporal crystal
17	1457	38.9	1176	2 JT0241	parasporal crystal
18	1451	38.8	1176	2 JC2219	parasporal crystal
19	1447	38.7	1176	2 A22617	parasporal crystal
20	1447	38.7	1176	2 S02215	parasporal crystal
21	1367	36.5	1174	2 A42459	parasporal crystal
22	1348	36.0	1156	2 A29838	parasporal crystal
23	1343	35.9	1138	2 A48944	parasporal crystal
24	1340.5	35.8	823	2 S04181	parasporal crystal
25	1331.5	35.6	1189	2 S00944	parasporal crystal
26	1326	35.4	1154	2 S39536	parasporal crystal
27	1292	34.5	1171	2 I40572	parasporal crystal
28	1282	34.5	1171	2 A37829	parasporal crystal
29	1286	34.4	1176	2 A48970	parasporal crystal

30 1232 32.9 1160 2 S32647 parasporal crystal  
31 1230.5 32.9 1165 2 S11446 parasporal crystal  
32 1220.5 32.6 655 2 JC7140 protoxin - Bacillu  
33 1196.5 32.0 1172 2 S32689 parasporal crystal  
34 1179 31.5 1160 2 I40589 parasporal crystal  
35 1178 31.5 652 2 A27323 parasporal crystal  
36 1165 31.1 1178 1 USBSXH parasporal crystal  
37 1164.5 31.1 1177 2 A49785 parasporal crystal  
38 1159 31.0 659 2 S10228 parasporal crystal  
39 1124.5 30.1 652 2 I39811 parasporal crystal  
40 995 26.6 649 1 JH0261 parasporal crystal  
41 938.5 25.1 618 2 S11445 parasporal crystal  
42 896 23.9 1156 2 S19306 parasporal crystal  
43 845 22.6 1136 1 USBS81 parasporal crystal  
44 662.5 17.7 934 2 B29838 parasporal crystal  
45 637 17.0 1180 2 I39870 parasporal crystal

ALIGNMENTS

RESULT 1

I40590  
CryV465 protein - Bacillus thuringiensis  
C:Species: Bacillus thuringiensis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996.#text-change-09-Jul-2004-----  
C:Accession: I40590  
R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A:Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis s  
tomocidus.  
A:Reference number: I39814; MUID:95314293; PMID:7739360  
A:Accession: I40590  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-719 <RES>  
A:Cross-references: UNIPROT:Q45709; EMBL:U07642; NID:g467234; PIDN:AAA82114.1; PID:g46723;  
C:Genetics:  
A:Gene: cryV465  
C:Superfamily: parasporal crystal protein

Query Match	100.0%	Score 3742	DB 2	Length 719
Best Local Similarity	100.0%	Pred. No. 3.1e-258		
Matches 719	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFVGSASTI	60	
Db	1	MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFVGSASTI	60	
Qy	61	QTGIGTAGKILGTGVPFAGQIASLYSIFLGELMPKGSQWEIFMEHVEEINQKILTYYA	120	
Db	61	QTGIGTAGKILGTGVPFAGQIASLYSIFLGELMPKGSQWEIFMEHVEEINQKILTYYA	120	
Qy	121	RNKALSDRLGLGDALAVYHESLESWVENNTRARSVVKNQYIALELMFVQKLPFAVSG	180	
Db	121	RNKALSDRLGLGDALAVYHESLESWVENNTRARSVVKNQYIALELMFVQKLPFAVSG	180	
Qy	181	BEVPLPIYAQAANLHLLLRDASI FGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN	240	
Db	181	BEVPLPIYAQAANLHLLLRDASI FGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN	240	
Qy	241	TGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI	300	
Db	241	TGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSQLTREVYTDAI	300	
Qy	301	GTVHPNQAFSTTWYNNNAPSFAIAEAVIRSPHLLDFLEKVTIYLSLSRSNTQYNNMW	360	
Db	301	GTVHPNQAFSTTWYNNNAPSFAIAEAVIRSPHLLDFLEKVTIYLSLSRSNTQYNNMW	360	
Qy	361	GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR	420	
Db	361	GGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR	420	

QY 421 VDFHWKFTPLPIASDNFYVLYGAVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPLPIASDNFYVLYGAVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYK 600  
 DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYK 600  
 QY 601 TFRITGFTTFFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRITGFTTFFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQIHIERNM 719

## RESULT 2

I39815  
 insecticidal protein cryV - Bacillus thuringiensis  
 C;Species: Bacillus thuringiensis  
 C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I39815  
 R;Gleave, A.P.; Williams, R.; Hedges, R.J.  
 Appl. Environ. Microbiol. 59, 1683-1687, 1993  
 A;Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for  
 iensis subsp. kurstaki.  
 A;Reference number: I39815; MUID:93298009; PMID:8517758  
 A;Accession: I39815  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-719 <RES>  
 A;Cross-references: UNIPROT:Q45752; GB:M98544; NID:G142767; PIDN:AAA22354.1; PID:G142768  
 C;Genetics:  
 A;Gene: cryV  
 C;Superfamily: parasporal crystal protein

Query Match 94.1%; Score 3520; DB 2; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 2e-242;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSNNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60  
 DB 1 MKLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGSKQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALSDRLGLDALAVVHESLSWENNRNTRARSVVKNQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDRLGLDALAVVHDSLSWGNRNTRARSVYVKSQYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFFNRQVERTRDYSCHCIKWYN 240  
 DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSCHVKWYS 240  
 QY 241 TGLNLRGNTAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTTSQLTREVYTDAL 300  
 DB 241 TGLNLRGNTAESWRYNQFRDMTLMVLDLVALFPSYDTQWYPIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 QY 361 GGHRLSRPTGGALNTSTOGSTNTSINPVTLOFTSRDVRYESLAGLNLFITQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTGLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFITQPVNGVPR 420

QY 421 VDFHWKFTPLPIASDNFYVLYGAVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPLPIASDNFYVLYGAVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYK 600  
 DB 541 TGTGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDDLYK 600  
 QY 601 TFRITGFTTFFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRITGFTTFFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKEKELFEIVKYAKQIHIERNM 719

## RESULT 3

S25383  
 parasporal crystal protein cryIIaI - Bacillus thuringiensis  
 N;Alternate names: delta-endotoxin; parasporal crystal protein cryV  
 C;Species: Bacillus thuringiensis  
 C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C;Accession: S25383  
 R;Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.  
 Mol. Microbiol. 6, 1211-1217, 1992  
 A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end  
 A;Reference number: S25383; MUID:92269582; PMID:1588820  
 A;Accession: S25383  
 A;Molecule type: DNA  
 A;Residues: 1-719 <TAI>  
 A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:G40289; PIDN:CAA44633.1; PID:G40290  
 C;Genetics:  
 A;Gene: cryV  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin

Query Match 93.8%; Score 3511; DB 2; Length 719;  
 Best Local Similarity 92.8%; Pred. No. 8.7e-242;  
 Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSNNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60  
 DB 1 MKLKNQDKHQSFSNNAKVDKISTDSLKNETDIELQNHEDCLKMEYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGSKQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALSDRLGLDALAVVHESLSWENNRNTRARSVVKNQYIALELMFVQKLPFAVSG 180  
 DB 121 RNKALTDRLGLDALAVVHDSLSWGNRNTRARSVYVKSQYIALELMFVQKLPFAVSG 180  
 QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFFNRQVERTRDYSCHCIKWYN 240  
 DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFFNRQVERAGDYSYHCVKWYS 240  
 QY 241 TGLNLRGNTAKSWRYNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTTSQLTREVYTDAL 300  
 DB 241 TGLNLRGNTAESWRYNQFRDMTLMVLDLVALFPSYDTQWYPIKTTAQLTREVYTDAL 300  
 QY 301 GTVHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMNW 360  
 DB 301 GTVHPHPSFTSTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSRWSNTQYMNW 360  
 QY 361 GGHRLSRPTGGALNTSTOGSTNTSINPVTLOFTSRDVRYESLAGLNLFITQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTGLNISTOGSTNTSINPVTLPFTSRDVRYESLAGLNLFITQPVNGVPR 420

QY 421 VDFHKKFPTLPASDNFYVLGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480  
DB 421 VDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGPQNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGCDLDYK 600  
DB 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGCDLDYK 600  
QY 601 TFRIGFTTTPFSFSDVQSTFTIGAMNFSNGNEVIIDRIEFVPEVTEYAEYDEFEKAQEKV 660  
DB 601 TFRIVGFTTTPFSFLDVQSTFTIGAMNFSNGNEVIIDRIEFVPEVTEYAEYDEFEKAQEKV 660  
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DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
RESULT 4  
I39814  
insecticidal protein cryVI - Bacillus thuringiensis  
C;Species: Bacillus thuringiensis  
C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
C;Accession: I39814  
R;Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.  
Appl. Environ. Microbiol. 61, 2402-2407, 1995  
A;Title: Distribution of cryV-type insecticidal protein genes in Bacillus thuringiensis  
tomocidus.  
A;Reference number: I39814; MUID:95314293; PMID:7793960  
A;Accession: I39814  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-719 <RES>  
A;Cross-references: GB:I36338; NID:g540281; PIDN:AAC36999.1; PID:g540282  
C;Genetics:  
A;Gene: cryVI  
C;Superfamily: parasporal crystal protein  
Query Match 93.6%; Score 3503; DB 2; Length 719;  
Best Local Similarity 92.5%; Pred. No. 3.2e-241;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;  
QY 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKNNNEDYLRNSESIDPVSASTI 60  
DB 1 MKLKNQDKHQSPSSNAKVDKISTDSLKNETDIELQNNHEDCLNSEYENVEPVSASTI 60  
QY 61 QTGIGIAGKILGTGVPAGQIASLYSFLGELWPKGKSQWEIFMEHVEEIIINOKILTYA 120  
DB 61 QTGIGIAGKILGTGVPAGQIASLYSFLGELWPKGKSQWEIFMEHVEEIIINOKISTYA 120  
QY 121 RNKALSDLRGLGDAVYHESLESWVENNTRARSVVKQYIALELMFVQKLPFAVSG 180  
DB 121 RNKALTDLKLGLGDAVYHDSLESWVGNRNTRARSVVKQYIALELMFVQKLPFAVSG 180  
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDRYSDHCICKWYN 240  
DB 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDRYSDHCICKWYS 240  
QY 241 TGLNLRGNTAKSWVRNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSLTREVYTTDAI 300  
DB 241 TGLNLRGNTAKSWVRNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSLTREVYTTDAI 300  
QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW 360  
DB 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW 360  
QY 361 GGHRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGNLFLTQPVNGVPR 420  
DB 361 GGHRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGNLFLTQPVNGVPR 420

QY 421 VDFHKKFPTLPASDNFYVLGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480  
DB 421 VDFHKKFVTHPIASDNFYYPGAGIGTQLODSENELPPEATGPQNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGCDLDYK 600  
DB 541 TGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGCDLDYK 600  
QY 601 TFRIGFTTTPFSFSDVQSTFTIGAMNFSNGNEVIIDRIEFVPEVTEYAEYDEFEKAQEKV 660  
DB 601 TFRIVGFTTTPFSFLDVQSTFTIGAMNFSNGNEVIIDRIEFVPEVTEYAEYDEFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
RESULT 5  
S00873  
parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis  
N;Alternate names: parasporal crystal protein cryA4  
C;Species: Bacillus thuringiensis subsp. thuringiensis  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: S00873  
R;Brizzard, B.L.; Whiteley, H.R.  
Nucleic Acids Res. 16, 2723-2724, 1988  
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t  
A;Reference number: S00873; MUID:88203216; PMID:3362680  
A;Accession: S00873  
A;Molecule type: DNA  
A;Residues: 1-1228 <BRI>  
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g58094;  
C;Genetics:  
A;Gene: cryA4  
A;Start codon: TTG  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin  
Query Match 62.0%; Score 2321.5; DB 2; Length 1228;  
Best Local Similarity 63.6%; Pred. No. 1e-156;  
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;  
QY 23 TDSLKNETDI-----ELKNNNEDYLRNSESIDPVSASTIQTGIGIAGKI 70  
DB 2 TSNRNKNEIINAVSNHSAQMDLLPDARIEDSLCIAEGNIDPVSASTVQTGINIAGRI 61  
QY 71 LGTLGVFFAGQIASLYSFLGELWPKGKSQWEIFMEHVEEIIINOKILTYARNKALSDLRG 130  
DB 62 LGVLGVFFAGQIASLYSFLGELWPKGKSQWEIFMEHVEEIIINOKITENARTALALQ 121  
QY 131 LGDALAVYHESLESWVENNTRARSVVKQYIALELMFVQKLPFAVSGEVPPLPIYA 190  
DB 122 LGDSFRAYQOSLEDWLENRDDARTRSVLTYQYIALELDLFLNAMPFLAIRNQEVPLMVYA 181  
QY 191 QAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDRYSDHCICKWYNLTGNNLRGNT 250  
DB 182 QAANLHLLLRDASIFGSEFGLTSQEIQRYYERQVTRDRYSDYCVWYNTGNSLRGNT 241  
QY 251 AKSWVRNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSLTREVYTTDAIGTVHPNQAF 310  
DB 242 AASWVRNQFRKDMTLMVLDLVALFPSYDTLVYPIKTTSLTREVYTTDAIGATGVN--MA 299  
QY 311 STTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNWGHRLSRPI 370  
DB 300 SNWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNWGHRLSRPI 359  
QY 371 GGALNTSTQGSTNTSINPVTLOFTSRDVRVRESLAGNLFLTQPVNGVPR 428  
DB 360 GGGLNTSTHGATNTSINPVTLOFTSRDVRVRESLAGNLFLTQPVNGVPR 419







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Db 228 RYNQFRRLTLVLDIVSLFPNYDSRYPIRTVSQLTREIYNPV-----L 273
QY 316 NNNAPSF-----SAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMWGGHRLBSRPIG 371
Db 274 ENFDGSRGSAQIEGS--IRSPHLMIDLNSITIYTDHR---GEY--YWSGHQIMASPVG 327
QY 372 -----GAL--NTSTQGSTNTSINPVTIQTSDRVYRTESLAGLNLFLTQPVNGVP 419
Db 328 FSGPEFTPLYGTMGNAAPQORIVAQLGGVYRTLSSTLYRRPFINIGIN---NQQLSVLD 384
QY 420 RVDHFKWFTPLPIASDNFYLYGAGVGTQLQDSNELPPETTGQPNVYESYSHRLSHIGLI 479
Db 385 GTEFAYG-----TSSNLPNAVYKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMF 436
QY 480 -----SASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTG 532
Db 437 RSGFNSSVSIIRAPMFSWIHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTG 496
QY 533 GDILRRNTGTGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATWN 592
Db 497 GDILRRNTGTGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATWN 556
QY 593 RGEDLDYKTRTIGFTTFFSDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAED 652
Db 557 SGNLQSGSFRTVGTFTTFFNFSGSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAED 616
QY 653 FEKAQKVTALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKQ 712
Db 617 LERAKAVNELFTSSNQIGLKTVDYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKR 676
QY 713 IHIERNM 719
Db 677 LSDERNL 683

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RESULT 12
A29125
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29125
R;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme
Bio/Technology 5, 807-813, 1987
A;Title: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-1156 <FIS>
A;Cross-references: UNIPROT:Q9F296; UNIPROT:Q93T21
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 39.6%; Score 1480.5; DB 2; Length 1156;
Best Local Similarity 46.5%; Pred. No. 6.9e-97;
Matches 310; Conservative 105; Mismatches 195; Indels 57; Gaps 12;

QY 76 VPFAGQIASLYSFIIGELWPKGSKQWEIFMEHVEEIIINQILTYARNKALSDLRGLGDAL 135
Db 51 VPGAGFVLGLVDIIWGIF--GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLESLNLY 107
QY 136 AVTHESLESWENRNNTARSVVKVQIALELMFVQKLPFAVSGEEVPLPIYAQAANL 195
Db 108 QIVAESFREWEDPTNPALEEMRIQFNDMNSALITAIPLFAVQVNYQVPLSVVQAANL 167
QY 196 HLLLLDASIFGKEWGLSASEISTFYNRQVVERTDYSDHCIKWNTGLNLRGTFNAKSWV 255
Db 168 HLSVLDRSVFVGQWGDAAATINSRYNDLRLIGNYTDHVRWNTGLERWVGDPDSRWI 227
QY 256 RYNQFRKDMTLMVLDLVALFPSTYDLYPIKTTSQLTSQREVVTDAIGTVHNPQAFSTTWY 315
Db 228 RYNQFRRLTLVLDIVSLFPNYDSRYPIRTVSQLTREIYNPV-----L 273

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QY 316 NNNAPSF-----SAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMWGGHRLBSRPIG 371
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QY 372 -----GAL--NTSTQGSTNTSINPVTIQTSDRVYRTESLAGLNLFLTQPVNGVP 419
Db 328 FSGPEFTPLYGTMGNAAPQORIVAQLGGVYRTLSSTLYRRPFINIGIN---NQQLSVLD 384
QY 420 RVDHFKWFTPLPIASDNFYLYGAGVGTQLQDSNELPPETTGQPNVYESYSHRLSHIGLI 479
Db 385 GTEFAYG-----TSSNLPNAVYKSGT--VDSLDEIPQNNVPPRQGFSHRLSHVSMF 436
QY 480 -----SASHVKALVYSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVVRGPGFTG 532
Db 437 RSGFNSSVSIIRAPMFSWIHRSABFNIIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTG 496
QY 533 GDILRRNTGTGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATWN 592
Db 497 GDILRRNTGTGDIRVNINPPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATWN 556
QY 593 RGEDLDYKTRTIGFTTFFSDVQSTFTIGAWNFSSGNEVYIDRIEFVVPVEVYEAED 652
Db 557 SGNLQSGSFRTVGTFTTFFNFSGSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAED 616
QY 653 FEKAQKVTALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKQ 712
Db 617 LERAKAVNELFTSSNQIGLKTVDYHIDQVSNLVESLSDEFYLDKRELFELVVKYAKR 676
QY 713 IHIERNM 719
Db 677 LSDERNL 683

RESULT 13
S02134
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai IC1)
N;Alternate names: delta-endotoxin IC1; entomocidal crystal protein
C;Species: Bacillus thuringiensis
A;Variety: strain aizawai IC1
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S02134; S04994
R;Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A;Title: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal
A;Reference number: S02134; MUID:89083518; PMID:3205732
A;Accession: S02134
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-1155 <HAI>
A;Cross-references: UNIPROT:P06578; EMBL:X13233; NID:G40277; PIDN:CAA31620.1; PID:G40278
A;Experimental source: strain aizawai IC1
R;Haider, M.Z.; Ellar, D.J.
J. Mol. Biol. 208, 183-194, 1989
A;Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes
A;Reference number: S04994; MUID:89362455; PMID:2769751
A;Accession: S04994
A;Molecule type: DNA
A;Residues: 429-449, 'A', 451-724 <HAW>
A;Cross-references: EMBL:X16315
A;Experimental source: strain aizawai IC1
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 39.1%; Score 1463.5; DB 2; Length 1155;
Best Local Similarity 46.0%; Pred. No. 1.1e-95;
Matches 307; Conservative 105; Mismatches 198; Indels 57; Gaps 12;

QY 76 VPFAGQIASLYSFIIGELWPKGSKQWEIFMEHVEEIIINQILTYARNKALSDLRGLGDAL 135
Db 51 VPGAGFVLGLVDIIWGIF--GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLESLNLY 107

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QY 136 AVYHESLESWVENNTRARSVVKNQYIALELMFVQKLPFAVSGEEVPLPIYAQAANL 195  
 Db 108 QIYAESFREWEADPTNPALREEMRIQFNDMSALTTAIPLFAVQNYQVPLLSVVYQAANL 167  
 QY 196 HLLLRDASIFGKWLGLSASEISTFYNRQVTRDYSCHIKWYNTGLNMLRGNTAKSWV 255  
 Db 168 HLSVLRDVSVFGQWGLDVAATINSRYNDLTRLIGNYTDHVRWYNTGLERWGPDSRDWI 227  
 QY 256 RYNQPRKMTLMVLDLVALFPSPYDTLVYPKTTSQLTREVYTDAGTVHPNQAFASSTWY 315  
 Db 228 RYNQPRRELTTLVLDIVSLFPNYSRYPIRTVSQLTREIYNPV-----L 273  
 QY 316 NNAAPSF-----SAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMWGGHRLSPIG 371  
 Db 274 ENFDGSRGSAQGLEGS-IRSPHLMOLINSIITYTDAHR---GEY--YWSGHQIMASPVG 327  
 QY 372 -----GAL-NTSQGSTNTSINPVTLOFTSRDVRVTESLAGLNLFLTOPVNGVP 419  
 Db 328 FSGPEFTFPLYGTMGNAAPQORIIVAQLGQGVYRTLSTLYRRPFNIGIN---NOQLSVLD 384  
 QY 420 RVDHFKWFTPLPIASDNFYLYGAGVGTQLODSENELPPTTQPNYESYSHRLSHIGLI 479  
 Db 385 GTEFAYG-----TSSNLPASAVYRKSGT--VDSLDEIPPNQNNVPPRQGFHRLSHVSMF 436  
 QY 480 -----SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTG 532  
 Db 437 RSGPNSSVSIIRPFMSWIHRSAEFNNIPSSQITQIPLTKSTNLGSGTSVVKGPFTG 496  
 QY 533 GDILRTNTGTGDIRVNNPFPQAQRYRIRYASTTDLQFHTSINGKAINQGNFSATWN 592  
 Db\* 497 GDILARTSPQISITLRVNTAPLSQRYRIRYASTTNLQFHTSIDGRINQGNFSATWS 556  
 QY 593 RGEDLDYKTPRTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVVEVTEAEYD 652  
 Db 557 SGSNLQSGFRIVGFTTTPNFSGSVFTLSAHVFNCSGNEVYIDRIEFVPAEVTFEAEYD 616  
 QY 653 FEKAQEKVTAFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQ 712  
 Db 617 LERAKAVNELFTSSNQIGLKTVDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQ 676  
 QY 713 IHIERNM 719  
 Db 677 LSDERNL 683  
 RESULT 14  
 A41052  
 parasporal crystal protein cryAel - Bacillus thuringiensis (strain alest1)  
 C;Species: Bacillus thuringiensis  
 C;Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 09-Jul-2004  
 C;Accession: A41052  
 R;Lee, C.S.; Aronson, A.I.  
 J. Bacteriol. 173, 6635-6638, 1991  
 A;Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp  
 A;Reference number: A41052; MUID:92011442; PMID:1655719  
 A;Accession: A41052  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1181 <LEE>  
 A;Cross-references: UNIPROT:Q03748; GB:M65252; NID:G142874; PIDN:AAA22410.1; PID:G142875  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin  
 Query Match 39.1%; Score 1463.5; DB 2; Length 1181;  
 Best Local Similarity 45.9%; Pred. No. 1.2e-95;  
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 QY 76 VPFAGQIASLYSFLIGELWPKGKSQWEIEMEHVEEIIINOKILTYARNKALSDRLGDL 135  
 Db 51 VPGAGFVLGLIDLIWGFV---GPSQWDAFLVQIEQLISQRIEEFARNQAIISRLGSLNLY 107  
 QY 136 AVYHESLESWVENNTRARSVVKNQYIALELMFVQKLPFAVSGEEVPLPIYAQAANL 195

Db 108 QIYAEAFREWEADPTNPALREEMRIQFNDMSALTTAIPLFTVQNYQVPLLSVVYQAANL 167  
 QY 196 HLLLRDASIFGKWLGLSASEISTFYNRQVTRDYSCHIKWYNTGLNMLRGNTAKSWV 255  
 Db 168 HLSVLRDVSVFGQWGLDVAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWGPDSRDWI 227  
 QY 256 RYNQPRKMTLMVLDLVALFPSPYDTLVYPKTTSQLTREVYTDAGTVHPNQAFASSTWY 315  
 Db 228 RYNQPRRELTTLVLDIVSLFPNYSRYPIRTVSQLTREIYNPV-----L 273  
 QY 316 NNAAPSF-----IRSPHLLDFLEKVTIYSLSRWSNTQYMMWGGHRLSPIG- 371  
 Db 274 ENFDGSRGSAQRIEQSIRSPHLMOLINSIITYT--DAHGGYVY---WSGHQIMASPVG 328  
 QY 372 -----GAL-NTSQGSTNTSINPVTLOFTSRDVRVTESLAGLNLFLTOPVNGVP 420  
 Db 329 SGPEFTFPLYGTMGNAAPQORIIVAQLGQGVYRTLSTLYRRPFNIGIN---NQLSVLDG 385  
 QY 421 VDFHFKWFTPLPIASDNFYLYGAGVGTQLODSENELPPTTQPNYESYSHRLSHIGLI- 479  
 Db 386 TEFAYG-----SSSNLPASAVYRKSGT--VDSLDEIPPNQNNVPPRQGFHRLSHVSMF 437  
 QY 480 -----SASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSGAAVVRGPGFTG 533  
 Db 438 SGFSNSSSVSIIRAPMFSWIHRSAEFNNIPSSQITQIPLTKSTNLGSGTSVVKGPFTG 497  
 QY 534 DILRTNTGTGDIRVNNPFPQAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNR 593  
 Db 498 DILRTSPQISITLRVNTAPLSQRYRIRYASTTNLQFHTSIDGRINQGNFSATMSS 557  
 QY 594 GEDLDYKTPRTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVVEVTEAEYD 653  
 Db 558 GGNLQSGFRIVGFTTTPNFSGSVFTLSAHVFNCSGNEVYIDRIEFVPAEVTFEAEYDL 617  
 QY 654 EKAQEKVTAFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQI 713  
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 QY 714 IHIERNM 719  
 Db 678 SDERNL 683  
 RESULT 15  
 I39838  
 parasporal crystal protein - Bacillus thuringiensis  
 C;Species: Bacillus thuringiensis  
 C;Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I39838  
 R;Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.  
 J. Biotechnol. 6, 307-322, 1987  
 A;Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki  
 A;Reference number: I39838  
 A;Accession: I39838  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1155 <RES>  
 A;Cross-references: UNIPROT:P06578; GB:M37263; NID:G142885; PIDN:AAA22420.1; PID:G142886  
 C;Superfamily: parasporal crystal protein  
 C;Keywords: delta-endotoxin  
 Query Match 39.1%; Score 1461.5; DB 2; Length 1155;  
 Best Local Similarity 46.2%; Pred. No. 1.6e-95;  
 Matches 308; Conservative 103; Mismatches 199; Indels 57; Gaps 12;  
 QY 76 VPFAGQIASLYSFLIGELWPKGKSQWEIEMEHVEEIIINOKILTYARNKALSDRLGDL 135  
 Db 51 VPGAGFVLGLVDIIWGFV---GPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGSLNLY 107  
 QY 136 AVYHESLESWVENNTRARSVVKNQYIALELMFVQKLPFAVSGEEVPLPIYAQAANL 195  
 Db 108 QIYAESFREWEADPTNPALREEMRIQFNDMSALTTAIPLFAVQNYQVPLLSVVYQAANL 167





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:52:12 ; Search time 98.4365 Seconds  
(without alignments)  
4202.652 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPDKHQSLSNAKVDK.....KRELFEIVKYAKQIHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3742	100.0	719	1	CIIB_BACTE
2	3598	96.2	719	2	Q9F0P8
3	3546	94.8	719	1	CIIC_BACTU
4	3520	94.1	719	1	CIIA_BACTK
5	3520	94.1	719	2	Q6X181
6	3520	94.1	719	2	AAP86782
7	3515	93.9	719	2	Q93NJ5
8	3514	93.9	719	2	O85796
9	3512	93.9	719	2	CAC85964
10	3510	93.8	719	2	Q8KV61
11	3311	88.5	719	1	CIID_BACTU
12	2459	65.7	1229	1	CIIB_BACTU
13	2459	65.7	1233	1	CIIC_BACTM
14	2322.5	62.1	1228	2	Q93T75
15	2321.5	62.0	1228	1	CIIB_BACTK
16	2313.5	61.8	1228	2	Q93NM5
17	2243	59.9	849	2	Q6PYW8
18	2243	59.9	849	2	AAS93797
19	2243	59.9	1227	1	CIIE_BACTU
20	2129	56.9	1231	2	Q8KNY2
21	2116	56.5	1231	1	CIID_BACTZ
22	1963	52.5	1215	1	CIIX_BACTM
23	1817	48.6	381	2	Q45740
24	1670	44.6	1144	2	Q8KZL7
25	1657.5	44.3	1157	1	C8AA_BACUK
26	1507	40.3	1157	1	C9CA_BACTO
27	1503.5	40.2	1166	1	CIIC_BACTU
28	1497.5	40.0	1169	1	CIIF_BACTM
29	1491.5	39.9	1174	2	Q45749
30	1484.5	39.7	1169	1	C8BA_BACUK
31	1480.5	39.6	1155	1	CIAB_BACTK

32	1480.5	39.6	1155	2	Q7BE98
33	1480.5	39.6	1155	2	Q9F296
34	1480.5	39.6	1155	2	AAN76494
35	1480.5	39.6	1155	2	AAO13302
36	1475.5	39.4	1156	2	Q6GUA7
37	1473.5	39.4	1118	2	Q9AM83
38	1470.5	39.3	793	2	Q6PYW7
39	1470.5	39.3	793	2	AAS93798
40	1470.5	39.3	1177	2	Q6EIX3
41	1468.5	39.2	1155	2	Q93T21
42	1468	39.2	1167	1	CIJA_BACTU
43	1463.5	39.1	1181	1	CIIE_BACTL
44	1459	39.0	1180	2	Q9SSV8
45	1457	38.9	1176	2	Q7WZT9

ALIGNMENTS

RESULT 1

CIIB\_BACTE  
ID CIIB\_BACTE STANDARD; PRT; 719 AA.  
AC Q45709;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryIIb (insecticidal delta-endotoxin  
DE CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name: cryIIb; Synonyms: cryII(b), cryV, cryV465;  
OS Bacillus thuringiensis (subsp. entomocidus).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1436;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BP465;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
RT thuringiensis and cloning of cryV-type genes from Bacillus  
RT thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
RT entomocidus.";  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
CC 1- FUNCTION: Promotes cell-to-cell lysis by binding to the midgut  
CC epithelial cells of certain coleopteran and lepidopteran species.  
CC Active on Plutella xylostella but not on Bombyx mori.  
CC 1- DEVELOPMENTAL STAGE: The crystal protein is produced during  
CC sporulation and is accumulated both as an inclusion and as part of  
CC the spore coat.  
CC 1- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
CC terminus.  
CC 1- SIMILARITY: Belongs to the delta endotoxin family.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; U07642; AAA82114.1; -  
CC PIR; I40590; I40590.  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal\_bind\_Like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
CC Sporulation; Toxin.  
CC SEQUENCE 719 AA; 81295 MW; E8210ABEAE97688E CRC64;

Query Match 100.0%; Score 3742; DB 1; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-250;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K L K N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60  
 D B 1 M K L K N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q K I L T Y A 120  
 D B 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q K I L T Y A 120

QY 121 R N K A L S D L R G L G D A L A V V H E S L E S W E N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
 D B 121 R N K A L S D L R G L G D A L A V V H E S L E S W E N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240  
 D B 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240

QY 241 T G L N L R G N T A K S W R Y N Q F R K D M T L M V L D L V A L P S Y D T L V P I K T S Q L T R E V Y T D A I 300  
 D B 241 T G L N L R G N T A K S W R Y N Q F R K D M T L M V L D L V A L P S Y D T L V P I K T S Q L T R E V Y T D A I 300

QY 301 G T V H P N Q A F A S T T W Y N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N M W 360  
 D B 301 G T V H P N Q A F A S T T W Y N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N M W 360

QY 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420  
 D B 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420

QY 421 V D F H W K F P T L P I A S D N F Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 D B 421 V D F H W K F P T L P I A S D N F Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 D B 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540

QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 D B 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

QY 601 T F R T I G F T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 D B 601 T F R T I G F T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719  
 D B 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719

## RESULT 2

Q9F0P8 PRELIMINARY; PRT; 719 AA.  
 AC Q9F0P8;  
 DT 01-MAR-2001 (TRENDELrel. 16, Created)  
 DT 01-MAR-2001 (TRENDELrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TRENDELrel. 26, Last annotation update)  
 DE Cr11.

GN Name=cr11;  
 OS Bacillus thuringiensis.  
 OG Plasmid pBTC19.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BTC007;  
 RX MEDLINE=22837682; PubMed=12957903;  
 RA Song F., Zhang J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,  
 RA Hu Y., Li G., Huang D.;  
 RT "Identification of cr11-type genes from Bacillus thuringiensis

RT strains and characterization of a novel cr11-type gene.";  
 RL Appl. Environ. Microbiol. 69:5207-5211 (2003).  
 DR EMBL; AF211190; AAG43526.1; --

DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid.

SQ SEQUENCE 719 AA; 81024 MW; 7E17481922C435E6 CRC64;

Query Match 96.2%; Score 3598; DB 2; Length 719;  
 Best Local Similarity 95.1%; Pred. No. 4.9e-240;  
 Matches 684; Conservative 23; Mismatches 12; Indels 0; Gaps 0;

QY 1 M K L K N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60  
 D B 1 M K L K N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60

QY 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q K I L T Y A 120  
 D B 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q K I L T Y A 120

QY 121 R N K A L S D L R G L G D A L A V V H E S L E S W E N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
 D B 121 R N K A L S D L R G L G D A L A V V H E S L E S W I K R N N A R A T S V V K S Q Y I A L E L L F V Q K L P S F A V S G 180

QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240  
 D B 181 E E V P L L P I Y A Q A A N L H L L L R D A S V F G K E W G L S N S Q I S T F Y N R Q V E R T S D H C V K W Y S 240

QY 241 T G L N L R G N T A K S W R Y N Q F R K D M T L M V L D L V A L P S Y D T L V P I K T S Q L T R E V Y T D A I 300  
 D B 241 T G L N L R G N T A E S W R Y N Q F R K D M T L M V L D L I A L P S Y D T L V P I K T S Q L T R E V Y T D A I 300

QY 301 G T V H P N Q A F A S T T W Y N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N M W 360  
 D B 301 G T V H N A S F A S T T W Y N N A P S F A I E A S A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360

QY 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420  
 D B 361 G G H R L E F R T I G G V L N T S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G N L F L T Q P V N G V P R 420

QY 421 V D F H W K F P T L P I A S D N F Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 D B 421 V D F H W K F A T L P I A S D N F Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480

QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540  
 D B 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540

QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 D B 541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

QY 601 T F R T I G F T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 D B 601 T F R T V G F T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719  
 D B 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719

## RESULT 3

Cr11c\_BACTu

ID Cr11c\_BACTu STANDARD; PRT; 719 AA.

087404;  
16-OCT-2001 (Rel. 40, Created)  
16-OCT-2001 (Rel. 40, Last sequence update)  
05-JUL-2004 (Rel. 44, Last annotation update)  
Pesticidal crystal protein cryIIc (insecticidal delta-endotoxin  
CryII(c)) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIIc; Synonyms=cryII(c);  
OS Bacillus thuringiensis.  
OG Plasmid.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C18 / Egypt;  
RA Osman Y.A., Madkour M.A., Bulla L.A. Jr.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut  
epithelial cells of insects.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
sporulation and is accumulated both as an inclusion and as part of  
the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
CC -----  
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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC EMBL; AF056933; AAC62933.1; --  
DR HSP; P02965; 1C1Y.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal bind like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_N; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
KW Plasmid; Sporulation; Toxin.  
SQ SEQUENCE 719 AA; 81210 MW; 8370B3F06B905DFF CRC64;  
  
Query Match 94.88; Score 3546; DB 1; Length 719;  
Best Local Similarity 95.08; Pred. No. 1.9e-236;  
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;  
  
QY 1 MKLKNPKHQSSNAKVDKIATDSLKNETDIELKNNMEDYLRMSEHESIDPFVSASTI 60  
Db 1 MKLKNPKHQTISSNAKVDKIATDSLKNETDIELKNNMEDYLRMSEHESIDPFVSASTI 60  
  
QY 61 QTGIGIAGKIILGTLPVFPAGQIASLYSFIIGELWPXKQWEIEMHVEEIIINQKILTYA 120  
Db 61 QTGIGIAGKIILGTLPVFPAGQIASLYSFIIGELWPXKQWEIEMHVEEIIINRKISITYA 120  
  
QY 121 RNKALSDRLGDLALAVYHESLESWENRNTRASVVKNQYIALELMPVQKLPSFAVSG 180  
Db 121 RNKALTDLKLGDALAVYHESLESWVGNRNTRASVVKNQYIALELMPVQKLPSFAVSG 180  
  
QY 181 EEPVLLPIYAQAANLHLLLDASIFGKWLGLSASEISTFYNQVERTRDYSDECIKWYN 240  
Db 181 EEPVLLPIYAQAANLHLLLDASIFEKGLSASEISTFYNQVERTRDYSYHCVKWNN 240  
  
QY 241 TGLNNLRGTNAKSWVRNQFRKMTLMVLVALPSPDYTLVYPIKTTSQLTRVYTDAI 300  
Db 241 TGLNNLRATNGOSWVRNQFRKDIEMVLVLRVPSPDYTLVYPIKTTSQLTRVYTDAI 300  
  
QY 301 GTVHPNQAFASITWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360  
Db 301 GTVDPNQALRSITWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYNNMW 360

QY 361 GGHRLSRPIGGALNTSTCGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR 420  
Db 361 GGHRLSRPIGGALNTSTCGSTNTSINPVTLOFTSRDVRTESWAGLNFLTQPVNGVPR 420  
  
QY 421 VDFHWKFPPLPIASDNFYLYGAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFPPLPIASDNFYLYGAGVGTQLQDSENELPPETTGQPNYESYSHRLSHIGLIS 480  
  
QY 481 ASHVKALVYSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTN 540  
Db 481 GSHVKALVYSWTHRSADRTNITPNSITQIPLVKAFNLSSGAAVVRGPGTGGHILRRTK 540  
  
QY 541 TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGDDLDYK 600  
Db 541 SGTFGHIRVNIINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATNWRGDDLDYK 600  
  
QY 601 TFRITGFTTFFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDFEKAQEKV 660  
Db 601 TFRITGFTTFFSFSDVQSTFTIGAWNFSSGNEVYIGRIEFPVVEVYEAEDFEKAQEKV 660  
  
QY 661 TALFTSTNPRGLKTDVDYHIDQVSNLVESLSDEFYLDKRELFELVYKAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVDYHIDQVSNLVESLSDELKRELFELVYKAKQIHIERNM 719  
  
RESULT 4  
CLIA\_BACTX STANDARD; PRT; 719 AA.  
ID Q45752; P71092; Q45750; Q45751; Q45756;  
AC 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin  
CryII(a)) (crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIIa; Synonyms=cryII(a), cryv, cryvI, CGCryv;  
OS Bacillus thuringiensis (subsp. kurstaki).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSIR732;  
RX MEDLINE=93298009; PubMed=8517758;  
RA Gleave A.P., Williams R., Hedges R.J.;  
RT "Screening by polymerase chain reaction of Bacillus thuringiensis  
serotypes for the presence of cryV-like insecticidal protein genes and  
characterization of a cryV gene cloned from B. thuringiensis subsp.  
kurstaki.";  
RL Appl. Environ. Microbiol. 59:1683-1687(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JHCC4835;  
RX MEDLINE=92269582; PubMed=1588820;  
RA Taylor R., Tippet J., Gibb G., Pells S., Pike D., Jordan L., Ely S.;  
RT "Identification and characterization of a novel Bacillus thuringiensis  
delta-endotoxin entomocidal to coleopteran and lepidopteran larvae.";  
RL Mol. Microbiol. 6:1211-1217(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HD-1;  
RX MEDLINE=95314293; PubMed=7793960;  
RA Shin B.-S., Park S.-H., Choi S.-K., Koo B.T., Lee S.T., Kim J.I.;  
RT "Distribution of cryV-type insecticidal protein genes in Bacillus  
thuringiensis and cloning of cryV-type genes from Bacillus  
thuringiensis subsp. kurstaki and Bacillus thuringiensis subsp.  
entomocidus.";  
RL Appl. Environ. Microbiol. 61:2402-2407(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AB88;  
RX MEDLINE=96178985; PubMed=8606196;  
RA Kostichka K., Warren G.W., Mullins M., Mullins A.D., Palekar N.V.,  
RA Craig J.A., Koziel M.G., Estruch J.J.;  
RT "Cloning of a cryV-type insecticidal protein gene from Bacillus

thuringiensis: the cryV-encoded protein is expressed early in stationary phase";  
 J. Bacteriol. 178:2141-2144 (1996).  
 [5]

RP SEQUENCE FROM N.A.

RA Selvapandian A., Bhatnagar R.K.;  
 "Isolation, cloning and expression of cryV gene";  
 Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Promotes colloidomotic lysis by binding to the midgut  
 epithelial cells of certain coleopteran and lepidopteran species.  
 CC Active on Plutella xylostella and Bombyx mori.

CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during  
 sporulation and is accumulated both as an inclusion and as part of  
 the spore coat.

CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-  
 terminus.

CC -!- SIMILARITY: Belongs to the delta endotoxin family.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; M98544; AAA22354.1; -  
 DR EMBL; X62821; CAA44633.1; -  
 DR EMBL; L36338; AAC36999.1; -  
 DR EMBL; L49391; AAB00958.1; -  
 DR EMBL; Y08920; CAA70124.1; -  
 DR PIR; I39815; I39815.  
 DR HSP; S25383; S25383.  
 DR HSP; P02965; ICIV.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 FT VARIANT 159 159 K -> R (in strain 61).  
 FT VARIANT 233 233 D -> Y (in strain JHCC4835 and strain HD-  
 FT VARIANT 1).  
 FT VARIANT 443 443 A -> V (in strain AB88).  
 FT VARIANT 711 712 KQ -> NE (in strain HD-1 and strain 61).  
 SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;

Query Match 94.1%; Score 3520; DB 1; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 1.2e-234;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHSIDPFVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALSDLRGLGDALAVYHESLESWENRNNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLXGLGDALAVYHDSLESWGNRNNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERTRDYSCHICKYN 240  
 DB 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERTRDYSCHICKYNYS 240  
 QY 241 TGLNLRGNTAKSWRYNQFRDMLMVLVALPFSYDILVPIKTTSQLTREYITDAI 300  
 DB 241 TGLNLRGNTAESWRYNQFRDMLMVLVALPFSYDITQMPYIKTTAQLTREYITDAI 300

QY 301 GTVHPNQAFASFTTWNNNAPSFAIEAAVIRSPHLDDLEKVTIYSLLSRWSNTQYMMNW 360  
 DB 301 GTVHPNPSFTSTTWNNNAPSFAIEAAVIRSPHLDDLEKVTIYSLLSRWSNTQYMMNW 360  
 QY 361 GGHRLSRPIGGALNTSTQGSTNTSINPVTLOFTSRDVRYESLAGLNLFQTQPVNGVPR 420  
 DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRYESLAGLNLFQTQPVNGVPR 420  
 QY 421 VDFHMKFPTLPIASDNFVYLGAVGVTGLODSENELPPTTGPQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHMKFVTHPIASDNFYPGYAGIGTQLODSENELPPEATGPQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAYVRGPGTGGDILRRTN 540  
 DB 481 ASHVKALVSWTHRSADRNTIENPNSITQIPLVKAFNLSSGAAYVRGPGTGGDILRRTN 540  
 QY 541 TGTGDIRVNNPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDDLDYK 600  
 DB 541 TGTGDIRVNNPFAQRYRVRIRYASTDLOPHTSINGKAINQGNFSATMNRGDDLDYK 600  
 QY 601 TFRITGTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKV 660  
 DB 601 TFRITVGTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEVYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNRGLKTDVKDHYHIDOVSNLVESLSDEFYLDKRELFELVYKAKQIHIERNM 719  
 DB 661 TALFTSTNRGLKTDVKDHYHIDOVSNLVESLSDEFYLDKRELFELVYKAKQIHIERNM 719

RESULT 5

Q6X181 PRELIMINARY; PRT; 719 AA.

ID Q6X181  
 AC Q6X181;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE CrvII.  
 GN Name=cryII;  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY262167; AAP86782.1; -  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 SQ SEQUENCE 719 AA; 81216 MW; 3627B5A6C25DAFF5 CRC64;

Query Match 94.1%; Score 3520; DB 2; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 1.2e-234;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHSIDPFVSASTI 60  
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKMSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALSDLRGLGDALAVYHESLESWENRNNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 DB 121 RNKALTDLXGLGDALAVYHDSLESWGNRNNTRARSVVKQYIALELMFVKQLPSFAVSG 180  
 QY 181 BEVPLLPYQAANLHLLLRDASIFGKEWGLSSSISTFYNRQVERTRDYSCHICKYN 240

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Db 181 EVVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSDHCWKYS 240
Qy 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALPSPSYDTLVYPIKTTSQLTREYVTDAL 300
Db 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALPSPSYDTLVYPIKTTSQLTREYVTDAL 300
Qy 301 GTVHPNQAFASHTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMW 360
Db 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMW 360
Qy 361 GGHRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDVTYRTESLAGNLFQTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLOFTSRDVTYRTESLAGNLFQTQPVNGVPR 420
Qy 421 VDFHWKFPPTLPASDNFYLYGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYLYGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600
Qy 601 TERTIGTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEFAEKAQEKV 660
Db 601 TERTVGTFTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEFAEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDKRELFEIVKYAKQIHIERNM 719

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RESULT 6

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AAP86782 PRELIMINARY; PRT; 719 AA.
ID AAP86782;
AC AAP86782;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE CryII.
GN CryII.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T01 328;
RA Espindola R., Lemos M.V.F., Lemos E.G.M., Sena J.A.D.;
RT "Complete sequence of cryII gene of isolate T01 328 from Bacillus
RL thuringiensis from Cubatao (SP - Brazil) soil."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY262167; AAP86782.1;
SQ SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5 CRC64;

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Query Match 94.1%; Score 3520; DB 2; Length 719;
Best Local Similarity 92.9%; Pred. No. 1.2e-234;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MKLKVPDKHQSLSSNAKVDKIATDSLKNETDIELKMNNEIDYLRMSEHSDIPFVSASTI 60
Db 1 MKLKQDKHQSPSSNAKVDKISTSLKNETDIELQINHEIDCLKMYENVEPFVSASTI 60
Qy 61 QTGIGIACKILGTGVFPAGQIASLYSFILGELWPKGKSWEIFMHEVHEIINQKILTYA 120
Db 61 QTGIGIACKILGTGVFPAGQVASLYSFILGELWPKGKQWEIFMHEVHEIINQKISTYA 120
Qy 121 RNKALSDIRGLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180

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Db 121 RNKALTDLKLGLGDALAVYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAVSG 180
Qy 181 EVVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERTRDYSDHCWKYN 240
Db 181 EVVPLPIYAQAANLHLLLRDASIFGKWLSSSEISTFYNRQVERAGDYSDHCWKYS 240
Qy 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALPSPSYDTLVYPIKTTSQLTREYVTDAL 300
Db 241 TGLNNLRGTNAKSWRYNQFRDMTLMVLDLVALPSPSYDTLVYPIKTTSQLTREYVTDAL 300
Qy 301 GTVHPNQAFASHTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMW 360
Db 301 GTVHPHPSFTSTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMMW 360
Qy 361 GGHRLSRPIGALNTSTQGSTNTSINPVTLOFTSRDVTYRTESLAGNLFQTQPVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLOFTSRDVTYRTESLAGNLFQTQPVNGVPR 420
Qy 421 VDFHWKFPPTLPASDNFYLYGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
Db 421 VDFHWKFPVTHPIASDNFYLYGYAGVGTQLODSENELPPTTGPQNYESYSHRLSHIGLIS 480
Qy 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540
Qy 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600
Db 541 TGTFGDIRVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600
Qy 601 TERTIGTTPFSFSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEFAEKAQEKV 660
Db 601 TERTVGTFTPFSLDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVTEAEYDEFAEKAQEKV 660
Qy 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDKRELFEIVKYAKQIHIERNM 719
Db 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFLDKRELFEIVKYAKQIHIERNM 719

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RESULT 7

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Q93NJ5 PRELIMINARY; PRT; 719 AA.
ID Q93NJ5;
AC Q93NJ5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CryIIa.
GN Name=CryIIa;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang J., Gu A., Huang D., Li G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373207; AAK66742.1;
DR HSSP; P02965; 1CIY.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 719 AA; 81225 MW; C629DF2C44827241 CRC64;

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Query Match 93.9%; Score 3515; DB 2; Length 719;
Best Local Similarity 92.8%; Pred. No. 2.7e-234;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

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QY 1 M K L N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60  
 D b 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K N S E Y E N V E P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P F A G Q A S L Y S F I L G E L M P K G S O W E I F M E H V E E I I N Q I L T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P F A G Q A S L Y S F I L G E L M P K G S O W E I F M E H V E E I I N Q I S T Y A 120  
 QY 121 R N K A L S D L R G L G D A L A V H S E S W E N R N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L G D A L A V H S E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I V A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F N R Q V E R T R D Y S D H C I K W N 240  
 D b 181 E E V P L L P I V A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F N R Q V E R A G D Y S D H C V K W Y S 240  
 QY 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S O L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P H P S T S T T W Y N N N A P S F A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 QY 361 G G H L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L F T S R D V Y T E S L A G L N L F L T H F V N G V P R 420  
 QY 421 V D F H W K F P T L P I A S D N F Y L G V A G V G T Q L O D S E N E L P P E T T G O P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
 D b 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T I G T T P F S D V S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 D b 601 T F R T V G F T T P F S F L D V S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719

RESULT 8

O85796 PRELIMINARY; PRT; 719 AA.  
 AC O85796;  
 DT 01-NOV-1998 (TREMELrel. 08, Created)  
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
 DE Insecticidal protein.  
 GN Name=crv101;  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Plasmid large plasmid.  
 CG Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=29339;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S101;  
 RA Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF076953; AAC26910.1; -  
 DR HSSP; P02965; 1CIY.  
 DR GO; GO:0005102; F:receptor binding; IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Plasmid.  
 SQ SEQUENCE 719 AA; 81230 MW; 42746D478359BBA7 CRC64;

Query Match 93.9%; Score 3514; DB 2; Length 719;  
 Best Local Similarity 92.8%; Pred. No. 3.2e-234;  
 Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 M K L N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60  
 D b 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K N S E Y E N V E P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P F A G Q A S L Y S F I L G E L M P K G S O W E I F M E H V E E I I N Q I L T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P F A G Q A S L Y S F I L G E L M P K G S O W E I F M E H V E E I I N Q I S T Y A 120  
 QY 121 R N K A L S D L R G L G D A L A V H S E S W E N R N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
 D b 121 R N K A L T D L K G L G D A L A V H S E S W G N R N N T R A R S V V K S Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E E V P L L P I V A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F N R Q V E R T R D Y S D H C I K W N 240  
 D b 181 E E V P L L P I V A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F N R Q V E R A G D Y S D H C V K W Y S 240  
 QY 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S O L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300  
 QY 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N W 360  
 D b 301 G T V H P H P S T S T T W Y N N N A P S F A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360  
 QY 361 G G H L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L F T S R D V Y T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F P T L P I A S D N F Y L G V A G V G T Q L O D S E N E L P P E T T G O P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G O P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
 D b 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T I G T T P F S D V S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 D b 601 T F R T V G F T T P F S F L D V S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N M 719

RESULT 9

CAC85964  
 ID CAC85964 PRELIMINARY; PRT; 719 AA.  
 AC CAC85964;  
 DT 02-MAR-2004 (TREMELrel. 27, Created)  
 DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)  
 DE Delta-endotoxin.  
 GN CRYIIA.  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

OC	Bacillus cereus group; Bacillus thuringiensis.	
OX	NCBI_TaxID=29339;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BNS3;	
RA	Tounsi S., Zouari N., Jaoua S.;	
RT	"Cloning and study of the expression of a novel cryIIa-type gene from	
RT	Bacillus thuringiensis subsp. kurstaki.",	
RL	J. Appl. Microbiol. 95:23-28(2003).	
DR	EMBL; AJ315121; CAC85964.1; -.	
SQ	SEQUENCE 719 AA; 81203 MW; 8676E5A6C25DAFE8 CRC64;	
Query Match	93.9%; Score 3512; DB 2; Length 719;	
Best Local Similarity	92.6%; Pred. No. 4.4e-234;	
Matches 666;	Conservative 32; Mismatches 21; Indels 0; Gaps 0;	
QY	1 M K L K N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60	
Db	1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K M S E Y E N V E P F V S A S T I 60	
QY	61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G K S Q W E I F M E H V E E I I N Q K I L T Y A 120	
Db	61 Q T G I G I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120	
QY	121 R N K A L S D L R G L G D A L A Y H S E S W E N R N N T R A R S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180	
Db	121 R N K A L T D L K G L G D A L A Y H D S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180	
QY	181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240	
Db	181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240	
QY	241 T G L N N L R G T N A K S W R Y N Q F R K D M T L M V D L V A L F P S Y D L V P I K T T S Q L T R E V Y T D A I 300	
Db	241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V D L V A L F P S Y D Q M Y P I K T T A Q L T R E V Y T D A I 300	
QY	301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L D F L E K V T I Y S L S R W S N T Q Y M N M W 360	
Db	301 G T V H P S F T S T T W Y N N N A P S F A I E A A V V R N P H L D F L E Q V T I Y S L S R W S N T Q Y M N M W 360	
QY	361 G G H R L E S R P I G G A L N T S T Q S T N T S I N P V T L Q F T S R D V R T E S L A G L N L F L T O P V N G V P R 420	
Db	361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V T L P F T S R D V R T E S L A G L N L F L T O P V N G V P R 420	
QY	421 V D F H W K F P T L P I A S D N F Y Y L G V A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480	
Db	421 V D F H W K F Y T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480	
QY	481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T T G G D I L R R T N 540	
Db	481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T T G G D I L R R T N 540	
QY	541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600	
Db	541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600	
QY	601 T F R T I G T T P F S D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660	
Db	601 T F R T V G T T P F S D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660	
QY	661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719	
Db	661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719	
RESULT 10		
Q8KY61	PRELIMINARY; PRT; 719 AA.	
ID	Q8KY61	
AC	Q8KY61;	
DT	01-OCT-2002 (TrEMBLrel. 22, Created)	
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Cry.	

OS	Bacillus thuringiensis.	
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
OX	NCBI_TaxID=1428;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Porcar M., Martinez C., Caballero P.;	
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF278797; AAM73516.1; -.	
DR	PIR; B42459; B42459.	
DR	HSSP; P02965; LC1Y.	
DR	GO; GO:0005102; F:receptor binding; IEA.	
DR	GO; GO:0006952; P:defense response; IEA.	
DR	GO; GO:0009405; P:pathogenesis; IEA.	
DR	InterPro; IPR001178; Endotoxin.	
DR	InterPro; IPR005638; endotoxin_C.	
DR	InterPro; IPR005639; endotoxin_N.	
DR	InterPro; IPR008979; Gal_bind_like.	
DR	Pfam; PF03944; Endotoxin_C; 1.	
DR	Pfam; PF00555; Endotoxin_M; 1.	
DR	Pfam; PF03945; Endotoxin_N; 1.	
SQ	SEQUENCE 719 AA; 80984 MW; 84F1287246264473 CRC64;	
Query Match	93.8%; Score 3510; DB 2; Length 719;	
Best Local Similarity	92.8%; Pred. No. 6e-234;	
Matches 667;	Conservative 31; Mismatches 21; Indels 0; Gaps 0;	
QY	1 M K L K N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H S I D P F V S A S T I 60	
Db	1 M K L K N P D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I H E D C L K I S E Y E N V E P F V S A S T I 60	
QY	61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G K S Q W E I F M E H V E E I I N Q K I L T Y A 120	
Db	61 Q T G I S I A G K I L G T L G V P F A G Q V A S L Y S F I L G E L W P K G K N Q W E I F M E H V E E I I N Q K I S T Y A 120	
QY	121 R N K A L S D L R G L G D A L A Y H S E S W E N R N N T R A R S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180	
Db	121 R N K A L T D L K G L G D A L A Y H S E S W G N R K N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180	
QY	181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240	
Db	181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240	
QY	241 T G L N N L R G T N A K S W R Y N Q F R K D M T L M V D L V A L F P S Y D L V P I K T T S Q L T R E V Y T D A I 300	
Db	241 T G L N N L R G T N A E S W R Y N Q F R K D M T L M V D L V A L F P S Y D L V P I K T T S Q L T R E V Y T D A I 300	
QY	301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L D F L E K V T I Y S L S R W S N T Q Y M N M W 360	
Db	301 G T V H P N A S F A S T T W Y N N N A P S F S T I E S A V R N P H L D F L E Q V T I Y S L S R W S N T Q Y M N M W 360	
QY	361 G G H R L E S R P I G G A L N T S T Q S T N T S I N P V T L Q F T S R D V R T E S L A G L N L F L T O P V N G V P R 420	
Db	361 G G H R L E F R I G G M L N T S T Q S T N T S I N P V T L P F T S R D V R T E S L A G L N L F L T O P V N G V P R 420	
QY	421 V D F H W K F P T L P I A S D N F Y Y L G V A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480	
Db	421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480	
QY	481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T T G G D I L R R T N 540	
Db	481 A S H V K A L Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T T G G D I L R R T N 540	
QY	541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600	
Db	541 T G T F G D I R V N I N P P F A Q R Y R V R I R Y A S T T D I Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600	
QY	601 T F R T I G T T P F S D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660	
Db	601 T F R T V G T T P F S D V Q S T F T I G A M N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660	
QY	661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719	
Db	661 T A L F T S T N P G G L K T N V T E Y H I D Q V S N L V E S L S N E F Y L D E K R E L F E I V K Y A K Q L H T G R N M 719	

RESULT 11  
CL1D\_BACTU STANDARD; PRT; 719 AA.  
AC Q9XDL1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryII (insecticidal delta-endotoxin)  
DE CryII(d) (Crystalline entomocidal protoxin) (81 kDa crystal protein).  
GN Name=cryIId; Synonyms=cryII(d), NRcryV;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BR30;  
RX MEDLINE=20374042; PubMed=10919402;  
RA Choi S.-K., Shin B.-S., Kong E.-M., Rho H.M., Park S.-H.;  
RT "Cloning of a new Bacillus thuringiensis cryII-type crystal protein gene."  
RL Curr. Microbiol. 41:65-69(2000).  
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae. Active on Plutella xylostella and on Bombyx mori.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
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CC  
CC EMBL; AF047579; AAD44366.1; -.  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.  
CC InterPro; IPR005638; endotoxin\_C.  
CC InterPro; IPR005639; endotoxin\_N.  
CC InterPro; IPR008979; Gal\_bind like.  
CC Pfam; PF03944; Endotoxin\_C; 1.  
CC Pfam; PF00555; Endotoxin\_M; 1.  
CC Pfam; PF03945; Endotoxin\_N; 1.  
CC Sporulation; Toxin.  
KW SEQUENCE 719 AA; 81403 MW; F335F5689D3B0C45 CRC64;  
Query Match 88.5%; Score 3311; DB 1; Length 719;  
Best Local Similarity 87.2%; Pred. No. 3.5e-220;  
Matches 62; Conservative 50; Mismatches 42; Indels 0; Gaps 0;  
QY 1 MKLKNPDKHQSLSSNAKYDKIATDSLAKNETDIELKNNEDYLRMSEHSIDPVSASTI 60  
DB 1 MKNKQNMRYFSNSNATVDKSFDPLEHNTNMLQNSHEDCLRMSEYSEVPFVSSTI 60  
QY 61 QTGIGIAGKILGTGVPPAGQATSLYSFILGELWPKGSKQWEIFMEHVEHIINOKILTYA 120  
DB 61 QTGIGIAGKILGNLGVPPAGQVSLYSFILGELWPKGSKQWEIFMEHVEBELINQISTYA 120  
QY 121 RNKALSDRLGLDALAVTHESLESWENRNTTRARSVVKQYIALELMFVKQLPSFVSG 180  
DB 121 RNKALADLKLGLDALAVTHESLESWENRNTTRARSVVKQYIALELMFVKQLPSFVSG 180  
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKWLGLSASISTFYNRQVTRDYSDHCIKWYN 240  
DB 181 EEVPLPIYAQAANLHLLLRDASIFGKWLGLSASISTFYNRQSSQTEYSYDCEWYN 240

QY 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDITLVYPIKTTTSOLTRVYTDI 300  
DB 241 TGLNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSTYDITLVYPIKTTTSOLTRVYTDI 300  
QY 301 GTVHPNQAFASSTWYNNAPSFSAIEAVIRSPHLLDFLEKVTIYSLLSRWSNTOYMMNW 360  
DB 301 GTVHPNASFASTWYNNAPSFSTIEAAVVRPHLLDFLEQVTIYSLLSRWSNTOYMMNW 360  
QY 361 GGHRLSPRPIGGALNTSTOGSTNTSINPVTLOFTSRDYVYRTESLAGINLFLTQPVNGVPR 420  
DB 361 GGHLEFRITGGTLNTSTOGSTNTSINPVTLPFTSRDYVYRTESLAGINLFLTQPVNGVPR 420  
QY 421 VDFHWKFPPLPIASDNFYLYGYAGVGQLOQDSENELPPTTGPQNPYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYLYGYAGIGTQLOQDSENELPPTTGPQNPYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRNTTIEPNSITQIPLVKAFLNLSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRNTTINSDSITQIPLVKAFLNLSGASVVRGPGFTGGDILRRTN 540  
QY 541 TGTGDIRVNINPPFAQRYRVRIRYASTDLQFHTSINGKAINQGNFSAATNVRGSDLDYK 600  
DB 541 TGTGDIRVNINPPFAQRYRLRIRYASTNLFTSINGKAINQGNFSAATNVRGSDLDYK 600  
QY 601 TERTIGTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEVPVVEVYEAAYDFEKAQEKV 660  
DB 601 AFRTVGFTTFFSFSAQSTFTIGAWNFSLGNEVYIDRIEVPVVEVYEAAYDYDKAQDEI 660  
QY 661 TALFSTNPRGLKTDVKDYHIDOVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TAMFTSTNLRLKTNVTCHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQNLIERNM 719  
RESULT 12  
CL1B\_BACTU STANDARD; PRT; 1229 AA.  
ID CL1B\_BACTU  
AC Q45739;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pesticidal crystal protein cryIbB (insecticidal delta-endotoxin)  
DE CryIb(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).  
GN Name=cryIbB; Synonyms=cryIb(b), cryE15;  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NRRL B-21110 / EG5847;  
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;  
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins toxic to lepidopteran insects."  
RL Patent number US5322687, 21-JUN-1994.  
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae.  
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.  
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.  
CC -!- SIMILARITY: Belongs to the delta endotoxin family.  
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CC  
CC EMBL; L32020; AAA22344.1; -.  
CC HSSP; P02965; 1CIY.  
CC InterPro; IPR001178; Endotoxin.



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Db 419 RFNF-----INPCNIYERGATTYSQPYQGVGQLFDFSETLPPTERRPNYESYSHRLS 472
QY 475 HIGLISASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGCD 534
Db 473 HIGLIGNTLRAPVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGCD 532
QY 535 ILRRTNTGFGDIRVNIWPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFATMNRG 594
Db 533 ILRRTNTGFGDIRVNIWPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFATMNRG 592
QY 595 ELDYKTFRTIGTTPPFSDVOSTFTIGAMNFSNGEVIIDRIEFPVVEVTEAEYDFE 654
Db 593 DNLEYSRFTAGSTPFPFLNAQSTFTLGAQSFN-QEVIIDRVFVPAEVTFAEYDLE 651
QY 655 KAOEKVTALFTSTNPRGLKTDVXDYHIDQVSNLVESISDEFYLDKRELFEIVKYAKQIH 714
Db 652 RAQKAVNALFTSTNPRGLKTDVXDYHIDQVSNLVESISDEFYLDKRELFEIVKYAKRLS 711
QY 715 IERNM 719
Db 712 DERNL 716

RESULT 14
Q93775 PRELIMINARY; PRT; 1228 AA.
ID Q93775;
AC Q93775;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Delta-endotoxin CryIba2.
GN Name=CryIba2;
OS Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-9;
RA Mat Isa M.N., Abdullah M.A.F., Mahadi N.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF363025; AAK51084.1; -
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
SQ SEQUENCE 1228 AA; 139620 MW; 3DA2A4DBF59C95C3 CRC64;

Query Match 62.1%; Score 2322.5; DB 2; Length 1228;
Best Local Similarity 63.6%; Pred. No. 1.9e-151;
Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

QY 23 TDSLKNETDI-----ELKMNNDYLRMSHEHSDPPFVSASTIQTGTGIGAKI 70
Db 2 TSNRKNENIINAVSNHSAQMDLLPDADIEDSLCIAEGNIDPPFVSASTVQTGINIAGRI 61
QY 71 LGTLGVPPFAQIASLYSIFLGLWPKGQSQWEIFMEHVEEIIQKILTYARNKALSDLRG 130
Db 62 LGVLGVPPFAQIASLYSIFLGLWPKGQSQWEIFMEHVEEIIQKILTYARNKALSDLRG 121
QY 131 LGDALAVHESLESWEVNRNTPARSVVKVQYIALHMFVKLPSPFAVSGEEVPLPIYA 190
Db 122 LGDSFRAYQQSLEDWLENRDDARTSRVLHTQYIALDLFLNAMPFAIRNQVEVPLMVA 181
QY 191 QAAHLHLLLRDASIFGKENGSGASEISTFYNRQVTRDRYSDHCIKWTNTGLNLRGTN 250

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Db 182 QAAHLHLLLRDASIFGSEFGLTSQEIORYYERQVTRDYSDYCVWYNTGLNLSRGTN 241
QY 251 AKSWRYNQFRKDMTLMVLDLVALFPSTYDTPVPIKTSQLTREVYTDAGTGHVNPQAF 310
Db 242 AASWRYNQFRDRLTLGVLVDLVALFPSTYDTPVPIKTSQLTREVYTDAGTGHVNPQAF 299
QY 311 STTWNNNAPSFAIEAAVIRSPHLLDLEKVTIYSLSRWSNTQYMMMGCHRLSRPI 370
Db 300 SMWNNNAPSFAIEAAVIRSPHLLDLEKVTIYSLSRWSNTQYMMMGCHRLSRPI 359
QY 371 GGALNTSTQSTNTSINPVTLOQTSRDYVYRTESLAGNLF--LTQPVNGVPRVDPHWKFP 428
Db 360 GGGLNTSTHGATNTSINPVTLPFASRDYVYRTESLAGNLF--LTQPVNGVPRVDPHWKFP 419
QY 429 -TLPTASDNFYLYGAGVGTOLQDSENELPPETTGQNYESYSHRLSHIGLISASHVKAL 487
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QY 488 VYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTNTGFGDI 547
Db 480 VYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGPGFTGCDILRRTNTGFGDI 539
QY 548 RVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINOGNFATMNRGEDDYKTRTIGF 607
Db 540 RVTVNGPLTQRYRIGFRYASTVDFDFVSRGGTTVANNFRFLRTMNSGDELKYGNEVRRAF 599
QY 608 TTPSFSDVQSTFTIGAMNFSNGEVIIDRIEFPVVEVTEAEYDFEKAQEKVTLFTST 667
Db 600 TTPFTFTQIDIIIRTSIQGLSGNCEVIIDKELIIPVTATFAEYDLERAQAVNALFTNT 659
QY 668 NPGRLKTDVXDYHIDQVSNLVESISDEFYLDKRELFEIVKYAKQIHIERNM 719
Db 660 NPRELKTVDYHIDQVSNLVESISDEFYLDKRELFEIVKYAKQIHIERNM 711

RESULT 15
C1BA_BACTK STANDARD; PRT; 1228 AA.
ID C1BA_BACTK
AC P05517; Q45731;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIba (insecticidal delta-endotoxin CryIb(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein).
GN Name=CryIba; Synonyms=cryIb(a), cryA4;
OS Bacillus thuringiensis (subsp. kurstaki), and
OC Bacillus thuringiensis (subsp. entomocidus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1436;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-2;
RC MEDLINE=88203216; PubMed=3362680;
RA Brizzard B.L., Whiteley H.R.;
RT "Nucleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis.";
RL Nucleic Acids Res. 16:2723-2723(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.entomocidus; STRAIN=HD-110;
RA Soetaert P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMEL; X06711; CAA29898.1; -;  
 DR EMEL; X95704; CAA65003.1; -;  
 DR PIR; S00873; S00873.  
 DR HSSP; P07130; 1DLC.  
 DR InterPro; IPR001178; Endotoxin.  
 DR InterPro; IPR005638; endotoxin\_C.  
 DR InterPro; IPR005639; endotoxin\_N.  
 DR InterPro; IPR008979; Gal\_bind\_Like.  
 DR Pfam; PF03944; Endotoxin\_C; 1.  
 DR Pfam; PF00555; Endotoxin\_M; 1.  
 DR Pfam; PF03945; Endotoxin\_N; 1.  
 KW Sporulation; Toxin.  
 FT VARIANT 150 150 Y -> H (in strain HD-110).  
 SQ SEQUENCE 1228 AA; 139647 MW; C8E3A19FB5D98575 CRC64;

Query Match 62.0%; Score 2321.5; DB 1; Length 1228;  
 Best Local Similarity 63.6%; Pred. No. 2.2e-151;  
 Matches 453; Conservative 80; Mismatches 162; Indels 17; Gaps 4;

QY 23 TDSLKNETDI-----ELKNNMEDYLRMSEHESIDPFVSASTIQTGIGIAGKI 70  
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 QY 71 LGTILGVPAGQIASLYSIFILGELWPKGKQWEIEMEHEVEIINQKILTYARNKALSDLRG 130  
 DB 62 LGVLGVPAGQIASLYSIFILGELWPKGKQWEIEMEHEVEIINQKILTYARNKALSDLRG 121  
 QY 131 LGDALAVTHESLESVVENNRNTRARVVKQYIAELMFVQKLPFAVSGEEVPLLPPIYA 190  
 DB 122 LGDSFRAYCQSLDLEWLNRRDARTSVLYTOYIALELDFLNAMPLFAIRNCEVPLLMVYA 181  
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 QY 429 -TLPIASDNFYLYGAGVGTQLODSENELPBTGQPNVYESYSHLSHIGLISASHVKAL 487  
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 QY 608 TTPFSFSDVQSTTIGAWNFSSGNEVYIDRIEFVPEVYVTEAEYDFEKAQEKYALFTST 667  
 DB 600 TTPFTFTQIIDIIRTSIQGLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVALFTNT 659  
 QY 668 NPREGLKTDVKYHIDQVSNLVESLSDFEYLBKRELFYVYAKQIHIERNM 719  
 DB 660 NPREGLKTDVTDYHIDQVSNLVACLSDFEYLBKRELFYVYAKQIHIERNM 711

Search completed: October 28, 2004, 18:30:12  
 Job time : 101.579 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:10:58 ; Search time 65.6795 Seconds  
(without alignments)  
3549.224 Million cell updates/sec

Title: US-10-019-823B-59

Perfect score: 3742

Sequence: 1 MKLKNPDKHQSLSNAKVDK.....KRELFEIVKYAKQIHIERNM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3520	94.1	719	17 US-10-782-020-10	Sequence 10, Appl
2	3520	94.1	719	17 US-10-782-141-8	Sequence 8, Appl
3	3520	94.1	719	17 US-10-782-096-10	Sequence 10, Appl
4	3520	94.1	719	17 US-10-782-570-7	Sequence 7, Appl
5	3368.5	90.0	710	14 US-10-428-961-42	Sequence 42, Appl
6	2324.5	62.1	1228	16 US-10-809-953-10	Sequence 10, Appl
7	2314.5	61.9	1207	10 US-09-988-462-7	Sequence 7, Appl
8	2234	59.7	1227	14 US-10-428-961-63	Sequence 63, Appl
9	2219	59.3	1186	9 US-09-826-660-23	Sequence 23, Appl
10	2170.5	58.0	1228	15 US-10-428-961-38	Sequence 38, Appl
11	2170.5	58.0	1228	15 US-10-614-524-2	Sequence 2, Appl
12	1982	53.0	643	9 US-09-826-660-25	Sequence 25, Appl
13	1734.5	46.4	1167	14 US-10-089-678-1	Sequence 1, Appl

14	1683.5	45.0	653	14	US-10-428-961-6	Sequence 6, Appl
15	1657.5	44.3	1157	17	US-10-782-141-16	Sequence 16, Appl
16	1657.5	44.3	1157	17	US-10-782-096-17	Sequence 17, Appl
17	1657.5	44.3	1157	17	US-10-782-570-13	Sequence 13, Appl
18	1514	40.5	1206	13	US-10-032-717-2	Sequence 2, Appl
19	1514	40.5	1206	14	US-10-414-637-2	Sequence 2, Appl
20	1514	40.5	1206	15	US-10-606-320-2	Sequence 2, Appl
21	1514	40.5	1206	17	US-10-746-914-2	Sequence 2, Appl
22	1500.5	40.1	1156	14	US-10-099-285-72	Sequence 72, Appl
23	1500.5	40.1	1156	14	US-10-428-961-28	Sequence 28, Appl
24	1494	39.9	1210	13	US-10-032-717-4	Sequence 4, Appl
25	1494	39.9	1210	14	US-10-414-637-4	Sequence 4, Appl
26	1494	39.9	1210	15	US-10-606-320-4	Sequence 4, Appl
27	1494	39.9	1210	17	US-10-746-914-4	Sequence 4, Appl
28	1480.5	39.6	1155	9	US-09-756-643-2	Sequence 2, Appl
29	1480.5	39.6	1155	10	US-09-988-462-9	Sequence 9, Appl
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31	1480.5	39.6	1181	10	US-09-988-462-11	Sequence 11, Appl
32	1480.5	39.6	1181	10	US-09-988-462-13	Sequence 13, Appl
33	1480.5	39.6	1181	10	US-09-988-462-15	Sequence 15, Appl
34	1480.5	39.6	1181	10	US-09-988-462-17	Sequence 17, Appl
35	1480.5	39.6	1181	10	US-09-988-462-28	Sequence 28, Appl
36	1480.5	39.6	1181	14	US-10-136-998A-4	Sequence 4, Appl
37	1480.5	39.6	1181	14	US-10-136-998A-8	Sequence 8, Appl
38	1480.5	39.6	1181	14	US-10-136-998A-10	Sequence 10, Appl
39	1480.5	39.6	1181	14	US-10-136-998A-12	Sequence 12, Appl
40	1475.5	39.4	1177	14	US-10-035-060-6	Sequence 6, Appl
41	1472.5	39.4	1177	14	US-10-102-469-24	Sequence 24, Appl
42	1470.5	39.3	1177	14	US-10-035-060-2	Sequence 2, Appl
43	1470.5	39.3	1177	14	US-10-035-060-8	Sequence 8, Appl
44	1447	38.7	1176	17	US-10-782-141-6	Sequence 6, Appl
45	1447	38.7	1176	17	US-10-782-096-7	Sequence 7, Appl

#### ALIGNMENTS

RESULT 1  
US-10-782-020-10  
; Sequence 10, Application US/10782020  
; Publication No. US20040197916A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-004, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for its Use  
; FILE REFERENCE: 045600/274139  
; CURRENT APPLICATION NUMBER: US/10/782,020  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: 60/448,810  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 719  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-782-020-10

Query Match 94.1%; Score 3520; DB 17; Length 719;  
Best Local Similarity 92.9%; Pred. No. 1.4e-286;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

QY 1 MKLKNPDKHQSLSNAKVDKIDSLKNETDIELKNMNNEDYLRMSHEHSDPFFVSASTI 60  
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Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

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QY 61 Q T G I G I A K I L G T L G V P F A G Q I A S L Y S F I L G E L M P K G K S Q W E I F M E H V E E I I N K I L T Y A 120
D b 61 Q T G I G I A K I L G T L G V P F A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E E I I N K I S T Y A 120
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D b 121 R N K A L T D L K G L G D A L A V Y H S L E S W G N R N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240
D b 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240
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D b 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
QY 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N M W 360
D b 301 G T V H P H S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
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RESULT 4
US-10-782-570-7
; Sequence 7, Application US/10782570
; Publication No. US20040210965A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-007, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for its Use
; FILE REFERENCE: 045600/274144
; CURRENT APPLICATION NUMBER: US/10/782,570
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: 60/448,812
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 719
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; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-570-7

Query Match 94.1%; Score 3520; DB 17; Length 719;
Best Local Similarity 92.9%; Pred. No. 1.4e-286;
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

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QY 241 T G L N N L R G T N A K S W R Y N Q F R K D M T L M V D L V A L P S Y D T L V Y P I K T T S Q L T R E V Y T D A I 300
D b 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V D L V A L P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300
QY 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N M W 360
D b 301 G T V H P H S F T S T T W Y N N N A P S F A I E A A V V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N M W 360
QY 361 G G H R L E S R P I G G A L N T S T Q S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
D b 361 G G H K L E F R T I G G T L N I S T Q S T N T S I N P V L P F T S R D V Y R T E S L A G L N L F L T O P V N G V P R 420
QY 421 V D F H W K F P T L P I A S D N F Y Y L G Y A G V G T Q L Q D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480
D b 421 V D F H W K F V T H P I A S D N F Y Y P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480
QY 481 A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540
D b 481 A S H V K A L V Y S W T H S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G T G G D I L R R T N 540
QY 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
D b 541 T G T F G D I R V N I N P P A Q R Y R V I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600
QY 601 T F R T I G T T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A B Y D F E K A Q E K V 660
D b 601 T F R I V G T T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A B Y D F E K A Q E K V 660
QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719
D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719

RESULT 5
US-10-428-961-42
; Sequence 42, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupa, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MCO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
```

; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 42  
 ; LENGTH: 710  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (200)..(200)  
 ; OTHER INFORMATION: The 'Xaa' at location 200 stands for any naturally occurring amino acid  
 US-10-428-961-42

Query Match 90.0%; Score 3368.5; DB 14; Length 710;  
 Best Local Similarity 89.2%; Pred. No. 7.2e-274;  
 Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;

QY	1	MKLKNDPKHQSLSSNAKVDKIATDSLKNEDTDLKNNEDYLRMSEHESIDPPVSASTI 60
DB	1	MKSKQNMHQSLSSNAKVDKIATDSLKNEDTDLKNNEDYLRMSEHESIDPPVSASTI 60
QY	61	QTGIGIAGKILGTGVPFAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINOKILTYA 120
DB	52	QTGIGIAGKILGNLGVPPFAGQVASLYSIFILGELWPKGKSQWEIFMEHVEEIIINOKILTYA 111
QY	121	RNKALSDRLGLDALAVHESLESWENRNNTRASVVKVQYIALELMFVQKLPFSFVSG 180
DB	112	RNKALADLGLDALAVHESLESWENRNNTRASVVKVQYIALELMFVQKLPFSFVSG 171
QY	181	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVVERTDYSDHCIKWYN 240
DB	172	EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVVERTDYSDHCIKWYN 231
QY	241	TGLNLRGNTAKSVRYNQFRDMTLMVLDLVALFPSYDTLVPIKTTSQLTRVYTDAL 300
DB	232	TGLNLRGNTAKSVRYNQFRDMTLMVLDLVALFPSYDTLVPIKTTSQLTRVYTDAL 291
QY	301	GTVHPNQAFASFTWYNNAPSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNW 360
DB	292	GTVHPNQAFASFTWYNNAPSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNW 351
QY	361	GGHLESRPIGGALNTSQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPR 420
DB	352	GGHLESRPIGGALNTSQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPR 411
QY	421	VDFHWKFTPLIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLIS 480
DB	412	VDFHWKFTPLIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLIS 471
QY	481	ASHVKALVSWTHRSADRTNTIEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540
DB	472	ASHVKALVSWTHRSADRTNTIEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 531
QY	541	TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600
DB	532	TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 591
QY	601	TFTTIGFTTSPSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEV 660
DB	592	TFTTIGFTTSPSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEV 651
QY	661	TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB	652	TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 710

RESULT 6  
 US-10-809-953-10  
 ; Sequence 10, Application US/10809953  
 ; Publication No. US2004018125A1  
 ; GENERAL INFORMATION:

; APPLICANT: Van Mellaert, Herman  
 ; APPLICANT: Botterman, Johan  
 ; APPLICANT: Van Rie, Jeroen  
 ; APPLICANT: Joos, Henk  
 ; TITLE OF INVENTION: RECOMBINANT PLANT EXPRESSING NON-COMPETITIVELY BINDING Bt INSECTIC  
 ; TITLE OF INVENTION: CRYSTAL PROTEINS  
 ; FILE REFERENCE: 021565-078  
 ; CURRENT APPLICATION NUMBER: US/10/809,953  
 ; CURRENT FILING DATE: 2004-03-26  
 ; PRIOR APPLICATION NUMBER: US/09/661,016  
 ; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/EP90/00905  
 ; PRIOR FILING DATE: 1990-05-30  
 ; PRIOR APPLICATION NUMBER: GB 89401499.2  
 ; PRIOR FILING DATE: 1989-05-31  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-809-953-10

Query Match 62.1%; Score 2324.5; DB 16; Length 1228;  
 Best Local Similarity 63.6%; Pred. No. 9.7e-186;  
 Matches 454; Conservative 85; Mismatches 166; Indels 9; Gaps 5;

QY	12	LSSNAKVDKIATDSLKN---ETDIELKNNEDYLRMSEHESIDPPVSASTIQTGIGIAG 68
DB	1	LTSNRKNENIINAVSNHSAQMDL-LPARIEDSLCIAEGNNIDPPVSASTVQTGINIAG 59
QY	69	KILGTGVPFAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINOKILTYARNKALSD 128
DB	60	RILGVLGVPPFAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINOKILTYARNKALSD 119
QY	129	RGLGDALAVHESLESWENRNNTRASVVKVQYIALELMFVQKLPFSFVSGEETVPLPI 188
DB	120	QGLGDSFRAYQSLDLEWLENRDDARTSVLHTQYIALELDFLNAFLFAIRNQEVPLLMV 179
QY	189	YAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVVERTDYSDHCIKWYNGLNLRG 248
DB	180	YAQAANLHLLLRDASIFGSEFGLTSQEIQRYVERQVTERDYSYCVENYNTGLNSLRG 239
QY	249	TNAKSWRVYRQFRDMTLMVLDLVALFPSYDTLVPIKTTSQLTRVYTDALGTVHPNQ 308
DB	240	TNAKSWRVYRQFRDMTLMVLDLVALFPSYDTLVPIKTTSQLTRVYTDALGTVHPNQ 297
QY	309	FASFTWYNNAPSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNWGGHLESR 368
DB	298	MASWYNNAPSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNWGGHLESR 357
QY	369	PIGGALNTSQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPRVDFHWK 426
DB	358	PIGGALNTSQGSTNTSINPVTLOFTSRDVRVYTESLAGLNLFLTQPVNGVPRVDFHWK 417
QY	427	FP-TLPIASDNFYLYGAGVGTQLODSENELPETTGQPNYESYSHRSLHIGLISASHVK 485
DB	418	NPQNISDRGTANYSQYESPGQLKDSSETLPPETTERPNYESYSHRSLHIGLISQSRV 477
QY	486	ALVTSWTHRSADRTNTIEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTPFG 545
DB	478	VPVTSWTHRSADRTNTIEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTPFG 537
QY	546	DIVNINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYKTFRTI 605
DB	538	PIRTVNGVPLTQRYRIGFRYASTVDFVSRGGTIVNNFRFLTMNSGDELKYNFVR 597
QY	606	GFTTFFPSDVQSTFTIGAMNFSNGNEVYIDRIEFVPEVYEAEDFEKAQEVTALEFT 665
DB	598	AFITPFTTQIQDIIRTSIQGLSGNEVYIDRIEFVPEVYEAEDFEKAQEVTALEFT 657
QY	666	STNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Db 658 NTPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELEKVKYAKRLSDERNL 711

RESULT 7

US-09-988-462-7

; Sequence 7, Application US/09988462

; Publication No. US20030046726A1

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; Desai, Nalini M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warren, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Launis, Karen L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Syngenta Biotechnology, Inc.

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/988,462

; FILING DATE: 20-NO. US20030046726A1-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/547,422

; FILING DATE: 11-APR-2000

; APPLICATION NUMBER: US 08/459,504

; FILING DATE: 02-JUN-1995

; APPLICATION NUMBER: US 07/951,715

; FILING DATE: 25-SEP-1992

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: S-188051

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8587

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1207 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-988-462-7

Query Match 61.9%; Score 2314.5; DB 10; Length 1207;

Best Local Similarity 65.4%; Pred. No. 6.5e-185;

Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSHESIDPFVFASTIQTGIGTAGKILGTLPFPAGQIASLYSFLGELWPKGKS 99

Db 10 EDSLCAEGNIDPFVFASTVGTGINAGRIILGVLGVFPAGQLASFYSFLVGLWPRGRD 69

QY 100 QWEIFMEHVEEIIKILTYARNKALSDRLGLGDALAVYHESLESWVENRNTARSVVK 159

Db 70 QWEIFLEHVEQLNQITENARNTALRQLGLGDSFRAYQQSLEDWLENRDDARTSVLY 129

QY 160 NOYIALELMFVQKLPFSFAVSGEEVPLLPITYAQAAHLHLLLRDASIFGKMWGLSASEIST 219

Db 130 TOYIALELDLFLNAMPFLFAIRNQEVPLLMVYQAANHLHLLLRDASLFGSEFGLTSQEIQR 189

QY 220 FYNQOVERTRDYSCHCIKWNTGLNNLRGTNAKSWVRYNQERKDMTLMVLVDVALRPSYD 279

Db 190 YYERQVERTRDYSYCVIEWYNTGLNLRGTNAASWVRYNQFRDLTLGLVDLVALRPSYD 249

QY 280 TLVYPIKTTSQLTREVYTDAGITVHPNQAFSTWYNNNAPSFAIAAARSPHLLDFFL 339

Db 250 TRTYPINTSAQLTREVYTDAGATGVN--MASMMWYNNNAPSFAIAAARSPHLLDFFL 307

QY 340 EKVITYLSLRWSNTQYMMWGGHRLSPGIGALNTSTQGSTNTSINPVLQFTSRDVI 399

Db 308 EQLTIFSASSRWSTNRHMTVWRGHTIQSRPIGGGLNTSTHGAINTSINPVLRFASRDVI 367

QY 400 RTESLAGNLFF--LTQPVNGVPRVDFHWKFP--TLPIASDNFYLYGAGVGTQLQDSNEL 456

Db 368 RTESYAGVLLWGIYLEPIHGVPTVRFTNPQNISDRGTANTYSPQYSPGLQKDSSETL 427

QY 457 PPETTQPNYESYSHRLSHIGLISASHVKALVSWTHRSADRTNITPNSITQIPLVKAF 516

Db 428 PPETTERPNYESYSHRLSHIGIILQSRVNVVSWTHRSADRTNITGNRITQIPMKAS 487

QY 517 NLSGGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPPFAQRYRVRIRYASTDLOFHTS 576

Db 488 ELPOGTTVVVRGPGFTGGDILRRNTGTGGPIRVTVNGSLTQRYRIGRYASTVDFDFVS 547

QY 577 INGKAINQGNFSATNVRGDLDYKTRFTIGFTTTPFSFSDVQSTFTTICANWSSGNEVYID 636

Db 548 RGGTTVNNFRFLRTMNSGDELKYGNFVRAFTTPTFTQIQDIIRTSIQLSGNGEYVID 607

QY 637 RIEFVPEVTEYAEYDFEZAQEKVTALTFTSTNPRGLKTDVDKDYHIDQVSNLVESLSDEFY 696

Db 608 KIEIIPVATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFY 667

QY 697 LDEKRELFVIVYAKQIHERNM 719

Db 668 LDEKRELEKVKYAKRLSDERNL 690

RESULT 8

US-10-428-961-63

; Sequence 63, Application US/10428961

; Publication No. US20030237111A1

; GENERAL INFORMATION:

; APPLICANT: Baum, James A.

; APPLICANT: Chu, Chih-Rei

; APPLICANT: Donovan, William P.

; APPLICANT: Gilmer, Amy J.

; APPLICANT: Ruper, Mark J.

; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin

; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

; FILE REFERENCE: MECO201--1

; CURRENT APPLICATION NUMBER: US/10/428,961

; CURRENT FILING DATE: 2003-05-02

; PRIOR APPLICATION NUMBER: 09/661,322

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,995

; PRIOR FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 63

; LENGTH: 1227

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-428-961-63

Query Match 59.7%; Score 2234; DB 14; Length 1227;

Best Local Similarity 60.8%; Pred. No. 3.9e-178;

Matches 434; Conservative 100; Mismatches 162; Indels 18; Gaps 3;

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QY 23 TDSLKNETDI-----ELKNNN-----EDYLRMSEHESIDPFVSASTIQTGIG 65
DB 2 TSNRKNENEINALSIPAVSNHSAQMNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTLGVFPFAGQIASLYSFLGELWPKGSKQWEIFMHEVEEIIINQKILTYARNKAL 125
DB 62 IAGRILGVLGVFPFAGQIASFYSLVGLWPRGRDPWEIFLEHVEHLIRQQVTENTRDTAL 121
QY 126 SDRGLGLDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSPFVSGEEVPL 185
DB 122 ARLOGLGNSFRAYQOSLEDWLENRDDATRSVLYTQYIALELDFLNAMPFAIRNQEVEPL 181
QY 186 LPIYAAQANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDYSDHCKIKWYNTGLNN 245
DB 182 LMVYAAQANLHLLLRDASLFGSEFGLTSQEIQRYRQVEKRETSYDYCARWYNTGLNN 241
QY 246 LRGTNAKSWRYNQPRKDMTLMVLDLVALFPSYDTLVYPIKTSQLTREVVTDAIGTVHP 305
DB 242 LRGTNAESWLRYNQPRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRNTA 301
QY 306 NQAFSTTWNNNAPSFSAIEAAVIRSHLLDFLEKTYIYLSRWSNTQYMNWVGHRLL 365
DB 302 PSGFASTNWFNNAPSFSAIEAAVIRPHLLDFPEQLTIFSVLSRWSNTQYMNWVGHRLL 361
QY 366 ESRPIGALNTSTQGSTNTSINPVTLOFTSRDVRYSLAGNLFITQPVNGVPRVDFFHW 425
DB 362 ESRTRGSLSTWTHGNTNTSINPVTLOFTSRDVRYSFAGINILLTTPVNGVPRVAFNW 421
QY 426 KPFTPLPIASDNFYLYGAGVGTQOLQDSNELPPTTQPNYESYSHRLSHIGLISASHVK 485
DB 422 RNPLSLRGSLLYTYIGTGTQVGLFDSETELPPTTERPNYESYSHRLSNIRLISGNTLR 481
QY 486 ALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDIILRRNTGTGFG 545
DB 482 APVYSWTHRSADRNTTISSDSITQIPLVKSFNLNGSVSGPFGTGGDIIRTNVNGSVL 541
QY 546 DIRVAINPPAQRVRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDIYKTERTI 605
DB 542 SMGLNFNNTSLQRYRVRYAASQTMVLRTVVGSGSTTFDQGFPTMSANESLTSQSFRFA 601
QY 606 GFTTSPFSVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFT 665
DB 602 EFPVGISASGSQ-TAGISISNAGRQTFHDKIEFIPITATLEAESDLERAQKAVNALFT 660
QY 666 STNPRGLKTDVYKHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 NTNPRRLKTVTDYHIDEVSNLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNL 714

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RESULT 9

```

US-09-826-660-23
; Sequence 23, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven E.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 1998-10-23
; PRIOR FILING DATE: 1998-10-23
; PRIOR FILING DATE: 1997-11-12
; PRIOR FILING DATE: 1998-03-02
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1186
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-23

Query Match 59.3%; Score 2219; DB 9; Length 1186;
Best Local Similarity 60.5%; Pred. No. 6.e-177;
Matches 432; Conservative 103; Mismatches 161; Indels 18; Gaps 3;

QY 23 TDSLKNETDI-----ELKNNN-----EDYLRMSEHESIDPFVSASTIQTGIG 65
DB 2 TSNRKNENEINALSIPAVSNHSAQMNLSTDARIEDSLCIAEGNNIDPFVSASTVQTGIN 61
QY 66 IAGKILGTLGVFPFAGQIASLYSFLGELWPKGSKQWEIFMHEVEEIIINQKILTYARNKAL 125
DB 62 IAGRILGVLGVFPFAGQIASFYSLVGLWPRGRDPWEIFLEHVEHLIRQQVTENTRDTAL 121
QY 126 SDRGLGLDALAVYHESLESWVENRNNTRARSVVKNQYIALELMFVQKLPSPFVSGEEVPL 185
DB 122 ARLOGLGNSFRAYQOSLEDWLENRDDATRSVLYTQYIALELDFLNAMPFAIRNQEVEPL 181
QY 186 LPIYAAQANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDYSDHCKIKWYNTGLNN 245
DB 182 LMVYAAQANLHLLLRDASLFGSEFGLTSQEIQRYRQVEKRETSYDYCARWYNTGLNN 241
QY 246 LRGTNAKSWRYNQPRKDMTLMVLDLVALFPSYDTLVYPIKTSQLTREVVTDAIGTVHP 305
DB 242 LRGTNAESWLRYNQPRRDLTLGVLDLVALFPSYDTRVYPMNTSAQLTREIYTDPIGRNTA 301
QY 306 NQAFSTTWNNNAPSFSAIEAAVIRSHLLDFLEKTYIYLSRWSNTQYMNWVGHRLL 365
DB 302 PSGFASTNWFNNAPSFSAIEAAVIRPHLLDFPEQLTIFSVLSRWSNTQYMNWVGHRLL 361
QY 366 ESRPIGALNTSTQGSTNTSINPVTLOFTSRDVRYSLAGNLFITQPVNGVPRVDFFHW 425
DB 362 ESRTRGSLSTWTHGNTNTSINPVTLOFTSRDVRYSFAGINILLTTPVNGVPRVAFNW 421
QY 426 KPFTPLPIASDNFYLYGAGVGTQOLQDSNELPPTTQPNYESYSHRLSHIGLISASHVK 485
DB 422 RNPLSLRGSLLYTYIGTGTQVGLFDSETELPPTTERPNYESYSHRLSNIRLISGNTLR 481
QY 486 ALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAVRGPFGTGGDIILRRNTGTGFG 545
DB 482 APVYSWTHRSADRNTTISSDSITQIPLVKSFNLNGSVSGPFGTGGDIIRTNVNGSVL 541
QY 546 DIRVAINPPAQRVRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDIYKTERTI 605
DB 542 SMGLNFNNTSLQRYRVRYAASQTMVLRTVVGSGSTTFDQGFPTMSANESLTSQSFRFA 601
QY 606 GFTTSPFSVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQKVTALFT 665
DB 602 EFPVGISASGSQ-TAGISISNAGRQTFHDKIEFIPITATLEAESDLERAQKAVNALFT 660
QY 666 STNPRGLKTDVYKHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719
DB 661 SNNQIGLKTVDYHIDRVSNLVESLSDEFCLDEKRELSEKVKYAKRLSDERNL 714

```

RESULT 10

```

US-10-428-961-38
; Sequence 38, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Ruper, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322

```

; PRIOR FILING DATE: 2000-09-13  
 ; PRIOR APPLICATION NUMBER: 60/153,995  
 ; PRIOR FILING DATE: 1999-09-15  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 38  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-428-961-38

Query Match 58.0%; Score 2170.5; DB 14; Length 1228;  
 Best Local Similarity 60.5%; Pred. No. 8.6e-173;  
 Matches 435; Conservative 98; Mismatches 171; Indels 15; Gaps 8;

QY	12	LSSNAK-----VDKIATDSLKN-ETDIELK-NMNNEDYLRMSHEHESIDPFVSASTIQTGI	64
DB	1	LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI	60
QY	65	GIAGKILGTGVFPAGQIASLYSIFLGLWPKGSQWEIFMEHVEEIIINQKILTYARKA	124
DB	61	NIAGRILGVLGVFPAGQIASFYSFLVGLWPRGRDQWEIFLHVEQLINQITENARNTA	120
QY	125	LSDLRGLGDALAVYHESLESWVENNRNTRARSVVKNOYIALLEMFVQKLPFAVSGEEVP	184
DB	121	LARLOGLGDSFRAYQQSLEDWLENRRDARTSVLYTQYIALLEDFLNAMPLFAIRNQEV	180
QY	185	LLPIYAQAANLHLLLRDASIFGKEWGLSAGEISFYFNROVERTRDYSCHCIKWYNTGLN	244
DB	181	LLMVAQAANLHLLLRDASLFGSEFGLTSQEIQRYVERQVEQTRDYSYCVWEYNTGLN	240
QY	245	NLRGTNAKSWRYNQFRKDMTLMVLDLVALFSPSYDTLVYPIKTTSQLTREVYTDAGTVH	304
DB	241	SLRGTTNAASWRYNQFRDLTLGLVLDLVALFSPYDTRTYPINTSAQLTREVYTDAGT	300
QY	305	PNQAFASWTWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNWGGHR	364
DB	301	VN--MASMWNWYNNAPSPSAIETAVIRSPHLLDFLEKVTIYSLSRWSATRHMTYWRGT	358
QY	365	LESPIGALNTSTQGSTNTSINPVLQFTSRDVTYTESLAGNLF--LTQPVNGVPRVD	422
DB	359	IQSRPIGGGLNTSTHGSINTSINPVLRSFSDRDVYTESYAGVLLWGIYLEPIHGVPVTR	418
QY	423	FWKFP--TLPIASDNFYLYGAGVGTQLODSENELPPTTQPNYESYSHRSLHIGLIS	480
DB	419	FNFRNPQNTFERGTAN--YSQPYESPGQLQKSETLPPTTERPNYESYSHRSLHIGLIS	477
QY	481	ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSGAAVVRGPGTGGDILRRTN	540
DB	478	QSRVHPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVVSVPFTGGDIIRTNV	537
QY	541	TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	600
DB	538	NGSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRVTVGSTTFDQGFPTMSANESLTSQ	597
QY	601	TFRITGFTTFFSDVQSTFTIGAWNPFSSGNEVYIDRIEFPVVEVTEAEYDEKAQEKV	660
DB	598	SFRFAEFPVGISASGSQ--TAGISISNNAGROTFFHDKIEFIPITATFAEYDLERAQEA	656
QY	661	TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM	719
DB	657	NALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL	715

RESULT 11  
 US-10-614-524-2  
 ; Sequence 2, Application US/10614524  
 ; Publication No. US20040016020A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arnaut, Greta  
 ; APPLICANT: Boets, Annemie  
 ; APPLICANT: Damme, Nicole  
 ; APPLICANT: Mathieu, Eva

; APPLICANT: Vanneste, Stijn  
 ; APPLICANT: Van Rie, Jeroen  
 ; TITLE OF INVENTION: Insecticidal proteins from Bacillus thuringiensis.  
 ; FILE REFERENCE: NEWBTSU2  
 ; CURRENT APPLICATION NUMBER: US/10/614,524  
 ; CURRENT FILING DATE: 2003-07-08  
 ; PRIOR APPLICATION NUMBER: US/09/739,243  
 ; PRIOR FILING DATE: 2000-12-19  
 ; PRIOR APPLICATION NUMBER: 60/173387  
 ; PRIOR FILING DATE: 1999-12-28  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1228  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-10-614-524-2

Query Match 58.0%; Score 2170.5; DB 15; Length 1228;  
 Best Local Similarity 60.5%; Pred. No. 8.6e-173;  
 Matches 435; Conservative 98; Mismatches 171; Indels 15; Gaps 8;

QY	12	LSSNAK-----VDKIATDSLKN-ETDIELK-NMNNEDYLRMSHEHESIDPFVSASTIQTGI	64
DB	1	LTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINPLVSASTVQTGI	60
QY	65	GIAGKILGTGVFPAGQIASLYSIFLGLWPKGSQWEIFMEHVEEIIINQKILTYARKA	124
DB	61	NIAGRILGVLGVFPAGQIASFYSFLVGLWPRGRDQWEIFLHVEQLINQITENARNTA	120
QY	125	LSDLRGLGDALAVYHESLESWVENNRNTRARSVVKNOYIALLEMFVQKLPFAVSGEEVP	184
DB	121	LARLOGLGDSFRAYQQSLEDWLENRRDARTSVLYTQYIALLEDFLNAMPLFAIRNQEV	180
QY	185	LLPIYAQAANLHLLLRDASIFGKEWGLSAGEISFYFNROVERTRDYSCHCIKWYNTGLN	244
DB	181	LLMVAQAANLHLLLRDASLFGSEFGLTSQEIQRYVERQVEQTRDYSYCVWEYNTGLN	240
QY	245	NLRGTNAKSWRYNQFRKDMTLMVLDLVALFSPSYDTLVYPIKTTSQLTREVYTDAGTVH	304
DB	241	SLRGTTNAASWRYNQFRDLTLGLVLDLVALFSPYDTRTYPINTSAQLTREVYTDAGT	300
QY	305	PNQAFASWTWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYMNWGGHR	364
DB	301	VN--MASMWNWYNNAPSPSAIETAVIRSPHLLDFLEKVTIYSLSRWSATRHMTYWRGT	358
QY	365	LESPIGALNTSTQGSTNTSINPVLQFTSRDVTYTESLAGNLF--LTQPVNGVPRVD	422
DB	359	IQSRPIGGGLNTSTHGSINTSINPVLRSFSDRDVYTESYAGVLLWGIYLEPIHGVPVTR	418
QY	423	FWKFP--TLPIASDNFYLYGAGVGTQLODSENELPPTTQPNYESYSHRSLHIGLIS	480
DB	419	FNFRNPQNTFERGTAN--YSQPYESPGQLQKSETLPPTTERPNYESYSHRSLHIGLIS	477
QY	481	ASHVKALVYSWTHRSADRTNTEPNSTQIPLVKAFNLSGAAVVRGPGTGGDILRRTN	540
DB	478	QSRVHPVYSWTHRSADRTNTISSDSITQIPLVKSFNLSGTSVVSVPFTGGDIIRTNV	537
QY	541	TGTFGDIRVNIINPPFAQRYRVRIRYASTTDLOFHTSINGKAINQGNFSATMNRGEDLDYK	600
DB	538	NGSVLSMGLNFNTSLQRYRVRVRYAASQTMVLRVTVGSTTFDQGFPTMSANESLTSQ	597
QY	601	TFRITGFTTFFSDVQSTFTIGAWNPFSSGNEVYIDRIEFPVVEVTEAEYDEKAQEKV	660
DB	598	SFRFAEFPVGISASGSQ--TAGISISNNAGROTFFHDKIEFIPITATFAEYDLERAQEA	656
QY	661	TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM	719
DB	657	NALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFCLDEKRELLEKVKYAKRLSDERNL	715

RESULT 12  
 US-09-826-660-25

; Sequence 25, Application US/09826660  
; Patent No. US20010026940A1  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Stelman, Steven J.  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/178,252  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: 60/065,215  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/076,445  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 643  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-09-826-660-25

Query Match 53.0%; Score 1982; DB 9; Length 643;  
Best Local Similarity 59.6%; Pred. No. 2.2e-157;  
Matches 383; Conservative 94; Mismatches 148; Indels 18; Gaps 3;  
QY 23 TDSLKNETDI---ELKMN---EDLRMSEHESIDPFVSASTIQTGIG 65  
Db 2 TSNRKNENIINALSIPAVNSHAQMLSTDAIEDSLCAEGNIDPFVSASTVQTGIN 61  
QY 66 IAGKILGTGVPPAGQIASLYSIFILGELWPKGQSEIFMEHVEELINQKILTARNKAL 125  
Db 62 IAGRLGLVGLVPPAGQIASLYSIFILGELWPKGQSEIFMEHVEELINQKILTARNKAL 121  
QY 126 SDRGLGLDALAVYHESLESVENNRNTRARSVVKNOYIALELMFVQKLPFAVSGEEVPL 185  
Db 122 ARLOGLGNFRAYQOSLEDWLENRDDARTSRVLYTQYIALELDLFLNAMPFAIRNQEVPL 181  
QY 186 LPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDYSDHCICKWNTGLNN 245  
Db 182 LMVYAQAANLHLLLRDASLFGSEFGLTSQEIORYERQVETREYSDYCARWNTGLNN 241  
QY 246 LRGTNAKSVRYNQFRKQMTLMVLDLVALFPSTYTLVYPIKTTLSOLTREVYTDAGTVHP 305  
Db 242 LRGTNAESWLYNQFRKQMTLMVLDLVALFPSTYTLVYPIKTTLSOLTREVYTDAGTVHP 301  
QY 306 NQAFASSTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMNWGGHRL 365  
Db 302 PSGFASSTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMNWGGHRL 361  
QY 366 ESRPTGALNTSTOGSTNTSINPVLQTSRDVRYTESLAGNLFILTPQVNGVRVDVFW 425  
Db 362 ESRITRGLSTSTHGTNTSINPVLQTSRDVRYTESLAGNLFILTPQVNGVRVDVFW 421  
QY 426 KFPTLPASDNFYLYGAVGTQLQDSNELPPTTQPNYESYSHRLSHIGLSASHVK 485  
Db 422 RNPLNSRGLSLLYIGYGVGTQLQDSNELPPTTQPNYESYSHRLSHIGLSASHVK 481  
QY 486 ALVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVRGPFTGGDILRRNTWTGPG 545  
Db 482 APVSWTHRSADRNTIENPSITQIPLVKAFNLSSGAAVRGPFTGGDILRRNTWTGPG 541  
QY 546 DIRVNNPPAQRVRYRYASTDQFHTSINGKAINQGNFSATNRGDDLDYKTFRTI 605  
Db 542 SMGLNFNTSLQRYRVRYRYASTDQFHTSINGKAINQGNFSATNRGDDLDYKTFRTI 601  
QY 606 GFTTFPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVYIE 648  
Db 602 EFPVGISASGSQ-TAGISISNAGRQTFHFDKIEFIPITATLE 643

RESULT 13  
US-10-089-678-1  
; Sequence 1, Application US/10089678  
; Publication No. US20030017967A1  
; GENERAL INFORMATION:  
; APPLICANT: ASANO, Shinichiro  
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, AN  
; FILE REFERENCE: Q68B21  
; CURRENT APPLICATION NUMBER: US/10/089,678  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: JP 2000-236140  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: PCT/JP01/06660  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1167  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-089-678-1

Query Match 46.4%; Score 1734.5; DB 14; Length 1167;  
Best Local Similarity 48.2%; Pred. No. 3.5e-136;  
Matches 366; Conservative 123; Mismatches 210; Indels 61; Gaps 14;  
QY 1 MKLKNDPKHQS---SSNAKVDKIATSLKNETDIELKMNEDYLRMSEHE-----SI 51  
Db 1 MSPNQNEVEILDASSSTSVSDNSVRYPLANDOTTITQNMVYKDYLRMSEGENPELFGNP 60  
QY 52 DPFVSASTIQTGIGIAGKILGTGVPPAGQIASLYSIFILGELWPKGK-SOWEIFMEHVEE 110  
Db 61 ETFISSSTVGTGIGLVGQVGLGALGVPFAGQIASFYSEIVGQLWPSSTVSWEMINKQVED 120  
QY 111 IINQKILTARNKALSDLRGLGDALAVYHESLESVENNRNTRARSVVKNOYIALELMFV 170  
Db 121 LIDQKITDSVRKTAGLQGLDGLVYQSKLNWLENRNDTRARSVVKNOYIALELDV 180  
QY 171 QKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRD 230  
Db 181 AKIPSPAISQEVPLLSVYAQAANLHLLLRDASIFGAEWGTGPEISTFYDRQVTRTAQ 240  
QY 231 YSDHCICKWNTGLNLRGNAKSVRYNQFRKQMTLMVLDLVALFPSTYTLVYPIKTTSQ 290  
Db 241 YSDYCVKWTNTGLDKLKGTAASWLYKHQFRREMTLLVLDLVALFPSTYTLVYPIETTAQ 300  
QY 291 LTREYVTDAGTVHPNQAFASSTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYLLS- 349  
Db 301 LTREYVTDPIVFNRETSGFCRRWSLNSDISFSEVESAVIRSPHLLDILSIEFTTTRAG 360  
QY 350 -RWSNTQYMNWGGHRLSRPIGALNTSTOGSTNTSINPVT-----LQTSRDVRYTE 402  
Db 361 LPLNNTEYLEYVWGHISIKYK-----NTNASSALERNYGTITSNKIKYYDLANKDIFQVR 414  
QY 403 SL-AGLNLFLTQPVNGVRVDVFWKFTPLPIASDNFYLYGAVGV-----T 447  
Db 415 SLGADLANVYQAQ-VYGVYPYASF-----TLIDKN-----TGSGSVGGFTYKPHHTMQVCT 463  
QY 448 QLQDSNELPPTTQPNYESYSHRLSHIGLSIS-----ASHVKALVYSWTHRSADR 499  
Db 464 QNYNTIDEIIPPE--NEPLSRGYSRLSHITSYSFSKNASSPARYGNLVPFANTHSADVT 521  
QY 500 NTIEPNSITQIPLVKAFNLSSGAAVRGPFTGGDILRRNTWTGTFGDIRVNNPPAQR 559  
Db 522 NTVYSDKITQIPVVKAKHTLVSGTTVIKGPFTGGNILKRTSSGPLAYTSVSKSPLSQRY 581  
QY 560 RVRIRYASTDQFHTSINGKAINQGNFSATNRGDDLDYKTFRTTGTFTTFFSFDVQST 619  
Db 582 PARIRYASTNLRFLVITSGTRIYSINVKTNKGGDDLTFNTFDLATIGTFTTFFSNYS 641

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QY 620 FTIGAWNFSSGNEVYIDRIEFPVVEVYEAEDYFEKAQEKVATLTSTNPRGLKTDVKDY 679
Db 642 LTVGADSPASGGEVYVDKFLFIPVNTFEAEEDLDVAKKAVNGLFTSKKD-ALQTSVTDY 700
QY 680 HDOVSNLVESLDEFLDEKRELFELVKYAKQIHENM 719
Db 701 QVNQAANLVCELSDELYPNEKRLMDAVKEAKRLVQARNL 740

RESULT 14
US-10-428-961-6
; Sequence 6, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rugar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)
; FILE REFERENCE: MECO201--1
; CURRENT APPLICATION NUMBER: US/10/428,961
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-428-961-6

Query Match 45.0%; Score 1683.5; DB 14; Length 653;
Best Local Similarity 51.3%; Pred. No. 2.8e-132;
Matches 345; Conservative 111; Mismatches 169; Indels 47; Gaps 15;

QY 13 SSNAKVCKIATSLKN---ETDIELKMNNDYLRSEHSIDPFSASTIQTGIGIAGK 69
Db 2 NENEIINALSIPAVSNHSAQMDLSL-DARIEDSLCIAEGNNINPLVASTVQTGINIAR 60
QY 70 ILGLVFPAGQIASLYSFLIGELWPKGQWEIEMEHVEEIIINQKILTYARNKALSCLR 129
Db 61 ILGLVFPAGQIASLYSFLIGELWPSGRDPWEIILEYVEQLIQVQVNTENTRTAIAELE 120
QY 130 GLGDALAVYHESLESWYENRNTRARSVVKNQYIALELMPVQKLPFSFVSGEEVPLPIY 189
Db 121 GLGGRYSYQQALETWLDNRNDARSIIILERYVALELDITTAFLFRTRNEEVPLLMVY 180
QY 190 AQAAHLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDDHCICKWYNTGLNNLRGT 249
Db 181 AQAAHLHLLLRDASLFGSEWGMASSDVNQYIQEIRYTBESNHCQVWYNTGLNNLRGT 240
QY 250 NAKSWVRVNCERKDMTLMVLDAVALPSSYDTLVYPIKTSQLTREYVTDAGTVHPNQAF 309
Db 241 NAEWSLRYNQFRDLTLGLVDLVALPSSYDTRTYPINTSAQLTREIYTDPIGRTNAPSGF 300
QY 310 ASTWYNNNAPSASIAEAAVTRSPHLLDFLEKVTIYSLLRWSNTQYNNWGGHRLSRP 369
Db 301 ASTWYNNNAPSASIAEAAIFRPHLLDFPEQLTIYSASSRWSSTQHMYWVGHRLNFRP 360
QY 370 IGAALNTSQGST-NTSINPVLQF-TSRDVRTESLAGNLFTQPVNGVPRVDFHWKF 427
Db 361 IGGTLNTSQGLTNTSINPVLHYSSRDVYRTESNAGNINLFTTPVNGVPRVAREN--F 418
QY 428 PTL-----PIASDN--FYILGAGVGTQLQDSENELPPTTGPQNYESYSHRLSHIG-- 477
Db 419 ITRIFMKEAPLPTVNIRELGNLYLOKLNHQK-----QONDQIMNHIVIDISYR 470
QY 478 LISASHVKALVYSWTHRSADRTNTIBPNSITQIPLVKAFNLSSGAAVVRGPGTGGDILR 537
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Db 471 LIIGNTRAPVYSWTHRSADRTNTIGPNRITQIPAVKGRFLFNG-SVISGPGFTGGDVVR 529
QY 538 -RTNIGTF---GDIRVNIN-PFPAQRYVRIRYASTTDLQFHTSINGKAINQGNFSATMN 592
Db 530 LNRNNGNIQNRGYIEVPIQFTSTSTRYVRVRYASVTSIELNVNLGNSSIFTNTLPATAA 589
QY 593 RGEDLDYKTFRTIGFTTTPFSFSDVQSTTT-----IGAWNPFSSGNEVYIDRIEFPVVEVT 646
Db 590 SLDNLQ-----SGDFGYVEINNATTSATGNIVGARNFSANAEEVIDRPEFIPVTAT 640
QY 647 YEAYDFEKAQE 658
Db 641 FEVEYDLERAQK 652

RESULT 15
US-10-782-141-16
; Sequence 16, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10/782,141
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-782-141-16

Query Match 44.3%; Score 1657.5; DB 17; Length 1157;
Best Local Similarity 48.9%; Pred. No. 1e-129;
Matches 368; Conservative 107; Mismatches 228; Indels 49; Gaps 19;

QY 1 MKNKPNDEKHSLSNAKVDKIATDS----LKNETDIELKMNNDYLRMSEHE-----S 50
Db 1 MSPNNQNEYELIDATPST-SVSSDSNRYPFANEPTDALQNNYKDYKMSGGENBELFGN 59
QY 51 IDPFVSASTIQTGIGIAGKIILGTLGVPPAGQIASLYSFLIGELWP-KGKSQWEIEMEHVE 109
Db 60 PETFSSSTIQTGIGIAGIILGALGVPPASQIASFYSFIVGQLWPKSVDTWGEINERVE 119
QY 110 EIIINQKILTYARNKALSCLRGLGDALAVYHESLESWYENRNTRARSVVKNQYIALELMP 169
Db 120 ELVDQKIEKYVKDKALAEKLGKLNALDVYQSLDLEWLENRNDARTRSWSNQFIALDLNF 179
QY 170 VQKLPSFVSGEEVPLPIYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTR 229
Db 180 VSSIISFVSGHEVLLAVYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVQLTA 239
QY 230 DYSRCHIKWYNTGLNNLRGTNAXSWRYNQFRKDMTLMVLDAVALPSSYDTLVYPIKTS 289
Db 240 EYSDYCVKWKYKIGLDKLGKTSKSWLVYHQFRREMILLVLDLVALFPNYDTHMYPETTA 299
QY 290 QLTREYVTDAGI-TVHPNQAFSTTWNNAAPSASIAEAAVTRSPHLLDFLEKVTIYSL 348
Db 300 QLTREVYTDPIAFNIVTSTGFCN-PWSTHSGILFYEVENNVIRPPLFDLILSSVEINT-- 356
QY 349 SR-----WSNTQYNNWGGHRLSRPIGGALNTST--QGSTNTSINPVLQTSRDVYRTE 402
Db 357 SRGGITLNDAYINYSWGHTLKYRRTADSTVTYTYTANYGRITSEKNSFALE--DRDIFEIN 414
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 17:51:02 ; Search time 86.6903 Seconds  
(without alignments)  
2975.262 Million cell updates/sec

Title: US-10-019-823B-59

Perfect score: 3742

Sequence: 1 MKLKNPDHQSLSSNAKYDK.....KRELFPIVKYAKQIHENM 719

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3742	100.0	719	4	AAB66912	Aab66912 Insectici
2	3742	100.0	719	6	AAB36276	Aae36276 B. thurin
3	3598	96.2	719	7	ADM74717	Adm74717 B. thurin
4	3546	94.8	719	2	AAW49089	Aaw49089 Bacillus
5	3520	94.1	719	4	AAB66908	Aab66908 Insectici
6	3520	94.1	719	5	AAB66272	Aae36272 B. thurin
7	3516	94.0	719	4	AAB66910	Aab66910 Insectici
8	3511	94.0	719	6	AAB36274	Aae36274 B. thurin
9	3511	93.8	719	4	AAU02095	Aau02095 Bacillus
10	3509	93.8	719	4	AAB66911	Aab66911 Insectici
11	3509	93.8	719	6	AAB36275	Aae36275 B. thurin
12	3503	93.6	719	4	AAB66909	Aab66909 Insectici
13	3503	93.6	719	6	AAB36273	Aae36273 B. thurin
14	3499	93.5	719	2	AAW08041	Aaw08041 81 kb end
15	3488.5	93.2	718	6	AAB36271	Aae36271 B. thurin
16	3482.5	93.1	718	4	AAB66907	Aab66907 Insectici
17	3368.5	90.0	710	4	AAU02041	Aau02041 B. thurin
18	3311	88.5	719	3	ABO7073	Abb07073 Bacillus
19	3060	81.8	1217	4	AAU02092	Aau02092 Bacillus
20	2645	70.7	1208	4	AAU02093	Aau02093 Bacillus
21	2460	65.7	1230	8	ADK98484	Adk98484 B thuring
22	2460	65.7	1230	8	ADK98489	Adk98489 B thuring
23	2460	65.7	1230	8	ADK98481	Adk98481 B thuring
24	2460	65.7	1230	8	ADK98491	Adk98491 B thuring
25	2460	65.7	1230	8	ADK98487	Adk98487 B thuring

26	2459	65.7	1229	2	AAR54074	Aar54074 CryET5. 2
27	2459	65.7	1229	2	AAW35259	Aaw35259 Bacillus
28	2459	65.7	1229	2	AAW17699	Aaw17699 CryET5. 3
29	2459	65.7	1229	2	AAW87633	Aaw87633 CryET5 pr
30	2459	65.7	1229	2	AAW30923	Aay30923 B. thurin
31	2459	65.7	1229	8	ADK98479	Adk98479 B thuring
32	2322.5	62.1	1228	2	AAR50955	Aar50955 Bacillus
33	2317.5	61.9	1209	4	AAU02094	Aau02094 Bacillus
34	2308.5	61.7	1227	2	AAW31990	Aay31990 Chimeric
35	2243	59.9	1227	2	AAW44321	Aaw44321 Bacillus
36	2243	59.9	1227	4	AAB19950	Aab19950 Bacillus
37	2234	59.7	1227	4	AAU02046	Aau02046 B. thurin
38	2233.5	59.7	488	2	AAW44322	Aaw44322 Bacillus
39	2233.5	59.7	488	4	AAB19947	Aab19947 Bacillus
40	2219	59.3	1186	2	AAW16796	Aay16796 Amino aci
41	2198.5	58.8	1221	4	AAU00421	Aau00421 B. thurin
42	2184.5	58.4	1221	4	AAU00420	Aau00420 B. thurin
43	2170.5	58.0	1228	4	AAB84628	Aab84628 Amino aci
44	2168.5	58.0	1228	4	AAU02039	Aau02039 B. thurin
45	1982	53.0	643	2	AAW16797	Aay16797 Amino aci

ALIGNMENTS

RESULT 1  
AAB66912  
ID AAB66912 standard; protein; 719 AA.  
XX  
AC AAB66912;  
XX  
DT 12-APR-2001 (first entry)  
XX  
DE Insecticidal protein cry1Ib1.  
XX  
KW Insecticide; transgenic plant; insect-resistance.  
XX  
OS Paecilomyces sp.  
XX  
PN WO200100841-A1.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-GB002457.  
XX  
PR 29-JUN-1999; 99GB-00015215.  
PR 23-DEC-1999; 99GB-00030536.  
XX  
(ZENE ) ZENECA LTD.  
Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
Vincent JL, Lee MD;  
WPI; 2001-123015/13.  
Novel insecticidal protein obtained from species of Paecilomyces for  
controlling insects, and for insect-resistant transgenic plant  
production.  
Claim 14; Page 64-66; 72pp; English.  
The present invention relates to novel insecticidal proteins obtained  
from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
insecticidal proteins can be used to produce transgenic plants, which are  
insect-resistant. Also, the insecticidal proteins are useful for  
controlling insects by providing them at a locus where insects feed

Query Match 100.0%; Score 3742; DB 4; Length 719;  
Best Local Similarity 100.0%; Pred. No. 2e-300;  
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M K L K N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H S I D P F V S A S T I 60  
 D b 1 M K L K N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H S I D P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q I L T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q I L T Y A 120  
 QY 121 R N K A L S D L R G L G D A L A V H E S L E S W E N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
 D b 121 R N K A L S D L R G L G D A L A V H E S L E S W E N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F F N R Q V E R T R D Y S D H C I K W Y N 240  
 D b 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F F N R Q V E R T R D Y S D H C I K W Y N 240  
 QY 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S Q L T R E V Y T D A I 300  
 QY 301 G T V H N Q A F A S T T W Y N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R S N T Q Y M N W 360  
 D b 301 G T V H N Q A F A S T T W Y N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R S N T Q Y M N W 360  
 QY 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F P T L P I A S D N F Y Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F P T L P I A S D N F Y Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S G A A V R G P G T G G D I L R R T N 540  
 D b 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S G A A V R G P G T G G D I L R R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T I G F T T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P E V T Y E A Y D F E K A Q E K V 660  
 D b 601 T F R T I G F T T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P E V T Y E A Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K E L F E I V K Y A K Q I H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K E L F E I V K Y A K Q I H I E R N M 719

RESULT 2  
 ID- AAE36276 standard; protein; 719 AA.  
 XX AAE36276;  
 AC AC  
 XX 26-JUN-2003 (first entry)  
 DT DT  
 XX B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cry1b1.  
 DE DE  
 XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 KW KW  
 XX Bacillus thuringiensis.  
 OS OS  
 XX WO200298911-A2.  
 PN PN  
 XX 12-DEC-2002.  
 PD PD  
 XX 30-MAY-2002; 2002WO-GB002666.  
 PF PF  
 XX 07-JUN-2001; 2001GB-00013900.  
 PR PR  
 XX (SYGN ) SYNGENTA LTD.  
 PA PA  
 XX

PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 DR New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PT Claim 12; Page 56-58; 67pp; English.  
 PS The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 CC Sequence 719 AA;  
 S Q  
 Query Match 100.0%; Score 3742; DB 6; Length 719;  
 Best Local Similarity 100.0%; Pred. No. 2e-300;  
 Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 M K L K N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H S I D P F V S A S T I 60  
 D b 1 M K L K N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H S I D P F V S A S T I 60  
 QY 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q I L T Y A 120  
 D b 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E E I I N Q I L T Y A 120  
 QY 121 R N K A L S D L R G L G D A L A V H E S L E S W E N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
 D b 121 R N K A L S D L R G L G D A L A V H E S L E S W E N N T R A R S V V K N Q Y I A L E M F V Q K L P S F A V S G 180  
 QY 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F F N R Q V E R T R D Y S D H C I K W Y N 240  
 D b 181 E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F F N R Q V E R T R D Y S D H C I K W Y N 240  
 QY 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S Q L T R E V Y T D A I 300  
 D b 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S Q L T R E V Y T D A I 300  
 QY 301 G T V H N Q A F A S T T W Y N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R S N T Q Y M N W 360  
 D b 301 G T V H N Q A F A S T T W Y N N A P S F A I E A A V I R S P H L L D F L E K V T I Y S L L S R S N T Q Y M N W 360  
 QY 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 D b 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
 QY 421 V D F H W K F P T L P I A S D N F Y Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 D b 421 V D F H W K F P T L P I A S D N F Y Y L G Y A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 QY 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S G A A V R G P G T G G D I L R R T N 540  
 D b 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S G A A V R G P G T G G D I L R R T N 540  
 QY 541 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 D b 541 T G T F G D I R V N I N P P F A Q R Y R V R I Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
 QY 601 T F R T I G F T T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P E V T Y E A Y D F E K A Q E K V 660  
 D b 601 T F R T I G F T T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P E V T Y E A Y D F E K A Q E K V 660  
 QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K E L F E I V K Y A K Q I H I E R N M 719  
 D b 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K E L F E I V K Y A K Q I H I E R N M 719

RESULT 3  
ADM74717  
ID ADM74717 standard; protein; 719 AA.  
XX  
AC ADM74717;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE B. thuringiensis cryIIel SEQ ID NO:2.  
XX  
KW cryII; toxicity; lepidoptera; cryIaB; coleoptera; diptera;  
KW cryIIel.  
XX  
OS Bacillus thuringiensis.  
XX  
PN CN1401772-A.  
XX  
PD 12-MAR-2003.  
XX  
PF 20-AUG-2001; 2001CN-00124163.  
XX  
PR 20-AUG-2001; 2001CN-00124163.  
XX  
PA (PLAN-) PLANT PROTECTION INST CHINESE ACAD AGRIC.  
XX  
PI Song F, Zhang J, Huang D;  
XX  
DR WPI; 2003-442339/42.  
DR N-PSDB; ADM74716.  
XX  
PT Bacillus thuringiensis cryI gene, expression vector, nucleotide sequence  
PT with high-toxicity to lepidoptera pests, encoded protein, primer  
PT sequences and the shuttle vector pSX422b, useful as a pesticide.  
XX  
PS Example 3; SEQ ID NO 2; 29pp; Chinese.  
XX  
CC The invention relates to a novel Bacillus thuringiensis cryI gene, gene  
CC combination, expression vector, nucleotide sequence of the B  
CC thuringiensis cryI gene with high-toxicity to lepidoptera pests and the  
CC amino acid sequence of the protein encoded by it, cooperative use of the  
CC cryI gene with the expression product of cryIaB or cryIbA, primer  
CC sequences for expressing the genes, and the constructed shuttle vector  
CC pSX422b. The gene in combination with the cryIaB or cryIbA genes  
CC displays high toxicity to the lepidoptera, coleoptera and diptera pests.  
CC The present sequence represents the cryIIel protein.  
XX  
SQ Sequence 719 AA;  
Query Match 96.2%; Score 3598; DB 7; Length 719;  
Best Local Similarity 95.1%; Pred. No. 1.7e-288;  
Matches 684; Conservative 23; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MLLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPFVSASTI 60  
DB 1 MLLKNPDKHQSLSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTILGVPAGQIASLYFILGELWPKGSKQWEIFMEHVEEIIINOKILTYA 120  
DB 61 QTGIGIAGKILGTILGVPAGQIASLYFILGELWPKGSKQWEIFMEHVEEIIINOKILTYA 120  
QY 121 RNKALSDRLGLDALAVYHESLESWENNRNTRARSVVKNCYIALELMFVKLPSPFVSG 180  
DB 121 RNIALADLGLDALAVYHESLESWENNRNTRARSVVKNCYIALELMFVKLPSPFVSG 180  
QY 181 EEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNQVETRDYSDHCIKWYN 240  
DB 181 EEVPLPIYAQAANLHLLLRDASVFGKEWGLSNSQISTFYNQVETRDYSDHCVKWYS 240  
QY 241 TGLNLRGNTAKSWRYNQFRKDMTLMVLDLVALFSDYDLTVYPKTTTSQLTREYVYTDI 300  
DB 241 TGLNLRGNTAKSWRYNQFRKDMTLMVLDLVALFSDYDLTVYPKTTTSQLTREYVYTDI 300

QY 301 GTVHPNQAFASSTWYNNAPSAEAAVIRSPHLDDLEKVTIYLLSRKSNTOYMMNW 360  
DB 301 GTVHPNASPASTWYNNAPSAEAAVIRSPHLDDLEKVTIYLLSRKSNTOYMMNW 360  
QY 361 GGHRLSPRIIGGALNTSTOGSTNTSINPVTLOFTSRDYYRTESLAGLNLFLOPVGVP 420  
DB 361 GGHRLSPRIIGGALNTSTOGSTNTSINPVTLOFTSRDYYRTESLAGLNLFLOPVGVP 420  
QY 421 VDFHWKFPPLPIASDNFYLYGAGVGTLQDSNELPPETTGQPNVYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFPPLPIASDNFYLYGAGVGTLQDSNELPPETTGQPNVYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
DB 481 ASHVKALVSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
QY 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
DB 541 TGTGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSATMNRGDLDYK 600  
QY 601 TFRITGFTTTPPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
DB 601 TFRITGFTTTPPSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
RESULT 4  
AAW49089  
ID AAW49089 standard; protein; 719 AA.  
XX  
AC AAW49089;  
XX  
DT 26-OCT-1998 (first entry)  
XX  
DE Bacillus thuringiensis isolate C-18 crystal II protein.  
XX  
KW Bacillus thuringiensis isolate C-18; BtC-18; Bt; crystal II; CryII;  
KW sporulation; insecticidal activity; pest control; rootworm; agriculture.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO9830700-A1.  
XX  
PD 16-JUL-1998.  
XX  
PF 09-JAN-1998; 98WO-US000357.  
XX  
PR 10-JAN-1997; 97US-0035361P.  
XX  
PA (OSMA/) OSWAN Y A.  
PA (MADK/) MADKOUR M A.  
XX (BULL/) BULLA L A.  
PI Osman YA, Madkour MA, Bulla LA;  
XX  
DR WPI; 1998-399145/34.  
XX N-PSDB; AAW32950.  
PT Bacillus thuringiensis strain with broad spectrum pesticidal activity -  
PT useful as insecticidal agent, and proteins and nucleotide(s) isolated  
PT from strain, useful as insecticides and to produce resistant plants.  
XX  
PS Disclosure; Fig 5; 50pp; English.  
XX  
CC The present sequence represents the Bacillus thuringiensis (Bt) isolate C  
CC -18 (BtC-18) crystal II (CryII) protein. Bt is a bacterium which produces  
CC crystalline inclusions during sporulation, composed primarily of a single  
CC polypeptide. These crystal proteins (Cry, e.g. class CryII) exhibit highly  
CC specific insecticidal activity, so that most Bt strains kill insects  
CC belonging to only one order. The invention claims for a stable BtC-18

CC strain which produces at least three different types of crystal proteins  
 CC and is therefore claimed to be capable of killing insects from at least  
 CC three orders, thus providing a suitable alternative for broad-spectrum  
 CC agricultural pest control. The isolated crystal proteins, for e.g. CryII  
 CC protein, can also be applied to control pests (alone or with e.g. other  
 CC insecticidal proteins) and is useful to produce antibodies to isolate  
 CC similar proteins from other strains/organisms. The invention also  
 CC provides a BtC-18 toxin protein which is active against rootworms. The  
 CC Cry encoding nucleic acids are claimed to be useful for expressing the  
 CC Cry proteins in plants, to produce pest-resistant transgenic plants and  
 CC plant products, or in micro-organisms, which can be applied to protect  
 CC agricultural crops. They are also useful to isolate nucleic acids  
 CC encoding potentially pesticidal proteins from other strains/organisms by  
 CC hybridisation  
 XX  
 SQ Sequence 719 AA;

Query Match 94.8%; Score 3546; DB 2; Length 719;  
 Best Local Similarity 95.0%; Pred. No. 3.4e-284;  
 Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

Qy 1 M K L N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H E S I D P F V S A S T I 60  
 Db 1 M K L N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H E S I D P F V S A S T I 60

Qy 61 Q T G I G I A G K I L G T L G V P P A G Q I A S L Y S F I L G E L W P K G S O W E I F M E H V E E I I N K I L T Y A 120  
 Db 61 Q T G I G I A G K I L G T L G V P P A G Q I A S L Y S F I L G E L W P K G S O W E I F M E H V E E I I N K I S T Y A 120

Qy 121 R N K A L S D L R G L G D A L A V Y H S E S W E N N T R A R S V V K Q Y I A L E L M F V Q K L P S F A V S G 180  
 Db 121 R N K A L T D L R G L G D A L A V Y H S E S W G N N N T R A R S V V K Q Y I A L E L M F V Q K L P S F A V S G 180

Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F N R Q V E R T R D Y S D H C I K W N 240  
 Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F N R Q V E R T R D Y S Y H C V K W N 240

Qy 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S O L T R E V Y T D A I 300  
 Db 241 T G L N L R A T G S W R Y N Q F R K D I E L M V L D L V R V F P S Y D T L V P I K T T S O L T R E V Y T D A I 300

Qy 301 G T V H P N Q A F A S T T W Y N N A P S A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N W 360  
 Db 301 G T V D P N Q A L R S T T W Y N N A P S A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N W 360

Qy 361 G G H L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y T E S L A G L N L F L T Q P V N G V P R 420  
 Db 361 G G H L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D F Y T E S W A G L N L F L T Q P V N G V P R 420

Qy 421 V D F H W K F P T L P I A S D N F Y L G A V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
 Db 421 V D F H W K F P T L P I A S D N F Y L G A V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480

Qy 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A P N L S G A A V R G P G T G G D I L R T N 540  
 Db 481 G S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A P N L S G A A V R G P G T G G H I L R T K 540

Qy 541 T G T F G D I R V N I N P P F A Q R Y R I R Y A S T T D I Q F H T S I N G K A I N Q N F S A T M N R C E D L D Y K 600  
 Db 541 S G T F G H I R V N I N P P F A Q R Y R V M S Y A S T T D I Q F H T S I N G K A I N Q N F S A T M N R C E D L D Y K 600

Qy 601 T F R I G T F T P F S D V Q S T F T T G A M P S S G N E V Y I D R I E F V P V E V T Y E A Y D F E K A Q E K V 660  
 Db 601 T F R I V G T F T P F S D V Q S T F T T G A M P S S G N E V Y I G R I E F V P V E V T Y E A Y D F E K A Q E K V 660

Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K A Q I H I E R N N 719  
 Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E L Y L D E K R E L F E I V K A Q I H I E R N N 719

RESULT 5  
 AAB66908  
 ID AAB66908 standard; protein; 719 AA.

XX AAB66908;  
 AC 12-APR-2001 (first entry)  
 DT Insecticidal protein cryIIa2.  
 DE Insecticide; transgenic plant; insect-resistance.  
 KW Paecilomyces sp.  
 OS WO200100841-A1.  
 PN 04-JAN-2001.  
 PD 23-JUN-2000; 2000WO-GB002457.  
 PF 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECA LTD.  
 PA Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 PT Claim 14; Page 55-57; 72pp; English.  
 PS The present invention relates to novel insecticidal proteins, obtained  
 XX from Paecilomyces sp. (see AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX Sequence 719 AA;

Query Match 94.1%; Score 3520; DB 4; Length 719;  
 Best Local Similarity 92.9%; Pred. No. 4.8e-282;  
 Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;

Qy 1 M K L N P D K H Q S L S S N A K V D K I A T D S L K N E T D I E L K N M N E D Y L R M S E H E S I D P F V S A S T I 60  
 Db 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60

Qy 61 Q T G I G I A G K I L G T L G V P P A G Q I A S L Y S F I L G E L W P K G S O W E I F M E H V E E I I N K I L T Y A 120  
 Db 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L W P K G N Q W E I F M E H V E E I I N Q I S T Y A 120

Qy 121 R N K A L S D L R G L G D A L A V Y H S E S W E N N T R A R S V V K Q Y I A L E L M F V Q K L P S F A V S G 180  
 Db 121 R N K A L T D L R G L G D A L A V Y H S E S W G N N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180

Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F N R Q V E R T R D Y S D H C I K W N 240  
 Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S S E I S T F N R Q V E R A G D Y S D H C V K W Y S 240

Qy 241 T G L N L R G T N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S O L T R E V Y T D A I 300  
 Db 241 T G L N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

Qy 301 G T V H P N Q A F A S T T W Y N N A P S A I E A A V I R S P H L L D F L E K V T I Y S L L S R W S N T Q Y M N W 360  
 Db 301 G T V H P H S T S T T W Y N N A P S A I E A A V R N P H L L D F L E Q V T I Y S L L S R W S N T Q Y M N W 360

Qy 361 G G H L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y T E S L A G L N L F L T Q P V N G V P R 420  
 Db 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y T E S L A G L N L F L T Q P V N G V P R 420

QY 421 VDFHWKFPPTLPASDNFYLLGYAGVGTQLODSENELPPPTTGPQNYESYSHRSLHIGLIS 480  
DB 421 VDFHWKFPVTHPIASDNFYYPGYAGIGTQLODSENELPPPTTGPQNYESYSHRSLHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGFGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGFGFTGGDILRRTN 540  
QY 541 TGFEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
DB 541 TGFEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 601 TPTTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
DB 601 TPTTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQHLIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQHLIERNM 719

RESULT 6  
AAE36272 standard; protein; 719 AA.  
AC AAE36272;  
DT 26-JUN-2003 . (first entry)  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa2.  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX Bacillus thuringiensis.  
OS WO200298911-A2.  
PN 12-DEC-2002.  
PD 30-MAY-2002; 2002WO-GB002666.  
PF 07-JUN-2001; 2001GB-00013900.  
PR (SYGN ) SYNGENTA LTD.  
PA Vincent JL, Viner R;  
PI WPI; 2003-175137/17.  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
PS Claim 12; Page 44-47; 67pp; English.  
XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
SQ Sequence 719 AA;

Query Match 94.1%; Score 3520; DB 6; Length 719;  
Best Local Similarity 92.9%; Pred. No. 4.8e-282;  
Matches 668; Conservative 31; Mismatches 20; Indels 0; Gaps 0;  
QY 1 MKLKNPDKHQSLSSNAKYDKIATDSLKNETDIELKMNEDYLRMSEHESIDPFVSASTI 60  
DB 1 MKLKNQDKHQSFSSNAKYDKISTDSLKNETDIELQNHEDCLKMSYENVEPFVSASTI 60

QY 61 QTGIGIAGKILGTLPAGQIASLYSFIILGELWPKGKQSEIFMEHVEEIIINQKILTYA 120  
DB 61 QTGIGIAGKILGTLPAGQIVASLYSFIILGELWPKGKQSEIFMEHVEEIIINQKISTYA 120  
QY 121 RNKALSDLRGLGDALAVYHESLESWENNRNTRARSVVKXQYIALELMFVQKLPFAVSG 180  
DB 121 RNKALTDLKGLGDALAVYHDSLESWGNRNTRARSVVKSQYIALELMFVQKLPFAVSG 180  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVETRDRYSDHCIKWYN 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDHCVKWYS 240  
QY 241 TGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFSDYDILVYPIKTTQSOLTREVVYTDAL 300  
DB 241 TGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSDYDQMPYPIKTTAQLTREVVYTDAL 300  
QY 301 GTVHPNQAFASFTWYNNNAPSFAIAEAAVIRSPHLLDFLEKVTIYLSLSRWNTQYMMNW 360  
DB 301 GTVHPHPSFTTWTWYNNNAPSFAIAEAAVVRNPHLLDFLEQVTIYLSLSRWNTQYMMNW 360  
QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRVYTESLAGNLFITQPVNGVPR 420  
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVRVYTESLAGNLFITQPVNGVPR 420  
QY 421 VDFHWKFPPLPIASDNFYLLGYAGVGTQLODSENELPPPTTGPQNYESYSHRSLHIGLIS 480  
DB 421 VDFHWKFPVTHPIASDNFYYPGYAGIGTQLODSENELPPPTTGPQNYESYSHRSLHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGFGFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFNLSSGAAVVRGFGFTGGDILRRTN 540  
QY 541 TGFEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
DB 541 TGFEGDIRVNINPPFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSAATMRGEDLDYK 600  
QY 601 TPTTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
DB 601 TPTTIGFTTTPFSFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQHLIERNM 719  
DB 661 TALFTSTNPRGLKTDVXDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQHLIERNM 719

RESULT 7  
AAB66910 standard; protein; 719 AA.  
XX AAB66910;  
AC AAB66910;  
XX 12-APR-2001 (first entry)  
DT Insecticidal protein cryIIa4.  
DE Insecticide; transgenic plant; insect-resistance.  
XX Paecilomyces sp.  
KW WO200100841-A1.  
XX 04-JAN-2001.  
XX 23-JUN-2000; 2000WO-GB002457.  
XX 29-JUN-1999; 99GB-00015215.  
XX 23-DEC-1999; 99GB-00030536.  
PA (ZENE ) ZENECA LTD.  
XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
PI Vincent JL, Lee MD;

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XX DR WPI; 2001-123015/13.
XX DR
XX PT Novel insecticidal protein obtained from species of Paecilomyces for
XX PT controlling insects, and for insect-resistant transgenic plant
XX PT production.
XX XX
XX PS Claim 14; Page 60-62; 72pp; English.
XX XX
XX CC The present invention relates to novel insecticidal proteins obtained
XX CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The
XX CC insecticidal proteins can be used to produce transgenic plants, which are
XX CC insect-resistant. Also, the insecticidal proteins are useful for
XX CC controlling insects by providing them at a locus where insects feed
XX XX
XX SQ Sequence 719 AA;

Query Match          94.0%; Score 3516; DB 4; Length 719;
Best Local Similarity 92.8%; Pred. No. 1e-281;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

Qy 1 M K L K N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H E S I D P F V S A S T I 60
Db 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K S E Y E N V E P F V S A S T I 60

Qy 61 Q T G I G I A G K I L G T L G V P P A G Q I A S L Y S F I L G E L M P K G S Q W E I F M E H V E R I I N O K I L T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E R I I N O K I S T Y A 120

Qy 121 R N K A L S D L R G L G D A L A V H S E S W E N N T R A R S V V K N Q V I A L E L M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A R S V V K S Q V I A L E L M F V Q K L P S F A V S G 180

Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F N R Q V E R T R D Y S D H C I K W N 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F N R Q V E R A G D Y S D H C V K W S 240

Qy 241 T G L N L R G N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S O L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

Qy 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A V I R S P H L D F L E K V T I Y S L L S W S N T Q Y M N W 360
Db 301 G T V H P H P S T S T T W Y N N N A P S F A I E A A V R N P H L D F L E Q V T I Y S L L S W S N T Q Y M N W 360

Qy 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q T S R D V Y R T E S L A G L N F L T Q P V N G V P R 420
Db 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N F L T Q P V N G V P R 420

Qy 421 V D F H W K F P T L P I A S D N F Y Y L G V A G V G T Q L O D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480
Db 421 V D F H W K F V T H P I A S D N F Y Y P G Y V G I G T Q L O D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480

Qy 481 A S H V K A L V S W T H E S A D R T N T I E P N S I T Q I P L A K A F N L S S G A A V R G P G T G G D I L R T N 540
Db 481 A S H V K A L V S W T H R S A D R T N T I E P N S I T Q I P L A K A F N L S S G A A V R G P G T G G D I L R T N 540

Qy 541 T G T F G D I R V N I N P P A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600
Db 541 T G T F G D I R V N I N P P A Q R Y R I R Y A S T T D L Q F H T S I N G K A I N Q N F S A T M N R G E D L D Y K 600

Qy 601 T F R T I G T T P F S D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A Y D P F K A Q E K V 660
Db 601 T F R T V G T T P F S L D V Q S T F T I G A W N F S S G N E V I D R I E F V P V E V T Y E A Y D P F K A Q E K V 660

Qy 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719
Db 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A K Q I H I E R N M 719

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XX AC AAE36274;
XX XX
XX DT 26-JUN-2003 (first entry)
XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa4.
XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.
XX OS Bacillus thuringiensis.
XX PN WO200298911-A2.
XX PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-GB002666.
XX PR 07-JUN-2001; 2001GB-00013900.
XX PA (SYGN ) SYNGENTA LTD.
XX PI Vincent JL, Viner R;
XX DR WPI; 2003-175137/17.
XX PS New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.
XX CC Claim 12; Page 50-53; 67pp; English.
XX CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.
XX CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention
XX SQ Sequence 719 AA;

Query Match          94.0%; Score 3516; DB 6; Length 719;
Best Local Similarity 92.8%; Pred. No. 1e-281;
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

Qy 1 M K L K N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K M N N E D Y L R M S E H E S I D P F V S A S T I 60
Db 1 M K L K N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K S E Y E N V E P F V S A S T I 60

Qy 61 Q T G I G I A G K I L G T L G V P P A G Q I A S L Y S F I L G E L M P K G S Q W E I F M E H V E R I I N O K I L T Y A 120
Db 61 Q T G I G I A G K I L G T L G V P P A G Q V A S L Y S F I L G E L M P K G K N Q W E I F M E H V E R I I N O K I S T Y A 120

Qy 121 R N K A L S D L R G L G D A L A V H S E S W E N N T R A R S V V K N Q V I A L E L M F V Q K L P S F A V S G 180
Db 121 R N K A L T D L K G L D A L A V H D S L E S W G N R N N T R A R S V V K S Q V I A L E L M F V Q K L P S F A V S G 180

Qy 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F N R Q V E R T R D Y S D H C I K W N 240
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F N R Q V E R A G D Y S D H C V K W S 240

Qy 241 T G L N L R G N A K S W R Y N Q F R K D M T L M V L D L V A L F P S Y D T L V P I K T T S O L T R E V Y T D A I 300
Db 241 T G L N L R G T N A E S W R Y N Q F R R D M T L M V L D L V A L F P S Y D T Q M Y P I K T T A Q L T R E V Y T D A I 300

Qy 301 G T V H P N Q A F A S T T W Y N N N A P S F A I E A V I R S P H L D F L E K V T I Y S L L S W S N T Q Y M N W 360
Db 301 G T V H P H P S T S T T W Y N N N A P S F A I E A A V R N P H L D F L E Q V T I Y S L L S W S N T Q Y M N W 360

Qy 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q T S R D V Y R T E S L A G L N F L T Q P V N G V P R 420
Db 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P F T S R D V Y R T E S L A G L N F L T Q P V N G V P R 420

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QY 421 VDFHWKFPPLPIASDNFYILGYAGVGTQLQDSENELPPETTTGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFPVTHPIASDNFYILGYAGVGTQLQDSENELPPETTTGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600  
QY 601 TFRGTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
DB 601 TFRGTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 9  
AAU02095  
ID AAU02095 standard; protein; 719 AA.

AC AAU02095;

DT 07-SEP-2001 (first entry)

XX Bacillus thuringiensis partial mutant CryIIa.

XX Crystal protein; CryIIa; CrylBa; moth; butterfly; Colorado potato beetle;  
KW mutant; mutain.

OS Bacillus thuringiensis.

FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal\_peptide  
FT Protein 20..719  
FT /label= Mature\_CryIIa

XX EPI099760-A1.

XX 16-MAY-2001.

XX 09-NOV-1999; 99EP-00203723.

XX 09-NOV-1999; 99EP-00203723.

XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.

XX De Maagd RA, Bosch HJ;

XX WPI; 2001-337141/36.

XX N-FSDB; AAS04855.

XX New hybrid Bacillus thuringiensis hybrid toxins comprising structural  
PT domains derived from at least 2 different crystal proteins, such as  
PT CryIIa and CrylBa, and having insecticidal activity, useful for combating  
PT insects.

XX Example; Page 30-32; 43pp; English.

XX The sequence is B. thuringiensis (Bt) crystal protein CryIIa, the DNA  
CC encoding which was mutated to allow cloning of domain III or domains I  
CC and II, to make the hybrid protoxins of the invention. The hybrid toxins  
CC of the invention, having structural domains I, II and III in this order  
CC starting from the N-terminal derived from at least 2 different crystal  
CC proteins, are useful for protecting plants against pest insects, e.g.  
CC moths, butterflies and Colorado potato beetle or for combating insects

SQ Sequence 719 AA;

Query Match 93.8%; Score 3511; DB 4; Length 719;  
Best Local Similarity 92.8%; Pred. No. 2.7e-281;  
Matches 667; Conservative 31; Mismatches 21; Indels 0; Gaps 0;

QY 1 MKLKNPDHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60  
DB 1 MKLKNPDHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60  
QY 61 QTGIGIAGKILGTLGVPFAGQIASLVSFILGELWPKGKSOWEIMFHEVVEEIIINOXILTVA 120  
DB 61 QTGIGIAGKILGTLGVPFAGQIASLVSFILGELWPKGKSOWEIMFHEVVEEIIINOXILTVA 120  
QY 121 RNKALSDLRGLDALAVYHESLESWENRNNTRARSVVKNQYIALELMFVQKLPFAVSG 180  
DB 121 RNKALSDLRGLDALAVYHESLESWENRNNTRARSVVKNQYIALELMFVQKLPFAVSG 180  
QY 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASELSTFYNQVERTRDYSDHCIKWYN 240  
DB 181 EEPVLLPIYAQAANLHLLLRDASIFGKEWGLSASELSTFYNQVERTRDYSDHCIKWYN 240  
QY 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTAQLTREVYTDAL 300  
DB 241 TGLNNLRGTNAESWVRYNQFRDWTLMVLDLVALFPSYDTQMPYIKTAQLTREVYTDAL 300  
QY 301 GTVHPNQAFASSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMNW 360  
DB 301 GTVHPNQAFASSTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMNW 360  
QY 361 GGHRLSRPTGGALNTSTCGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR 420  
DB 361 GGHRLSRPTGGALNTSTCGSTNTSINPVTLOFTSRDVRTESLAGLNFLTQPVNGVPR 420  
QY 421 VDFHWKFPPLPIASDNFYILGYAGVGTQLQDSENELPPETTTGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFPVTHPIASDNFYILGYAGVGTQLQDSENELPPETTTGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATNRGDLDYK 600  
QY 601 TFRGTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
DB 601 TFRGTGTTTSPFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 10  
AAB66911  
ID AAB66911 standard; protein; 719 AA.

XX AAB66911;

XX 12-APR-2001 (first entry)

XX Insecticidal protein cryIIa5.

XX Insecticide; transgenic plant; insect-resistance.

XX Paecilomyces sp.

XX WO200100841-A1.

XX 04-JAN-2001.

XX

PF 23-JUN-2000; 2000WO-GB002457.  
 XX 29-JUN-1999; 99GB-00015215.  
 PR 23-DEC-1999; 99GB-00030536.  
 XX (ZENE ) ZENECALTD.  
 XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;  
 PI Vincent JL, Lee MD;  
 XX WPI; 2001-123015/13.  
 DR Novel insecticidal protein obtained from species of Paecilomyces for  
 XX controlling insects, and for insect-resistant transgenic plant  
 PT production.  
 XX Claim 14; Page 62-64; 72pp; English.  
 XX The present invention relates to novel insecticidal proteins obtained  
 CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
 CC insecticidal proteins can be used to produce transgenic plants, which are  
 CC insect-resistant. Also, the insecticidal proteins are useful for  
 CC controlling insects by providing them at a locus where insects feed  
 XX  
 SQ Sequence 719 AA;  
 Query Match 93.8%; Score 3509; DB 4; Length 719;  
 Best Local Similarity 92.5%; Pred. No. 3.9e-281;  
 Matches 665; Conservative 33; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 MRLKNDPKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPFVSASTI 60  
 DB 1 MRLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLPVFPAGQASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTLPVFPAGQASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALSDLRGLDALAVYHESLESWENNRNTRARSVVKQYIALELMFVKLPSPFVSG 180  
 DB 121 RNKALSDLRGLDALAVYHDSLESWGNRNRNTRARSVRSQYIALELMFVKLPSPFVSG 180  
 QY 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFNRQVETRDYSDHCWKYN 240  
 DB 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFNRQVETRDYSDHCWKYS 240  
 QY 241 TGLNLRGNTAKSWVRYNQFRKDMTLMVLDLVALPFSYDTLVPIKTTQLTREYVTDI 300  
 DB 241 TGLNLRGNTAKSWVRYNQFRKDMTLMVLDLVALPFSYDTLVPIKTTQLTREYVTDI 300  
 QY 301 GTVHPNQAFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 DB 301 GTVHPNPFSTTWNNAAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMW 360  
 QY 361 GGHLESPIGGALNTSQGSTNTSINPVTLOFTSRDVRTTESLAGNLPLTOPVNGVPR 420  
 DB 361 GGHLEFRITGGTINISTQGSTNTSINPVTLPFTSRDVRTTESLAGNLPLTOPVNGVPR 420  
 QY 421 VDFHWKFTPLFIASDNFYLYGAGVGQLODSNELPPTTGPQNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPLFIASDNFYLYGAGVGQLODSNELPPTTGPQNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVYSWTHRSADRTNTTNPNSITQIPLVKAPNLSSGAAVVRGPGFTGGDILRTN 540  
 DB 481 ASHVKALVYSWTHRSADRTNTTNPNSITQIPLVKAPNLSSGAAVVRGPGFTGGDILRTN 540  
 QY 541 TGTFGDIRVINPFAQYRVRIRYASTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 DB 541 TGTFGDIRVINPFAQYRVRIRYASTDLQFHTSINGKAINQGNFSATMNRGEDLDYK 600  
 QY 601 TFRITGFTTFFSDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660  
 DB 601 TFRITGFTTFFSDVQSTFTTGAWNFSSGNEVYIDRIEFVPEVYEAEDFEKAQEKV 660

QY 661 TALFTSTNPRGLKTDVYKHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOIHBRNM 719  
 DB 661 TALFTSTNPRGLKTDVYKHIDQVSNLVESLSDEFYLDKRELFEIVKYANELHBRNM 719  
 RESULT 11  
 AAE36275  
 ID AAE36275 standard; protein; 719 AA.  
 XX AC AAE36275;  
 XX DT 26-JUN-2003 (first entry)  
 XX DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa5.  
 XX KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
 XX OS Bacillus thuringiensis.  
 XX PN WO200298911-A2.  
 XX PD 12-DEC-2002.  
 XX PF 30-MAY-2002; 2002WO-GB002666.  
 XX PR 07-JUN-2001; 2001GB-00013900.  
 XX PA (SYGN ) SYNGENTA LTD.  
 XX PI Vincent JL, Viner R;  
 XX WPI; 2003-175137/17.  
 PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 PS Claim 12; Page 53-56; 67pp; English.  
 XX The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects. Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 SQ Sequence 719 AA;  
 Query Match 93.8%; Score 3509; DB 6; Length 719;  
 Best Local Similarity 92.5%; Pred. No. 3.9e-281;  
 Matches 665; Conservative 33; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 MRLKNDPKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSEHESIDPFVSASTI 60  
 DB 1 MRLKNQDKHQSFSSNAKVDKISTDSLKNETDIELQNHEDCLKSEYENVEPVSASTI 60  
 QY 61 QTGIGIAGKILGTLPVFPAGQASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKILTYA 120  
 DB 61 QTGIGIAGKILGTLPVFPAGQASLYSIFILGELWPKGKQWEIFMEHVEEIIINOKISTYA 120  
 QY 121 RNKALSDLRGLDALAVYHESLESWENNRNTRARSVVKQYIALELMFVKLPSPFVSG 180  
 DB 121 RNKALSDLRGLDALAVYHDSLESWGNRNRNTRARSVRSQYIALELMFVKLPSPFVSG 180  
 QY 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFNRQVETRDYSDHCWKYN 240  
 DB 181 EEVPLLPYQAANLHLLLRDASIFGKEWGLSSSEISTFNRQVETRDYSDHCWKYS 240  
 QY 241 TGLNLRGNTAKSWVRYNQFRKDMTLMVLDLVALPFSYDTLVPIKTTQLTREYVTDI 300

Db 241 TGLNLRGTNAESWVRVYQFRDMDTLMVLDLVALPSPYDTQMPYPIKTTAQLTREYVYDAI 300  
QY 301 GTVHPNQAFSTWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW 360  
Db 301 GTVHPNPSTTWTYNNAPSPSAIEAAVVRNPPLLDLFLEQVTIYSLLSRWSTQYMNW 360  
QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVTSTESLAGLNFLTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVTSTESLAGLNFLTQPVNGVPR 420  
QY 421 VDFHWKFTPLPIASDNFYLYGACVGTQLODSENELPPETTCQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHWKFVTHPIASDNFYLYGACVGTQLODSENELPPETTCQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
Db 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRITGFTTFFSFDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
Db 601 TFRITGFTTFFSFDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
Db 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 12

AAE36273  
ID AAE36273 standard; protein; 719 AA.

AC AAE36273;

DT 12-APR-2001 (first entry)

DE Insecticidal protein cryIIa3.

XX Insecticide; transgenic plant; insect-resistance.

OS Paecilomyces sp.

XX WO200100841-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-GB002457.

PR 29-JUN-1999; 99GB-00015215.

PR 23-DEC-1999; 99GB-00030536.

XX (ZENE ) ZENECA LTD.

XX Griffin J, Carlile AJ, Cayley PJ, Mackay EA, Warner SAJ;

PI Vincent JL, Lee MD;

XX WPI; 2001-123015/13.

XX Novel insecticidal protein obtained from species of Paecilomyces for  
PT controlling insects, and for insect-resistant transgenic plant  
PT production.

XX Claim 14; Page 57-59; 72pp; English.

XX The present invention relates to novel insecticidal proteins obtained  
CC from Paecilomyces sp. (see AAB66899 to AAB66901 and AAB66913). The  
CC insecticidal proteins can be used to produce transgenic plants, which are  
CC insect-resistant. Also, the insecticidal proteins are useful for  
CC controlling insects by providing them at a locus where insects feed

SQ Sequence 719 AA;  
Query Match 93.6%; Score 3503; DB 4; Length 719;  
Best Local Similarity 92.5%; Pred. No. 1.2e-280;  
Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;  
QY 1 MKLKNPDKHOSLSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSRHESIDPFVSASTI 60  
DB 1 MKLKNQDKHOSFSSNAKVDKISTDSLKNETDIELQININDELCKMSEYENPFVSASTI 60  
QY 61 QTGIGTAGKTLGTLGVPPAGQIASLYSFTLGELWPKGKQWEIFMEHVEEIIINOKILTYYA 120  
DB 61 QTGIGTAGKTLGTLGVPPAGQVASLYSFTLGELWPKGKQWEIFMEHVEEIIINOKISTYYA 120  
QY 121 RNKALSDRLGDLALAVYHESLESWENRNNTRARSVVKNQYIALELMFVKLPSPFAVSG 180  
DB 121 RNKALTDLKGDLALAVVHDSLESWVGNNRNNTRARSVVKQYIALELMFVKLPSPFAVSG 180  
QY 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRTRDYSHCIKWYN 240  
DB 181 BEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKWYS 240  
QY 241 TGLNLRGTNAKSWVRVYQFRDMDTLMVLDLVALPSPYDTQMPYPIKTTAQLTREYVYDAI 300  
DB 241 TGLNLRGTNAESWVRVYQFRDMDTLMVLDLVALPSPYDTQMPYPIKTTAQLTREYVYDAI 300  
QY 301 GTVHPNQAFSTWYNNAPSPSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSTQYMNW 360  
DB 301 GTVHPNPSTTWTYNNAPSPSAIEAAVVRNPPLLDLFLEQVTIYSLLSRWSTQYMNW 360  
QY 361 GGHRLSPRIGGALNTSTQGSTNTSINPVTLOFTSRDVTSTESLAGLNFLTQPVNGVPR 420  
DB 361 GGHKLEFRITGGTLNISTQGSTNTSINPVTLPFTSRDVTSTESLAGLNFLTQPVNGVPR 420  
QY 421 VDFHWKFTPLPIASDNFYLYGACVGTQLODSENELPPETTCQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFVTHPIASDNFYLYGACVGTQLODSENELPPETTCQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540  
DB 481 ASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPFTGGDILRRTN 540  
QY 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
DB 541 TGTFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQGNFSAATMNRGEDLDYK 600  
QY 601 TFRITGFTTFFSFDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
DB 601 TFRITGFTTFFSFDVOSTFTIGAMNFSNGNEVYIDRIEFVPEVTEYAEYDPEKAQEKV 660  
QY 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVYHIDQVSNLVESLSDEFYLDKRELFEIVKYANLHIERNM 719

RESULT 13

AAE36273  
ID AAE36273 standard; protein; 719 AA.

AC AAE36273;

DT 26-JUN-2003 (first entry)

DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, cryIIa3.

XX Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.

XX Bacillus thuringiensis.

OS WO200298911-A2.

PD 12-DEC-2002.

PF 30-MAY-2002; 2002WO-GB002666.  
 XX  
 PR 07-JUN-2001; 2001GB-00013900.  
 XX  
 PA (SYGN ) SYNGENTA LTD.  
 XX  
 PI Vincent JL, Viner R;  
 XX  
 DR WPI; 2003-175137/17.  
 XX  
 XX New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
 XX  
 PS Claim 12; Page 47-50; 67pp; English.  
 XX  
 CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant constructs that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
 CC Antibodies raised to the insecticidal proteins can be used to identify other proteins with insecticidal activity. The present sequence is Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This sequence is used in the invention  
 XX  
 SQ Sequence 719 AA;  
 Query Match 93.6%; Score 3503; DB 6; Length 719;  
 Best Local Similarity 92.5%; Pred. No. 1.2e-280;  
 Matches 665; Conservative 32; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 MKLKNPKDQKSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSHEHSDIDPFVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCKMSEYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGLGVPFAGQIASLVSFILGELWPKGKQSEIFMEHVEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKILGTGLGVPFAGQVASLVSFILGELWPKGKQSEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALSDRLGLDALAVVHDSLESWENNRNTRARSVVKNQYIAELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLXGLDALAVVHDSLESWGNRNTRARSVVKQSVIAELMFVQKLPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLGSASEISTFYNQVERTRYSCHCIKWYN 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKWLGSASEISTFYNQVERTRYSCHCIKWYN 240  
 QY 241 TGLNLRGNTAKSWRYNQFRDMTLMVLDLVALFSPYDTLVPYIKTTSQLTREYVTDAL 300  
 DB 241 TGLNLRGNTAKSWRYNQFRDMTLMVLDLVALFSPYDTLVPYIKTTSQLTREYVTDAL 300  
 QY 301 GTVHPNQAFASFTTWNNAFSAIEAIVRSFPHLLDFLEKVTIYSLLSRWSNTQYMMNW 360  
 DB 301 GTVHPNPSFTTWNNAFSAIEAIVRVNPHLLDFLEQVTIYSLLSRWSNTQYMMNW 360  
 QY 361 GGHRLSPRIAGALNTSTOGSTNTSINPVLQFTSRDVRYESLAGLNLFLTQPVNGVPR 420  
 DB 361 GGHKLEFRTIGTLNISTOGSTNTSINPVLPTSRDVRYESLAGLNLFLTQPVNGVPR 420  
 QY 421 VDFHWKFPPLPIASDNFYVLGYAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTVTHPIASDNFYVPGYAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
 QY 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVRGPFGTGGDILLRRTN 540  
 DB 481 ASHVKALVSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVRGPFGTGGDILLRRTN 540  
 QY 541 TGTGDIRVNPFPQAVRVRIRYASTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600  
 DB 541 TGTGDIRVNPFPQAVRVRIRYASTDLQFHTSINGKAINQGNFSATMNRGDDLDYK 600  
 QY 601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 DB 601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660

DB 601 TFRITGFTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKV 660  
 QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
 DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVSLSDEFYLDKRELFEIVKYANELHIERNM 719  
 RESULT 14  
 AAR08041  
 ID AAR08041 standard; protein; 719 AA.  
 AC AAR08041;  
 XX  
 DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 27-FEB-1991 (first entry)  
 XX  
 DE 81 kD endotoxin deduced from DNA carried on pUHL2.  
 KW Crystal; insecticide; toxin; delta endotoxin.  
 XX  
 OS Bacillus thuringiensis; JHCC 4353 and 4835.  
 XX WO9013651-A.  
 PN  
 PD 15-NOV-1990.  
 XX  
 PF 09-MAY-1989; 89GB-00010624.  
 XX  
 PR 09-MAY-1989; 89GB-00010624.  
 XX  
 PA (ICIL ) IMPERIAL CHEM IND PLC.  
 XX  
 PI Blenk RG, Ely S, Tailor RH, Tippett JM;  
 DR WPI; 1990-361486/48.  
 DR N-PSDB; A3Q06636.  
 XX  
 PT Bacillus thuringiensis strains - used for producing an endotoxin for protecting plants against insects, partic. Lepidoptera and Coleoptera.  
 XX  
 PS Claim 5; Fig 5-10; 66pp; English.  
 XX  
 CC The sequence carried on pUHL2 which was isolated from B. thuringiensis strains JHCC4835 and JHCC 4353 (NCIB 40091 and 40090 resp.). The DNA can be used to produce transformants E.coli strain MC12022/pJH12 (NCIB 40278, or bacteriophage EMBL4 vector (NCIB 40279) or E.coli strain BL21/pJH11 (NCIB 40275). The delta-endo-toxin produced by the transformants can be used in formulations for combatting Lepidoptera and Coleoptera pests.  
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 719 AA;  
 Query Match 93.5%; Score 3499; DB 2; Length 719;  
 Best Local Similarity 92.5%; Pred. No. 2.7e-280;  
 Matches 665; Conservative 31; Mismatches 23; Indels 0; Gaps 0;  
 QY 1 MKLKNPKDQKSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSHEHSDIDPFVSASTI 60  
 DB 1 MKLKNQDKHQSFSNAKVDKISTDSLKNETDIELQNHEDCKMSEYENVEPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGLGVPFAGQIASLVSFILGELWPKGKQSEIFMEHVEEIIINQKILTYA 120  
 DB 61 QTGIGIAGKILGTGLGVPFAGQVASLVSFILGELWPKGKQSEIFMEHVEEIIINQKISTYA 120  
 QY 121 RNKALSDRLGLDALAVVHDSLESWENNRNTRARSVVKNQYIAELMFVQKLPFAVSG 180  
 DB 121 RNKALTDLXGLDALAVVHDSLESWGNRNTRARSVVKQSVIAELMFVQKLPFAVSG 180  
 QY 181 BEVPLPIYAQAANLHLLLRDASIFGKWLGSASEISTFYNQVERTRYSCHCIKWYN 240  
 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKWLGSASEISTFYNQVERTRYSCHCIKWYN 240

QY 241 TGLNNLRGNAKSWVRNQFRKDMTLMVLDLVALPFSYDYLVPYIKTTSQLTRREYVYDAI 300  
DB 241 TGLNNLRGNAKSWVRNQFRKDMTLMVLDLVALPFSYDYLVPYIKTTSQLTRREYVYDAI 300  
QY 301 GTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLLSRWNSNTQYMMNW 360  
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QY 361 GGHLESPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHLESPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480  
QY 481 ASHVKALVYSWTHRSADRTNTEPNSTIQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
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QY 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719  
DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 15  
AAE36271  
ID AAE36271 standard; protein; 718 AA.  
XX AAE36271;  
DT 26-JUN-2003 (first entry)  
XX  
DE B. thuringiensis insecticidal crystal endotoxin (CRY) protein, crystallal.  
XX  
KW Insecticidal protein; pesticide; insecticidal crystal endotoxin; CRY.  
XX  
OS Bacillus thuringiensis.  
XX  
PN WO200298911-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 30-MAY-2002; 2002WO-GB002666.  
XX  
PR 07-JUN-2001; 2001GB-00013900.  
XX  
PA (SYGN ) SYNGENTA LTD.  
XX  
PI Vincent JL, Viner R;  
XX  
DR WPI; 2003-175137/17.  
XX  
PT New insecticidal protein comprising an X-glycine motif at the amino-terminus, useful as an active ingredient of a pesticide.  
XX  
PS Claim 12; Page 42-44; 67pp; English.  
XX

CC The invention relates to insecticidal protein comprising an X-glycine motif at the amino-terminus. Polynucleotide or DNA constructs of the invention are useful for producing plants or plant parts that are resistant to insects. The protein or synergistic combination is useful as an active ingredient of a pesticide or for controlling insects.  
CC Antibodies raised to the insecticidal proteins can be used to identify

CC other proteins with insecticidal activity. The present sequence is  
CC Bacillus thuringiensis insecticidal crystal endotoxin (CRY) protein. This  
CC sequence is used in the invention  
XX  
SQ Sequence 718 AA;  
Query Match 93.2%; Score 3488.5; DB 6; Length 718;  
Best Local Similarity 92.5%; Pred. No. 2e-279;  
Matches 665; Conservative 31; Mismatches 22; Indels 1; Gaps 1;  
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QY 361 GGHLESPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
DB 361 GGHLESPRIGGALNTSTQGSTNTSINPVTLOFTSRDVRTESLAGLNLFLTQPVNGVPR 420  
QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480  
DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSNELPPETTGQPNYESYSHRLSHIGLIS 480  
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DB 661 TALFTSTNPRGLKTDVQYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKQIHIERNM 719

Search completed: October 28, 2004, 18:20:08  
Job time : 89.6903 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 28, 2004, 18:06:07 ; Search time 22.3343 Seconds  
(without alignments)  
2134.948 Million cell updates/sec

Title: US-10-019-823B-59  
Perfect score: 3742  
Sequence: 1 MKLKNPDKHQSLSSNAKVX.....KRELFIVKYAKQIHIERNM 719

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3546	94.8	719	2	US-09-003-217-2	Sequence 2, Appli
2	3541	94.6	719	3	US-09-218-942-2	Sequence 2, Appli
3	3516	94.0	719	3	US-08-286-870A-8	Sequence 8, Appli
4	3368.5	90.0	710	4	US-09-661-322A-42	Sequence 42, Appli
5	3160	84.4	648	3	US-08-286-870A-4	Sequence 4, Appli
6	2573	68.8	535	3	US-08-286-870A-6	Sequence 6, Appli
7	2459	65.7	1229	1	US-08-100-709-4	Sequence 4, Appli
8	2459	65.7	1229	1	US-08-176-865-4	Sequence 4, Appli
9	2459	65.7	1229	1	US-08-474-038-4	Sequence 4, Appli
10	2459	65.7	1229	2	US-08-779-046-4	Sequence 4, Appli
11	2459	65.7	1229	2	US-08-881-340-4	Sequence 4, Appli
12	2314.5	61.9	1207	1	US-07-951-715A-7	Sequence 7, Appli
13	2314.5	61.9	1207	2	US-08-459-448A-7	Sequence 7, Appli
14	2314.5	61.9	1207	3	US-08-459-595A-7	Sequence 7, Appli
15	2314.5	61.9	1207	3	US-08-459-504B-7	Sequence 7, Appli
16	2314.5	61.9	1207	3	US-08-459-444-7	Sequence 7, Appli
17	2314.5	61.9	1207	3	US-09-053-549-8	Sequence 8, Appli
18	2314.5	61.9	1207	3	US-09-547-422-7	Sequence 7, Appli
19	2314.5	61.9	1207	4	US-09-988-462-7	Sequence 7, Appli
20	2308.5	61.7	1227	3	US-09-053-549-2	Sequence 2, Appli
21	2243	59.9	1227	1	US-08-448-170-8	Sequence 8, Appli
22	2243	59.9	1227	3	US-08-961-803-9	Sequence 9, Appli
23	2234	59.7	1227	4	US-09-661-322A-63	Sequence 63, Appli
24	2233.5	59.7	488	1	US-08-448-170-10	Sequence 10, Appli
25	2233.5	59.7	488	3	US-08-961-803-10	Sequence 10, Appli
26	2219	59.3	1186	3	US-09-178-252-23	Sequence 23, Appli
27	2219	59.3	1186	4	US-09-826-660-23	Sequence 23, Appli

28	2168.5	58.0	1228	4	US-09-661-322A-38	Sequence 38, Appli
29	1982	53.0	643	3	US-09-178-252-25	Sequence 25, Appli
30	1982	53.0	643	4	US-09-826-660-25	Sequence 25, Appli
31	1813	48.5	380	5	PCT-US91-02560-4	Sequence 4, Appli
32	1683.5	45.0	653	4	US-09-661-322A-6	Sequence 6, Appli
33	1657.5	44.3	1157	1	US-07-876-280-30	Sequence 30, Appli
34	1657.5	44.3	1157	1	US-07-812-180A-2	Sequence 2, Appli
35	1657.5	44.3	1157	1	US-08-315-468-2	Sequence 2, Appli
36	1657.5	44.3	1157	3	US-07-941-650A-2	Sequence 2, Appli
37	1519.5	40.6	1176	1	US-08-257-999-2	Sequence 2, Appli
38	1507	40.3	1157	2	US-08-532-547-5	Sequence 5, Appli
39	1507	40.3	1157	2	US-08-379-656B-5	Sequence 5, Appli
40	1507	40.3	1157	3	US-08-455-838-5	Sequence 5, Appli
41	1507	40.3	1157	3	US-09-019-809-5	Sequence 5, Appli
42	1507	40.3	1157	4	US-09-471-177-5	Sequence 5, Appli
43	1507	40.3	1157	4	US-09-220-806-5	Sequence 5, Appli
44	1506.5	40.3	1168	1	US-08-291-368-4	Sequence 4, Appli
45	1506.5	40.3	1168	2	US-08-962-190-4	Sequence 4, Appli

# ALIGNMENTS

RESULT 1  
US-09-003-217-2  
; Sequence 2, Application US/09003217  
; Patent No. 5986177  
; GENERAL INFORMATION:  
; APPLICANT: Osman, Yehia A.  
; APPLICANT: Madkour, Magdy A.  
; APPLICANT: Bulla, Lee A.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES WITH  
; TITLE OF INVENTION: BROAD SPECTRUM ACTIVITY  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)  
; STREET: 3605 Glenwood Ave. Suite 310  
; CITY: Raleigh  
; STATE: NC  
; COUNTRY: US  
; ZIP: 27622  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/003,217  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spruill, W. Murray  
; REGISTRATION NUMBER: 32,943  
; REFERENCE/DOCKET NUMBER: 5718-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919 420 2202  
; TELEFAX: 919 881 3175  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 719 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-003-217-2

Query Match 94.8%; Score 3546; DB 2; Length 719;  
Best Local Similarity 95.0%; Pred. No. 5.6e-318;  
Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

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Db 1 MKLKNPDKHQSLSSNAKVXKIATDSLKNETDIELKNNEDYLRMSHESIDPFFVSASTI 60

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 DB 61 QTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKGSQWEIFMEHVEEIIINQKILTYA 120  
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 DB 121 RNKALTDLKGLDALAVYHESLESVENNRNTARSVVKNQYIALELMFVQKLPFAVSG 180  
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 DB 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240  
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 DB 301 GTVHPNQAFSTTTWYNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWSNTQYMMNW 360  
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 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 2

US-09-218-942-2  
 ; Sequence 2, Application US/09218942  
 ; Patent No. 6232439  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Osman, Yehia  
 ; TITLE OF INVENTION: Bacillus Thuringiensis Isolates with Broad Spectrum  
 ; FILE REFERENCE: CryII  
 ; CURRENT APPLICATION NUMBER: US/09/218,942  
 ; CURRENT FILING DATE: 1998-12-22  
 ; EARLIER APPLICATION NUMBER: 60/035,361  
 ; EARLIER FILING DATE: 1997-01-10  
 ; EARLIER APPLICATION NUMBER: 09/003,217  
 ; EARLIER FILING DATE: 1998-01-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 719  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus thuringiensis  
 US-09-218-942-2

Query Match 94.6%; Score 3541; DB 3; Length 719;  
 Best Local Similarity 95.0%; Pred. No. 1.5e-317;  
 Matches 683; Conservative 11; Mismatches 25; Indels 0; Gaps 0;  
 QY 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60

DB 1 MKLKNPKHQSLSSNAKVDKIATDSLKNETDIELKNMNNEDYLRMSEHESIDPFVSASTI 60  
 QY 61 QTGIGIAGKILGTGVPFAGQIASLYSFLGELWPKGSQWEIFMEHVEEIIINQKILTYA 120  
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 QY 361 GGHRLSPRIGGALNTSTOGSTNTSINPVTLQFTSRDYRTESWAGLNLFLTPQVNGVPR 420  
 DB 361 GGHRLSPRIGGALNTSTOGSTNTSINPVTLQFTSRDYRTESWAGLNLFLTPQVNGVPR 420  
 QY 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSNELPPTTQPNYESYSHRLSHIGLIS 480  
 DB 421 VDFHWKFTPLPIASDNFYLYGAGVGTQLQDSNELPPTTQPNYESYSHRLSHIGLIS 480  
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 DB 541 TGTFGDIRVNINPPPAQRYRVRIRYASTTDLOPHTSINGKAINQGNFSATWNRGDLDYK 600  
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 DB 601 TFRITGFTTFFSDFSDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQEKV 660  
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 DB 661 TALFTSTNPRGLKTDVKDYHIDQVSNLVSLSDEFYLDKRELFEIVKYAKQIHIERNM 719

RESULT 3

US-08-286-870A-8  
 ; Sequence 8, Application US/08286870A  
 ; Patent No. 6063605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELY, S  
 ; APPLICANT: TAILOR, RH  
 ; APPLICANT: TIPPETT, JM  
 ; APPLICANT: BLENN, RG  
 ; TITLE OF INVENTION: BACTERIAL GENES  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 ; ADDRESSEE: Intellectual Property Group of  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
 ; STREET: 1100 New York Avenue, N.W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3918  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30

;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/286,870A  
;; FILING DATE: 05-AUG-1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/520228  
;; FILING DATE: 09-MAY-1990  
;; APPLICATION DATA:  
;; APPLICATION NUMBER: GB 8910624.9  
;; FILING DATE: 09-MAY-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: PAUL N. KOKULIS  
;; REGISTRATION NUMBER: 16,773  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 861-3000  
;; TELEFAX: (202) 822-0944  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 719 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-286-870A-8

Query Match 94.0%; Score 3516; DB 3; Length 719;  
Best Local Similarity 92.8%; Pred. No. 2.9e-315;  
Matches 667; Conservative 32; Mismatches 20; Indels 0; Gaps 0;

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Db 1 M K L N Q D K H Q S F S S N A K V D K I S T D S L K N E T D I E L Q N I N H E D C L K M S E Y E N V E P F V S A S T I 60  
QY 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E I I N K I L T Y A 120  
Db 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E I I N K I S T Y A 120  
QY 121 R N K A L S D L R G L G D A L A V Y H E S L E S W E N V E N N T R A R S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
Db 121 R N K A L T D L K G L G D A L A V Y H S L E S W G N N T R A R S V V K S Q Y I A L E L M F V Q K L P S F A V S G 180  
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240  
Db 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S S E I S T F Y N R Q V E R A G D Y S D H C V K W Y S 240  
QY 241 T G L N N L R G T N A K S W R Y N Q F R D M T L M V L D L V A L F P S Y D T L V P I K T S Q L T R E V Y T D A I 300  
Db 241 T G L N N L R G T N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 300  
QY 301 G T V H P N Q A F A S T T W Y N N N A P S F S A I E A A V I R S P H L L D F L E K V T I Y S L L S R S N T Q Y M N M W 360  
Db 301 G T V H P H P S T S T T W Y N N N A P S F S A I E A A V R N P H L L D F L E Q V T I Y S L L S R S N T Q Y M N M W 360  
QY 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
Db 361 G G H K L E F R T I G G T L N I S T Q G S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
QY 421 V D F H W K F P T L P I A S D N F Y L G A G V G T Q L Q D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
Db 421 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 480  
QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G P T G G D I L R R T N 540  
Db 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G P T G G D I L R R T N 540  
QY 541 T G T F G D I R V N I N P P F A Q R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
Db 541 T G T F G D I R V N I N P P F A Q R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600  
QY 601 T F R T I G T F T P F S D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660  
Db 601 T F R T V G T F T P F S F L D V Q S T F T I G A W N F S S G N E V Y I D R I E F V P V E V T Y E A E Y D F E K A Q E K V 660

QY 661 T A L F T S T N P R G L K T D V K D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A Q I H I E R N M 719  
Db 661 T A L F T S T N P R G L K T D V Q D Y H I D Q V S N L V E S L S D E F Y L D E K R E L F E I V K Y A Q I H I E R N M 719  
RESULT 4  
US-09-661-322A-42  
; Sequence 42, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos  
; FILE OF INVENTION: and Methods of Use  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 42  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (200)-(200)  
; OTHER INFORMATION: No. 6593293-Coding  
US-09-661-322A-42

Query Match 90.0%; Score 3368.5; DB 4; Length 710;  
Best Local Similarity 89.2%; Pred. No. 1.2e-301;  
Matches 641; Conservative 32; Mismatches 37; Indels 9; Gaps 1;

QY 1 M K L N P D K H Q S L S N A K V D K I A T D S L K N E T D I E L K N M N N E D Y L R M S E H S I D P F V S A S T I 60  
Db 1 M K S K N Q M H Q S L S N A T V D K N F T G S L E N T N T E L Q N F N - - - - - H E G I E P F V S V S T I 51  
QY 61 Q T G I G I A G K I L G T L G V P F A G Q I A S L Y S F I L G E L W P K G S Q W E I F M E H V E I I N K I L T Y A 120  
Db 52 Q T G I G I A G K I L G N L G V P F A G Q V A S L Y S F I L G E L W P K G S Q W E I F M E H V E I I N K I S T Y A 111  
QY 121 R N K A L S D L R G L G D A L A V Y H E S L E S W E N V E N N T R A R S V V K N Q Y I A L E L M F V Q K L P S F A V S G 180  
Db 112 R N K A L A D L K G L G D A L A V Y H E S L E S W I E N R N N T R S V V K S Q Y I T L E L M F V Q S L P S F A V S G 171  
QY 181 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K E W G L S A S E I S T F Y N R Q V E R T R D Y S D H C I K W Y N 240  
Db 172 E E V P L L P I Y A Q A A N L H L L L R D A S I F G K X W G L S D S E I S T F Y N R Q S G K S E Y S D H C V K W Y N 231  
QY 241 T G L N N L R G T N A K S W R Y N Q F R D M T L M V L D L V A L F P S Y D T L V P I K T S Q L T R E V Y T D A I 300  
Db 232 T G L N R L M G N N A E S W R Y N Q F R D M T L M V L D L V A L F P S Y D T Q M Y P I K T A Q L T R E V Y T D A I 291  
QY 301 G T V H P N Q A F A S T T W Y N N N A P S F S A I E A A V I R S P H L L D F L E K V T I Y S L L S R W N T Q Y M N M W 360  
Db 292 G T V H P H P S F S T T W Y N N N A P S F S T I E A A V R N P H L L D F L E Q V T I Y S L L S R W N T Q Y M N M W 351  
QY 361 G G H R L E S R P I G G A L N T S T Q G S T N T S I N P V T L Q F T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 420  
Db 352 G G H K L E F R T I G G T L N T S T Q G S T N T S I N P V T L P T S R D V Y R T E S L A G L N L F L T Q P V N G V P R 411  
QY 421 V D F H W K F P T L P I A S D N F Y L G A G V G T Q L Q D S E N E L P P E T T G Q P N Y E S Y S H R L S H I G L I S 480  
Db 412 V D F H W K F V T H P I A S D N F Y P G Y A G I G T Q L Q D S E N E L P P E A T G Q P N Y E S Y S H R L S H I G L I S 471  
QY 481 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G P T G G D I L R R T N 540  
Db 472 A S H V K A L V Y S W T H R S A D R T N T I E P N S I T Q I P L V K A F N L S S G A A V V R G P G P T G G D I L R R K N 531  
QY 541 T G T F G D I R V N I N P P F A Q R V R I R Y A S T T D L Q F H T S I N G K A I N Q G N F S A T M N R G E D L D Y K 600

Db 532 TGTGDIRVNINPPFAQRVIRYASTDLOPHTSINGKAINQGNFSATMNRGDLKY 591  
Qy 601 TFRITGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKV 660  
Db 592 TFRITGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAEYDFEKAQKV 651  
Qy 661 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDYFDEKRELFEIVKYAKQIHERNM 719  
Db 652 TALFTSTNPRGLKTDVKYHIDQVSNLVESLSDYFDEKRELFEIVKYAKQIHERNM 710

## RESULT 5

US-08-286-870A-4  
; Sequence 4, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PAUL N. KOKULIS  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 70608/220720  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 648 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-286-870A-4

Query Match 84.4%; Score 3160; DB 3; Length 648;  
Best Local Similarity 92.3%; Pred. No. 1.7e-282;  
Matches 598; Conservative 30; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 MCLKNPKHQSLSSNAKYDKIATDSLKNETDIELKNNEDYLRMSEHESIDPVSASTI 60  
Db 1 MCLKNQDKHQSFSSNAKYDKISTDSLKNETDIELQNHEDCLKNSEYENVEPVFSASTI 60  
Qy 61 QTGIGIAGILGTGVPFAGQIASLYSIFILGELWPKGKSQWEIFMEHVEEIIINOKILTVA 120  
Db 61 QTGIGIAGILGTGVPFAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINOKISTVA 120

Qy 121 RNKALSDLRGIGDALAVYHESLESWEVNRNNTARSVVNQVIALELMFVOKLPSPAVSG 180  
Db 121 RNKALTDLKGIGDALAVYHDSLESWVGNNRNTARSVVKSQVIALELMFVOKLPSPAVSG 180  
Qy 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSASESTFYNRQVTRDYSCHICKWYN 240  
Db 181 BEVPLPIYAQAANLHLLLRDASIFGKEWGLSSSESTFYNRQVTRDYSCHICKWYS 240  
Qy 241 TGLNLRGTNAKSWRYNOFRKDMTLMVLDLVALFPSTDTLVYPIKTTTSQLTREVTDAI 300  
Db 241 TGLNLRGTNAESWRYNOFRDMTLMVLDLVALFPSTDTLVYPIKTTAQLTREVTDAI 300  
Qy 301 GTVHPNCAFSTTWNNAAPSFAIAEAAVIRSPHLLDLEKVTIYSLSRKSNTOYMMNW 360  
Db 301 GTVHPNCFSTTWNNAAPSFAIAEAAVVRNPHLLDLEQVTIYSLSRKSNTOYMMNW 360  
Qy 361 GGHRLSRPIGGALNTSTQSTNTSINPVTLOFTSRDYRTESLAGNLFLTQPVNGVPR 420  
Db 361 GGHKLEFRITGGTLNISTQSTNTSINPVTLPFTSRDYRTESLAGNLFLTQPVNGVPR 420  
Qy 421 VDFHMKFPTLPIDSNFYLYGAGVGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Db 421 VDFHMKFVTHPIASDNFYLYGAGIGTQLODSENELPPEATGQPNYESYSHRLSHIGLIS 480  
Qy 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Db 481 ASHVKALVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTN 540  
Qy 541 TGTGDIRVNINPPFAQRVIRYASTDLOPHTSINGKAINQGNFSATMNRGDLKY 600  
Db 541 TGTGDIRVNINPPFAQRVIRYASTDLOPHTSINGKAINQGNFSATMNRGDLKY 600  
Qy 601 TFRITGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAE 648  
Db 601 TFRITGTTTFFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEAE 648

## RESULT 6

US-08-286-870A-6  
; Sequence 6, Application US/08286870A  
; Patent No. 6063605  
; GENERAL INFORMATION:  
; APPLICANT: ELY, S  
; APPLICANT: TAILOR, RH  
; APPLICANT: TIPPETT, JM  
; APPLICANT: BLENK, RG  
; TITLE OF INVENTION: BACTERIAL GENES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/286,870A  
; FILING DATE: 05-AUG-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/520228  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 8910624.9  
; FILING DATE: 09-MAY-1989

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; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-286-870A-6

Query Match      68.8%; Score 2573; DB 3; Length 535;
Best Local Similarity 91.0%; Pred. No. 1.9e-228;
Matches 487; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

QY 1 MKLKNQDKHQSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFVSASTI 60
Db 1 MKLKNQDKHQSSNAKVDKIATDSLKNETDIELQNNHEDCLKMSYENVEPFVSASTI 60

QY 61 QTGIGIACKILGTGVFPAGQIASLYSFLGELWPKGKQWEIFMEHVBEIINQKILTYA 120
Db 61 QTGIGIACKILGTGVFPAGQVASLYSFLGELWPKGKQWEIFMEHVBEIINQKISTYA 120

QY 121 RNKALSLRGLGDALAVYHESLESWVENNRNTRSVKQYIALELMFVQKLPSPFVSG 180
Db 121 RNKALSLRGLGDALAVYHDSLESWGNRNTRSVKQYIALELMFVQKLPSPFVSG 180

QY 181 EYVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYN 240
Db 181 EYVPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCVKWYS 240

QY 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTTSQLTREVYTDI 300
Db 241 TGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTTSQLTREVYTDI 300

QY 301 GTVHPNQAFASWTWYNNAPSAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMNW 360
Db 301 GTVHPNPSTSTWYNNAPSAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMNW 360

QY 361 GGHRLSPIGGALNTSTQGSTNTSINPVTLPFTSRDVRVTSAGLNFLTPQVNGVPR 420
Db 361 GGHKLEFRTIGTGLNISTQGSTNTSINPVTLPFTSRDVRVTSAGLNFLTPQVNGVPR 420

QY 421 VDFHWKFTPLPIASDNFYLYGVAGVGTQLODSENELPPTTQPNYESYSHRISHIGLIS 480
Db 421 VDFHWKFTVTHPIASDNFYLYGVAGVGTQLODSENELPPEATGQPNYESYSHRISHIGLIS 480

QY 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535
Db 481 ASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI 535

RESULT 7
US-08-100-709-4
; Sequence 4, Application US/08100709
; Patent No. 532687
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jan, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYETS
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia

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; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoft, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-100-709-4

Query Match      65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.5e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKHQSSNAKVDKIATDSLKNETDIELKNNNEDYLRMSEHESIDPFVSASTIQT 62
Db 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNDIPFVSASTVQT 58

QY 63 GIGIAGKILGTGVFPAGQIASLYSFLGELWPKGKQWEIFMEHVBEIINQKILTYARN 122
Db 59 GINIAGRIILGVLPVFPAGQLASFSYFLGELWPSGRDPWEIFLEHVBEIINQKILTYARN 118

QY 123 KALSRLRGLGDALAVYHESLESWVENNRNTRSVKQYIALELMFVQKLPSPFVSGEE 182
Db 119 TAIARLEGLGRYSYQQALETWLDNRNDARSIIILERYVALELITTAIPLFRNEE 178

QY 183 VPLLPYQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSDHCIKWYNTG 242
Db 179 VPLMVYQAANLHLLLRDASIFGSEWGMASDVNQYQEQIRYTEYSNHCVQWYNTG 238

QY 243 LNNLGTNAKSWRYNQFRKDMTLMVLDLVALPSPYDTLVPIKTTTSQLTREVYTDI 302
Db 239 LNNLGTNAESWLRYNQFRDLTLGLVLDLVALPSPYDTLVPIKTTTSQLTREVYTDI 298

QY 303 VHPNQAFASWTWYNNAPSAIEAAVIRSPHLLDFLEKVTIYLLSRWSNTQYMNWGG 362
Db 299 TNAPSGFASTWYNNAPSAIEAAVIRSPHLLDPPEQLTIYSASSRWSSTQHMYWVG 358

QY 363 HRLESRPIGGALNTSTQGST-NTSINPVTLPFTSRDVRVTSAGLNFLTPQVNGVPRV 421
Db 359 HRLNFRPIGGTGLNTSTQGLTNNTSINPVTLPFTSRDVRVTSAGLNFLTPQVNGVPRV 418

QY 422 DFHWKFTPLPIASDNFYLYG-----YAGVGTQLODSENELPPTTQPNYESYSHRIS 474
Db 419 RFNF-----INPQNIYERGATTYSQYQGVGLQDFSETLPPTTERPNYESYSHRIS 472

QY 475 HIGLISASHVKALVSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534
Db 473 HIGLIIGNTLRAPVYSWTHRSADRTNTIEPNSITQIPLVKALNLHSGVTVVGGPGFTGGD 532

QY 535 ILRRNTGFGDIRVNIINPPFAQRYRIRYASTTDLQPHFISINGKAINQGNFSATMNRG 594
Db 533 ILRRNTGFGDIRVNIINPPFAQRYRIRYASTTDLQPHFISINGKAINQGNFSATMNRG 592

QY 595 ELDYKTRFTIGTTPFSDVOSTFTTGAMNPFSSGNEVYIDRIEFVPEVTEYAEYDFE 654
Db 593 DNLEYSRFTAGTFTPFNFNAOSTFTTGAQSFNS-QEYVIDRVEFPVPAEYFEAYDLE 651

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QY 655 KAEKVTALFTSTNPRGKTDVYDHYDQVSNLVESLDEFLYDEKRELFEIVKAKQH 714  
 Db 652 RAQKAVNALFTSTNPRRLKTDVTDYHDQVSNVACLSDREKRELFEKVKYAKRLS 711  
 QY 715 IERNM 719  
 Db 712 DERNL 716

RESULT 8  
 US-08-176-865-4  
 ; Sequence 4, Application US/08176865  
 ; Patent No. 5616319  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYVET4 AND CYVET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/100,709  
 ; FILING DATE: 29-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Egoif, Christopher  
 ; REGISTRATION NUMBER: 27633  
 ; REFERENCE/DOCKET NUMBER: 7205-49  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-757-1590  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-176-865-4

Query Match 65.7%; Score 2459; DB 1; Length 1229;  
 Best Local Similarity 64.8%; Pred. No. 2.5e-217;  
 Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPDKHQSLSSNAKVDKIATDSLKNETDIELKNNEDYLRMSHESIDPFVSASTIQT 62  
 Db 20 VSNFSTQMLSPDARI-----EDSLCAEVANNIDPFVSASTVQT 58  
 QY 63 GIGIAGKILGTLGVFPAGQIASYSLFGLWPKGSKQWEIFMEHVEEINQKILTYARN 122  
 Db 59 GINIAGRILGLVGFPAQQLASFSYFLVGLWPSGRDPWFLEHVEQLIRQQVTENTN 118  
 QY 123 KALSRLGLGALAVYHESLESVNNRNRARSVVKVQXIALELMFVQKLPSFAVSGEE 182  
 Db 119 TAIARLEGJRGVRSYQQALETWLDNRNDRSRIILERYVALELDITTAIFLRNEE 178  
 QY 183 VPLPIYAAANLHLLLRDASIFGKEWGLSASEISTFYNRQVTRDYSCHICKWYNTG 242

Db 179 VPELLMYAQAANLHLLLRDASLFGSEWGMASDVNOYYQBOIRYTEEYSHCHVOMYNTG 238  
 QY 243 LNNLACTNAKSWRYNQFRKDMTLMVLVDLVALPSPYDYLVPKIKTTSQLTREVYTDAGT 302  
 Db 239 LNNLRTGNAESWLRNQFRRLDTLGLVDLVALPSPYDYLVPKIKTTSQLTREVYTDPIGR 298  
 QY 303 VHPNOAFASTWYNNAPSFSAIEAAIRSPHLLDFLEKVTIYSLLSRWSTQYNNWGG 362  
 Db 299 TNAPSGFASTWNNAPSFSAIEAAIRSPHLLDFLEKVTIYSLLSRWSTQYNNWGG 358  
 QY 363 HRLESRPIGGALNTSTQST-NTSINPVTLOFTSRDYRTSLAGNLFLTQPVNGVPRV 421  
 Db 359 HRLNFRPIGGLTNTSTQGLTNTSINPVTLOFTSRDYRTSLAGNLFLTQPVNGVPRV 418  
 QY 422 DFHWKFPPLPIASDNFYVLG-----YAGVGTQLODSENELPPTTGPQNYESYSHRLS 474  
 Db 419 RFPF-----INPONIYERGATTYSQYQGVGLQLFSETELPPTTERPNYESYSHRLS 472  
 QY 475 HIGLISASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAPNLSSGAAVVRGPGFTGGD 534  
 Db 473 HIGLIGNTURAPYVSWTHRSADRTNTIEPNSITQIPLVKAPNLSSGAAVVRGPGFTGGD 532  
 QY 535 ILRRNTGTGDIRVNINPPFAQRYRYRIYASTTDLQFHTSINGKAINQGNFSATMNRG 594  
 Db 533 ILRRNTGTGDIRVNINPPFAQRYRYRIYASTTDLQFHTSINGKAINQGNFSATMNRG 592  
 QY 595 EDLDYKTRTIGFTTTPFSFSDVOSTFTIGAMWPFSSGNEVYIDRIEFVPEVTEYAEYDFE 654  
 Db 593 DNLEYSRFTAGFTPTPEFLNAQSTFTLGAQSPSN-QEVYIDRVEFVPAEVTFEABYDLE 651  
 QY 655 KAEKVTALFTSTNPRGKTDVYDHYDQVSNLVESLDEFLYDEKRELFEIVKAKQH 714  
 Db 652 RAQKAVNALFTSTNPRRLKTDVTDYHDQVSNVACLSDREKRELFEKVKYAKRLS 711  
 QY 715 IERNM 719  
 Db 712 DERNL 716

RESULT 9  
 US-08-474-038-4  
 ; Sequence 4, Application US/08474038  
 ; Patent No. 5679343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donovan, William P.  
 ; APPLICANT: Tan, Yiping  
 ; APPLICANT: Jany, Christine S.  
 ; APPLICANT: Gonzalez Jr., Jose M.  
 ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYVET4 AND CYVET5  
 ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
 ; ADDRESSEE: Nadel  
 ; STREET: 1601 Market Street, 36th Floor  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,038  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/176,865  
 ; FILING DATE: 30-DEC-1993  
 ; APPLICATION NUMBER: US 08/100,709

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; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-038-4

Query Match          65.7%; Score 2459; DB 1; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.5e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKDQHSLSSNAKVDTSLKNEITDIELKMNMDYLRMSHESIDPFVSASTIQT 62
Db 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNDPFVSASTVQT 58

QY 63 GIGIAGKILGTGVFPFAGQIASLYSFLIGELWPKGKSQWEIFMEHVEEIIQKILTYARN 122
Db 59 GINIAGRILGVLGVFPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQQVTENTRN 118

QY 123 KALSDLRGLGDALAVYHESLESWVENRNNTRARSVVNQYIALELMFVKLPFAVSGEE 182
Db 119 TAIARLEGLGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPFRIRNEE 178

QY 183 VPLLPIYQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVERTRDYSDBCIKWYNTG 242
Db 179 VPLLVMYQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSHCHVQWYNTG 238

QY 243 LNNLRGTNAKSWRYNQPRKDMTLMVLDLVALFSPSYDTLVYPIKTTSQLTRREVYTDAGT 302
Db 239 LNNLRGTNAESWLRYNQPRRDLTLGVLDLVALFSPSYDTRTYPINTSAQLTREIYTDPIGR 298

QY 303 VHPNOAPASTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNTQYNNMWGG 362
Db 299 TNAPSGFASTWNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVG 358

QY 363 HRLESRPFGALNTSTQGST-NTSINPVLQTSRDVYRTESLAGNLFLTPQVNGVPRV 421
Db 359 HRLNFRPIGGTLNTSTQGLTNNTSINPVLQTSRDVYRTESNAGTNILFTTPVNGVPEWA 418

QY 422 DFHWKFPPLPIASDNFYLG-----YAGVGTQLQDSENELPPETTGQPNYESYSHRLS 474
Db 419 RFNF-----INPQNIYERGATYSQYQGVGIQLFDSYELPPEPTTERPNYESYSHRLS 472

QY 475 HIGLISASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGSD 534
Db 473 HIGLIIGNTLRAPVYSWTHRSADRTNIGPNRITQIPLVKALNLHSGVTVVGPGFTGSD 532

QY 535 ILRRTNTGFGDIRVNIINPPPAQRYRVRIRYASTTDLQHTSINGKAINQGNFSAATMNRG 594
Db 533 ILRRTNTGFGDIRLNIINVPUSQRYRVRIRYASTTDLQFFTRINGTNIGNFSRTMNRG 592

QY 595 EDLDYKTRTIGTTPFSFSDVSTFTIGAWNFSSNVEYIDRIEFVPVEVTVYAEAYDPE 654
Db 593 DNLEYSRPTAGSPFPFNLAQSTFTLGAQSFN-QUEYIDRVFVPAEVTPEAEYDLE 651

QY 655 KAQEKVTLFTSTNPRGLKTDVKDYHIDQVNLVLSLSDPFLYDEKRELFEIVKYAKIHH 714
Db 652 RAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVVACLSDPFLYDEKRELFEIVKYAKRLS 711

QY 715 IERNM 719
Db 712 DERNL 716
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RESULT 10

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US-08-779-046-4
; Sequence 4, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-046-4

Query Match          65.7%; Score 2459; DB 2; Length 1229;
Best Local Similarity 64.8%; Pred. No. 2.5e-217;
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;

QY 3 LKNPKDQHSLSSNAKVDTSLKNEITDIELKMNMDYLRMSHESIDPFVSASTIQT 62
Db 20 VSNPSTQMNLSPDARI-----EDSLCVAEVNNDPFVSASTVQT 58

QY 63 GIGIAGKILGTGVFPFAGQIASLYSFLIGELWPKGKSQWEIFMEHVEEIIQKILTYARN 122
Db 59 GINIAGRILGVLGVFPFAGQLASFYSFLVGELWPSGRDPWEIFLEHVEQLIRQQVTENTRN 118

QY 123 KALSDLRGLGDALAVYHESLESWVENRNNTRARSVVNQYIALELMFVKLPFAVSGEE 182
Db 119 TAIARLEGLGRGYSYQQALETWLDNRDARSIIILERYVALELDITTAIPFRIRNEE 178

QY 183 VPLLPIYQAANLHLLLRDASIFGKEWGLSASEISTFYNNQVERTRDYSDBCIKWYNTG 242
Db 179 VPLLVMYQAANLHLLLRDASLFGSEWGMASDVNQYQEQIRYTEEYSHCHVQWYNTG 238

QY 243 LNNLRGTNAKSWRYNQPRKDMTLMVLDLVALFSPSYDTLVYPIKTTSQLTRREVYTDAGT 302
Db 239 LNNLRGTNAESWLRYNQPRRDLTLGVLDLVALFSPSYDTRTYPINTSAQLTREIYTDPIGR 298

QY 303 VHPNOAPASTTWNNNAPSFSAIEAAVIRSPHLLDFLEKVTIYSLLSRWNTQYNNMWGG 362
Db 299 TNAPSGFASTWNNNAPSFSAIEAAIFRPPHLLDFPEQLTIYSASSRWSSTQHMNYWVG 358
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QY 363 HRLSRPIGALNTSTQGST-NTSINPVTLQFTSRDVRYSAGLNLFLTPQVNGVPRV 421  
Db 359 HRLNFRPIGTLNTSTQGLTNTSINPVTLQFTSRDVRYSAGLNLFLTPQVNGVPRV 418  
QY 422 DFHWKPTLPIASDNFYVIG-----YAGVGTQLODSENELPPTTGPQNYESYSHRLS 474  
Db 419 RFNF-----INPQNIYERGATTSQPYQGVGIQLFDSFELPPTTTERNYESYSHRLS 472  
QY 475 HIGLISASHVKALVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534  
Db 473 HIGLIIGNTLRAPYVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 532  
QY 535 ILRRTNTGFGDIRVNIINPPLPFAQRYRIRYASTTDLQFTSINGKAINOGNFSATMNRG 594  
Db 533 ILRRTNTGFGDIRVNIINPPLPFAQRYRIRYASTTDLQFTSINGKAINOGNFSATMNRG 592  
QY 595 ELDYKTFRTIGFTTFFSPDSVOSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDFE 654  
Db 593 DNLEYSRFTAGSTFPFNLAQSTFTLGAQSFNS-GEVYIDRVEFPVPAEVTFEAEYDLE 651  
QY 655 KAEQKVTALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDPEYLDKRELFELVKYAKQIH 714  
Db 652 RAQKAVNALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDPEYLDKRELFELVKYAKRLS 711  
QY 715 IERNM 719  
Db 712 DERNL 716

RESULT 11  
US-08-881-340-4  
; Sequence 4, Application US/08881340  
; Patent No. 5942658  
; GENERAL INFORMATION:  
; APPLICANT: Donovan, William P.  
; APPLICANT: Tan, Yiping  
; APPLICANT: Jany, Christine S.  
; APPLICANT: Gonzalez Jr., Jose M.  
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYVET4 AND CYVET5  
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.  
; ADDRESS: Nadel  
; STREET: 1601 Market Street, 36th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/881,340  
; FILING DATE: 24-JUN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION NUMBER: 08/100,709  
; FILING DATE: 29-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Egolf, Christopher  
; REGISTRATION NUMBER: 27633  
; REFERENCE/DOCKET NUMBER: 7205-49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-757-1590  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1229 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-881-340-4  
Query Match 65.7%; Score 2459; DB 2; Length 1229;  
Best Local Similarity 64.8%; Pred. No. 2.5e-217;  
Matches 470; Conservative 91; Mismatches 128; Indels 36; Gaps 5;  
QY 3 LKNPKHQSSNAKVDKIATDSLKNETDIELKMNMDYELRMSEHESIDPFVSASTIQT 62  
Db 20 VSNPTQMLNSPDARI-----EDSLCAEVNNIDPFVSASTVQT 58  
QY 63 GIGIAGKILGTGVFPFAGQIASLYSFIILGELWPKGKOWEIMFMEHVEEIIINQILTYARN 122  
Db 59 GINIAGRILGLVGVFPFAGQLASFSFLVGEIWPGRDFWEIHFLEHVEQLIRQQVNTNRN 118  
QY 123 KALSILRGLDALAVYHESLESWVENNTRARSVKNQYIALELMFVQKLPSFAVSGEE 182  
Db 119 TAIARLEGLGRGYSYQQALETWLDNRNDARSIIILERYVALELDITTAIPLFRIRNEE 178  
QY 183 VPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQVERTRDYSCHICKWYNTG 242  
Db 179 VPLLMVYQAANLHLLLRDASLFGSEWGMASDVNOYQEQIIRYTEEYSHCVQWYNTG 238  
QY 243 LNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSSYDTLVYPIKTTSQLTREYVYDAIGT 302  
Db 239 LNNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSSYDTLVYPIKTTSQLTREYVYDAIGT 298  
QY 303 VHPNQAFASFTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIYSLSRWSNTQYNNMGG 362  
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QY 363 HRLSRPIGALNTSTQGST-NTSINPVTLQFTSRDVRYSAGLNLFLTPQVNGVPRV 421  
Db 359 HRLNFRPIGTLNTSTQGLTNTSINPVTLQFTSRDVRYSAGLNLFLTPQVNGVPRV 418  
QY 422 DFHWKPTLPIASDNFYVIG-----YAGVGTQLODSENELPPTTGPQNYESYSHRLS 474  
Db 419 RFNF-----INPQNIYERGATTSQPYQGVGIQLFDSFELPPTTTERNYESYSHRLS 472  
QY 475 HIGLISASHVKALVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 534  
Db 473 HIGLIIGNTLRAPYVSWTHRSADRNTNTPNSITQIPLVKAFNLSSGAAVVRGPGFTGGD 532  
QY 535 ILRRTNTGFGDIRVNIINPPLPFAQRYRIRYASTTDLQFTSINGKAINOGNFSATMNRG 594  
Db 533 ILRRTNTGFGDIRVNIINPPLPFAQRYRIRYASTTDLQFTSINGKAINOGNFSATMNRG 592  
QY 595 ELDYKTFRTIGFTTFFSPDSVOSTFTIGAMNFSNGNEVYIDRIEFPVPEVTEAEYDFE 654  
Db 593 DNLEYSRFTAGSTFPFNLAQSTFTLGAQSFNS-GEVYIDRVEFPVPAEVTFEAEYDLE 651  
QY 655 KAEQKVTALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDPEYLDKRELFELVKYAKQIH 714  
Db 652 RAQKAVNALFTSTNPRGLKTDVVDYHIDQVSNLVESLSDPEYLDKRELFELVKYAKRLS 711  
QY 715 IERNM 719  
Db 712 DERNL 716

RESULT 12  
US-07-951-715A-7  
; Sequence 7, Application US/07951715A  
; Patent No. 5625136  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.

```

; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-951-715A-7

Query Match 61.9%; Score 2314.5; DB 1; Length 1207;
Best Local Similarity 65.4%; Pred. No. 5.3e-204;
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSEHSDPFSASTIQTGIGAGKILGTIGVPPFAGQIASLYSFLGELWPKGS 99
DB 10 EDSLCAIEGNNIDPFSASTVQTGINIAGRIILGVLGVPPFAGQLASFYSFLVGLWPRGRD 69
QY 100 QWEIFMEHVEEINOKILTYARNKALSDRLGLGDALAVYHESLESWVENNTRARSVK 159
DB 70 QWEIFLEHVEQLNQITENARNALALQGLGDGFRAYQQSLEDWLENKRDARTSRVLY 129
QY 160 NQVIALELMFVQKLPSFAVSGEEVPLPIYAQAANLHLLLRDASIFGKMWGLSASEIST 219
DB 130 TQVIALELDLFLNAMPFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQ 189
QY 220 FYNRQVTRDSDHCKIKWNTGLNNLRGTNAKSWRYNQFRKDMTLMVLDLVALFPSYD 279
DB 190 YFERQVTRDSDYCVIEWYNTGLNLRGTNAASWRYNQFRRLDTLGLVLDLVALFPSYD 249
QY 280 TLVYPIKTSQLTREVYTDAGTVHPNQAFASITWYNNNAPSFAIAEAAVIRSPHLLDPL 339
DB 250 TRYPINTSAQLTREVYTDAGTGVN--MASMNNYNNNAPSFAIAEAAVIRSPHLLDPL 307
QY 340 EKVTIYSLRSWNTQYMMWGGHRLSRPIGGALNTSTOGSTNTSINPVTLOFTSRDVI 399
DB 308 EQLTIFSASSRSWNTHTMYWRGHTIQSRPIGGGLTSTHCAATNTSINPVTLPASRDVI 367
QY 400 RTESLAGLNLF--LTQPVNGVPRVDPHWKFP-TLPIASDNFYILGAGVGTQLQDSENEL 456

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DB 368 RTESVAGVLLWGIYLEPIHGVPVTFVRFNPNQNISDRGTANYSQPYSPGLQKDSFTEL 427
QY 457 PPETTGQPNYESYSHRLSHIGLISASHVKALVYSWTHRSADRTNTIBPNSITQIPLVKAF 516
DB 428 PPETTERPNYESYSHRLSHIGIILQSRVNVVYVSWTHRSADRTNTICPNRITQIPMKAS 487
QY 517 NLSGAAVVRGPGFTGGDILRRNTGTGDIRVNNINPFAQRYRVRIRYASTDLOPHTS 576
DB 488 ELPOGTTVVRGPGFTGGDILRRNTGGPGPIRVTVNGPLTQRYRIGFRYASTVDFPFVS 547
QY 577 INGKAINQGNFSATMNRGEBLDYKTFRTIGTTPFSFSDVQSTFTTICAWNFSNGNEVYID 636
DB 548 RGGTTVNNFRFLRTMNSGDELKGNFVRRAFTTPTFTQIQDIIRTSIQGLSGNGEYIID 607
QY 637 RIEFVPEVTVYEAEDFEKAQEKVTALFTSTNPRGLXTDKYHIDOVSNLVESLSDEFY 696
DB 608 KIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDFC 667
QY 697 LDEKRELFIEIVKYAKQIHIERNM 719
DB 668 LDEKRELLKVKYAKRLSDERNL 690

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RESULT 13
US-08-459-448A-7
; Sequence 7, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.

```

REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-448A-7

Query Match 61.9%; Score 2314.5; DB 2; Length 1207;

Best Local Similarity 65.4%; Pred. No. 5.3e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSHESIDPFVSASTIQIGIAGKILGTGVPFAGQIASLYSFLIGELWPKGKS 99  
DB 10 EDSLCTAEGNIDPFVSASTVQTGINIAGRILGVLGVFPFAGQIASLYSFLIGELWPKGRD 69  
QY 100 QWEIFMEHVEEIIINQILTYARNKALSDRLGDLAVYHESLESWVENNTRARSVK 159  
DB 70 QWEIFLEHVEQLINQITENARTALRQLGDSFRAYQOSLEDWLENRDDARTSVLY 129  
QY 160 NOYIALELMFVQKLPSFAVSGEEVPLPIYAOAANLHLLLRDASIFGKEWGLSASEIST 219  
DB 130 TOYIALELDFLNAMEPLFAIRNQEVPLLMVYAOAANLHLLLRDASIFGSEGLTSEIOR 189  
QY 220 FYNQVTRDYSCHCIKWNTGLNLRGTNAKSWRYNQFRKMTLMVLDLVALFPSPYD 279  
DB 190 YERQVTRDYSCHCIKWNTGLNLRGTNAKSWRYNQFRKMTLMVLDLVALFPSPYD 249  
QY 280 TLVYPIKTSQLTREYVTDAGTVHPNCAFASITWYNNAPSFSAEAAVIRSPHLLDFL 339  
DB 250 TRTYPIKTSQLTREYVTDAGTVHPNCAFASITWYNNAPSFSAEAAVIRSPHLLDFL 307  
QY 340 EKVTIYSLSRWSNTQYNNMGHRLSRPIGGLNLTSTQSTNTSINPVTLOFTSRDYY 399  
DB 308 EQLTIFSASSRWSTHRTYWRGHTIQSRPIGGLNLTSTHGTATNTSINPVTLPFASRDYY 367  
QY 400 RTESLAGLNF--LTQPNVGVPRVDFHWKFP--TLPIASDNFYVLGAGVGTQLQDSENL 456  
DB 368 RTESYAGVLLWGIYEPHGVPTVRFNFTNPQNISDRGTANYQPYESPGLQKXSETL 427  
QY 457 PPETTGQPNYESYSHRLSHIGLSASHYKALVYSWTHRSADRTNTEPNSITQPLVKAF 516  
DB 428 PPETTERPNYESYSHRLSHIGLSASHYKALVYSWTHRSADRTNTEPNSITQPLVKAS 487  
QY 517 NLSGAAVVRGPGTGGDILRRNTGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTS 576  
DB 488 ELPOGTVTVRGPFGTGGDILRRNTGTGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTS 547  
QY 577 INKAINQGNFSAWNRGDLVDKFTERTIGFTTFFSPSDVQSTFTTGAMNFSNGEYVID 636  
DB 548 RGGTIVNPNFRFLRNTMNGSDKLYGNFVRAFTPTFTTQIQDIIFTSIQGLSGNGEYVID 607  
QY 637 RIEFVPVEVYEAEDFEKAQKVTALTSTNPRGLKTDVVDYHIDQVSNLVESISDEFY 696  
DB 608 KIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDEFY 667  
QY 697 LDEKRELFEIVKAKQIHIERNM 719  
DB 668 LDEKRELFEIVKAKRLSDERNL 690

RESULT 14

US-08-459-595A-7  
Sequence 7, Application US/08459595A  
Patent No. 6018104  
GENERAL INFORMATION:  
APPLICANT: Kozziel, Michael G.  
APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6018104artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,595A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1207 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-595A-7

Query Match 61.9%; Score 2314.5; DB 3; Length 1207;

Best Local Similarity 65.4%; Pred. No. 5.3e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;

QY 40 EDYLRMSHESIDPFVSASTIQIGIAGKILGTGVPFAGQIASLYSFLIGELWPKGKS 99  
DB 10 EDSLCTAEGNIDPFVSASTVQTGINIAGRILGVLGVFPFAGQIASLYSFLIGELWPKGRD 69  
QY 100 QWEIFMEHVEEIIINQILTYARNKALSDRLGDLAVYHESLESWVENNTRARSVK 159  
DB 70 QWEIFLEHVEQLINQITENARTALRQLGDSFRAYQOSLEDWLENRDDARTSVLY 129  
QY 160 NOYIALELMFVQKLPSFAVSGEEVPLPIYAOAANLHLLLRDASIFGKEWGLSASEIST 219  
DB 130 TOYIALELDFLNAMEPLFAIRNQEVPLLMVYAOAANLHLLLRDASIFGSEGLTSEIOR 189  
QY 220 FYNQVTRDYSCHCIKWNTGLNLRGTNAKSWRYNQFRKMTLMVLDLVALFPSPYD 279

Db 190 YERQVERTRDSDYCVWYNTGLNSLGTNAASWRYNQPRDLTLGLVLDLVALFPSYD 249  
Qy 280 TLVPIKITSQLTREVYTDAGTVHPNQAFSTWYNNAPSFSAIEAAVIRSPHLLDFL 339  
Db 250 TRTYPINTSAQLTREVYTDAGTGVN--MASMWNWNNAPSFSAIEAAVIRSPHLLDFL 307  
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Db 308 EQLTIFSASSRWNTRHMTYWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLRFSRDYY 367  
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Db 368 RTESYAGVLLWGIYLEPIHGVTFRFNTPNQNISDRGTANYSQPYESPGQLKXDSDEL 427  
Qy 457 PPETGQPNYESYSHRLSHIGLSASHVYKALVYSWTHRSADRTNTPNSITQIPLVKAF 516  
Db 428 PPETTERPNYESYSHRLSHIGILQSRVNPVYSWTHRSADRTNTPNRTIQIPMVKAS 487  
Qy 517 NLSGAAVVRGPGFTGGDLRLRTNTGFGDIRVNPFPFAQRYRVRIRYASTTDLQFHTS 576  
Db 488 ELPGGTVVRGPGFTGGDLRLRTNTGFGDIRVNPVNGPLTQRYRIGFRYASTVDFDFVS 547  
Qy 577 INGKAINQGNFSAATMRGDLTKFTRTIGFTTFFSFDVQSTFTIGAMNFSNGEVYID 636  
Db 548 RGGTVNNFRFLRTWNSGDELKYGNFVRRAFTTPTFTTQIIDIIRTSIQGLSGNGEVYID 607  
Qy 637 RIEFVPEVYEAEDYFEKAQEKVTALTSTNPRGLTKDVXDYHIDQVSNLVESLSDEFY 696  
Db 608 KIEIIPVTATFEAYDLERAQEAVALFTNTPRRLTKDVTDYHIDQVSNLVACLSDEF 667  
Qy 697 LDEKRELPEIVYAKQIHIERNM 719  
Db 668 LDEKRELLEKVKYAKRLSDERNL 690

RESULT 15

US-08-459-504B-7  
; Sequence 7, Application US/08459504B  
; Patent No. 6075185  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6075185artis Corporation  
; STREET: 3054 Cornwalis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,504B

; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: US 08/459,595  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1207 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-459-504B-7  
Query Match 61.9%; Score 2314.5; DB 3; Length 1207;  
Best Local Similarity 65.4%; Pred. No. 5.3e-204;  
Matches 447; Conservative 77; Mismatches 154; Indels 5; Gaps 3;  
Qy 40 EDYLRMSEHSIDPFVSASTIQTGIGAKILGTGVFPFAGQIASLYSFIIGELWPKGKS 99  
Db 10 EDSLCTAEGNNIDPFVSASTVQTGINIAGRIILGVLPVFPFAGQIASFYSFLVGLWPRGRD 69  
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Qy 280 TLVPIKITSQLTREVYTDAGTVHPNQAFSTWYNNAPSFSAIEAAVIRSPHLLDFL 339  
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Qy 577 INGKAINQGNFSAATMRGDLTKFTRTIGFTTFFSFDVQSTFTIGAMNFSNGEVYID 636  
Db 548 RGGTVNNFRFLRTWNSGDELKYGNFVRRAFTTPTFTTQIIDIIRTSIQGLSGNGEVYID 607  
Qy 637 RIEFVPEVYEAEDYFEKAQEKVTALTSTNPRGLTKDVXDYHIDQVSNLVESLSDEFY 696  
Db 608 KIEIIPVTATFEAYDLERAQEAVALFTNTPRRLTKDVTDYHIDQVSNLVACLSDEF 667

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